Soil Microbiome Diversity on Sable Island, Nova Scotia

By

Alyssa N. Rice

A Thesis Submitted to

Saint Mary's University, Halifax, Nova Scotia

in Partial Fulfillment of the Requirements for

the Degree of Bachelor of Science with Honours in Biology

May 2024, Halifax, Nova Scotia

Approved: _____

Dr. Erin K. Cameron

Supervisor

Approved: _____

Dr. Ronald W. Russell

Thesis Reader

May 8, 2024

Soil Microbiome Diversity on Sable Island, Nova Scotia

By

Alyssa N. Rice

Abstract

The soil microbiome is essential for ecosystem functioning and influences both above- and below-ground communities. Sable Island is a sand bar with a large feral horse population, which has been shown to affect marram grasslands more than heathlands. Feral horses can have negative effects on soil microbiomes by reducing microbial diversity and abundance, but there has been no previous research on soil microbes on Sable Island. Determining the microbial composition and the driving factors of diversity is crucial for effective ecosystem management. Our goal was to determine differences in microbial α-diversity and β-diversity across vegetation types, soil pH, organic matter, and phosphorous. This study also serves as an overall survey of bacterial and fungal diversity. We expected microbial α-diversity to be lower in marram grasslands than in heathlands, and the microbial β-diversity to differ between vegetation types. Using eDNA from soil samples, we identified bacteria with 16S and fungi with ITS2 DNA barcodes and performed soil analyses from 80 samples from 16 sites on the island. We identified a total of 812 bacterial and 336 fungal ASVs. Our results indicate that bacterial α-diversity was significantly ($p < 0.05$) affected by the vegetation type, soil pH, and organic matter content, but not phosphorous concentration. In contrast, fungi were robust to variation in the environmental factors and fungal α-diversity was not significantly affected by any variables. Microbial α-diversity was not lower in marram grasslands than in heathlands, potentially due to horse activities damaging the vegetation types similarly and an increase in nutrient deposition in the marram. Microbial β-diversity of presence/absence was not significantly affected by any variable. Identifying drivers of soil microbiome diversity is important for effective ecosystem management in vulnerable ecosystems such as Sable Island.

May 8, 2024

Table of Contents

1. Introduction

1.1 Microbes in the environment

Microbes in the soil consist of bacteria, fungi, archaea, viruses, and protozoa; together these microbes form the soil microbiome (Fierer, 2017). Soil contains a high abundance of diverse taxa even though only approximately 0.000001% of the soil surface area is inhabited by microbes (Young & Crawford, 2004). Of the microbes that are present, only 0.1-5% are active at a given moment, and 10-60% can be activated within hours of stimuli (Blagodatskaya & Kuzyakov, 2013). This means that most microbes are dormant until conditions permit, at which point they become engaged in processes such as decomposition. The microbiome composition varies widely depending on many factors, including the vegetation type and soil characteristics such as aggregate size, texture, nutrient content, and pH; however, no particular factor is consistently an overarching determinant of the composition (Fierer, 2017).

The soil microbiome is fundamental to ecosystem functioning; it is responsible for nutrient cycling, decomposition, and carbon sequestration (Mishra et al., 2023). These three processes often work simultaneously when breaking down organic matter. Nitrogen is cycled by ammonification followed by nitrification; this is when organic nitrogen is converted to ammonia by one set of microorganisms, and then another group of microorganisms convert the ammonia into nitrites and nitrates (Mishra et al., 2023). Microorganisms convert phosphorous from an organic to an inorganic form which is soluble and more bioavailable to plants (Mishra et al., 2023). Microbes feed on the organic carbon in decomposing organic material to use it for their biomass. Additionally, the microbiome affects atmospheric carbon dioxide (CO_2) concentrations despite their low cumulative biomass (Liang et al., 2017). Carbon sequestration occurs when autotrophic microbes take CO_2 from the atmosphere to build biomass or release non-gaseous carbon forms

into the rhizosphere (Jansson & Hofmockel, 2020). Dead microbial biomass, containing carbon, adheres to soil substrates and acts as a carbon sink (Liang et al., 2017). Some microbe species can also transform CO_2 into carbonate minerals that remain in the soil for extensive periods (Jiang et al., 2022). However, when the microbial pool is affected by increased temperature or nitrogen, the microbial contribution to the carbon sink is decreased which can result in a carbon source-sink imbalance (Liang & Balser, 2012).

Shifts in the microbial taxa can impact how the microbiome operates and what ecological function is served (Fierer, 2017). Diversity of the microbiome can depend on abiotic factors such as pH, soil nutrient concentrations, precipitation, and temperature; physical disturbance such as compaction and erosion; and anthropogenic factors such as pollutants, invasive species, and climate change (Mishra et al., 2023). As the soil microbiome is important for the functioning of ecosystems, impacts on the microbiome can lead to reduced functionality with downstream consequences.

1.1.1 Bacteria and Fungi

Bacterial and fungal taxonomic diversity is affected by abiotic and biotic factors. As bacteria and fungi both live in similar environments, they are competing for the same resources (Bahram et al., 2018). Bacterial taxa differ among climatic regions suggesting niche specialization, which may make them more susceptible to climate change (Bahram et al., 2018). Bahram et al. (2018) suggested that fungi are more tolerant to nutrient and water limitations than bacteria, as they possess structures like hyphae which improve their ability to access water and can use more complex carbon sources. Both taxonomic groups have evolved mechanisms to increase their competitive advantage: fungi will express antimicrobial compounds, and in response, bacteria

express antibiotic-resistance genes (ARGs) (Bahram et al., 2018). Bacteria expressing ARGs are found more often when in competition with fungi than with other bacteria (Bahram et al., 2018).

The relative abundance of bacteria or fungi in the soil fluctuates based on environmental factors. This is often due to pH, nutrients, soil moisture, soil temperature, disturbance, and the presence of organic matter; however, the outcome of bacterial or fungal dominance can be inconsistent with the general expectations (Strickland & Rousk, 2010). This is likely due to both groups having similar functions in ecosystem processes, as they can be symbiotic with plants, break down organic matter, or cause disease (Clark, 2012; Money, 2016). Also, the high diversity within the microbiome can allow shifts in dominance depending on environmental conditions (i.e., saprophytic fungi decrease with nitrogen limitation, but mycorrhizal fungi are unaffected) (Strickland & Rousk, 2010). Bacterial or fungal dominance can not be directly related to functionality within the soil; the specific functional groups of bacteria or fungi must be compared to assess relevant dominances and functional shifts (Strickland & Rousk, 2010). However, determining the functionality of specific taxa remains a difficult task (Fierer, 2017).

Some taxa of bacteria and fungi form mutualistic associations that benefit both their plant host and the microbe itself. These associations help the plant and promote growth by providing nutrients that are difficult to access, making plants more stress tolerant and providing resistance to disease by pathogenic microbes (Amoo et al., 2023; Trillas & Segarra, 2009). Protection of the plant by a beneficial microorganism is done by parasitizing the pathogenic microorganism, antibiosis (i.e., production of antibiotics), or competition (Amoo et al., 2023).

The association some bacteria form with plants results in a nitrogen-carbon exchange. Two major groups of bacteria are nitrogen-fixing: rhizobia and *Frankia*; these bacteria form associations with plants and receive carbon while providing nitrogen to the plant (Franche et al.,

2009). Both groups of bacteria enter the plant through root hairs intracellularly or intercellularly, and once the infection is established the plant forms a nodule at that site (Vessey et al., 2004). Rhizobia forms a symbiosis with leguminous plants or non-leguminous *Parasponia* sp. where plants form root nodules for the bacteria to live in (Franche et al., 2009); the rhizobia give the plant ammonium and receive carbon in return (Prell & Poole, 2006). *Frankia* bacteria form a symbiosis with actinorhizal plants, leading to a similar exchange of nitrogen and carbon (Vessey et al., 2004).

Several types of fungi, such as endophytic and ectophytic, form beneficial associations with plants, which live in and outside the plant's body, respectively. Examples of endophytic fungi include arbuscular mycorrhizae and ericoid mycorrhizae. Arbuscular and ericoid mycorrhizae form associations via penetrating the plant cells by growing branched or coiled structures, respectively (Trillas & Segarra, 2009). Fungi that form an association without penetrating the host are known as ectomycorrhizal, or ectophytic, fungi which form structures around the root of the plant (Trillas & Segarra, 2009). Like rhizobia and *Frankia*, the associated fungi receive carbon from the host plant, while providing nutrients such as phosphorous, nitrogen, potassium, and other metals to the plant (Marschner & Dell, 1994). The colonization of the plant with the fungi elicits a defence response by the plant to prevent invasion into the endodermis and vessels by pathogenic microbes, and thereby help protect the plant from pathogenic fungi (Trillas & Segarra, 2009).

1.2 Grazer effects on the environment

Terrestrial grazers are animals that feed on plants like grasses; often, these animals form herds such as cattle and horses. Grazers affect biotic and abiotic factors in their environment through activities such as grazing, trampling, and producing excrement (Eldridge et al., 2020). Biotic effects of grazing include the herbivory of plant species which reduces plant relative abundances, facilitates exotic species, and alters the plant community composition (e.g., grasslands

to shrublands) with increasing grazing intensity (Mikola et al., 2009; Eldridge et al., 2020; McSherry & Ritchie, 2013). Grazers also have biotic effects on the presence of soil macrofauna (e.g., nematodes, ants), and can induce the growth of mycorrhizal hyphae (Mikola et al., 2009; Eldridge et al., 2020; McSherry & Ritchie, 2013). Abiotic effects of grazing consist of increased soil pH, increased soil density (as trampling removes soil pores), increased soil moisture, increased erosion, and reduced litter cover and depth (Mikola et al., 2009; Eldridge et al., 2020). Grazers also cause nutrient patchiness due to herbivory; they remove plant biomass and thus nutrients, and later return the nutrients in patches through excrement (Mikola et al., 2009).

Depending on vegetation and soil type, the effects of grazers can differ. Intense grazing on sandy soils reduces vegetation, which can make the soil more vulnerable to erosion and potentially lead to net carbon release from the soil (McSherry & Ritchie, 2013). Whether plants use C_3 or C_4 photosynthesis affects whether the carbon is sequestered or released under grazing pressures. The C_3 and C_4 photosynthesis pathways differ in the enzymes (RuBP carboxylase *vs.* PEP carboxylase, respectively) and mechanisms used to create the sugar, allowing for different adaptations to their environments, such as cold tolerance (Pearcy & Ehleringer, 1984). Under heavy grazing intensity, C_4 grasses have a positive interaction by increasing soil carbon sequestration, this is in contrast to C_3 grasses which have a negative interaction by decreasing the soil carbon (McSherry & Ritchie, 2013). This may partly be due to mycorrhizal associations with C_4 grasses which enhance soil stability by fungal glomalin production (McSherry & Ritchie, 2013).

Detrimental environmental effects on the vegetation and soil are caused by overstocking grazing animals which leads to the over-utilization of land and food resources (Rickert, 1996). Horses spend more time foraging and travelling than cattle resulting in increased damage to vegetation and soil through their varied grazing and trampling at high stocking densities (Nolte et

al., 2017). Feral horses significantly negatively affect environmental quality by causing reductions in plant biomass, increases in erosion, reductions in animal richness, and reductions in microbial abundances which leads to ecosystem functioning disruptions (Eldridge et al., 2020).

1.3 Sable Island

Sable Island is a sand bar southeast of Nova Scotia, Canada. The crescent-shaped island is approximately 40 km long and has a maximum width of 1.5 km, located at 43.9333 °N, -60.0000 °W in the North Atlantic Ocean (Eamer et al., 2022; Catling et al., 2009). As the island is a sand bar, there is accumulation and erosion of sediment, both of which affect the vegetation communities; currently, the island has more retreat occurring than sedimentation (Eamer et al., 2022). There is a possibility of eastward migration of the island due to how the sediment is accumulating, though the retreat trends are stronger which indicates the island is shrinking, rather than migrating (Eamer et al., 2022). Sable Island experiences strong winds averaging 25.7 km/h which help shape the dunescape as well as the vegetation communities (Byrne & McCann, 1995).

From 1553 to 1633, animals such as cattle and pigs were transported by Portuguese settlers to live on the island, but the animals were then removed and slaughtered by Acadians and New Englanders (Christie, 1980). Reverend Andrew Le Mercier brought cattle, sheep, hogs, and horses to the island in 1737, but abandoned them by 1753, and just before 1760, Thomas Hancock also brought horses, hogs, sheep, and goats to the island (Christie, 1980). Though many animals were taken to the island over the years, they were often stolen or sold, with only horses establishing long-term survival (Christie, 1980). Either the introduction of horses by Le Mercier or Hancock led to an established population of horses which persists today (Christie, 1980).

1.3.1 Sable Island Biodiversity

Sable Island is an important habitat on which a number of animal species, including birds and seals, depend. Bird species include the Least Sandpiper (*Calidris minutilla*), Spotted Sandpiper (*Actitis macularia*), Ipswich Sparrow (*Passerculus sandwichensis princeps*), and endangered Roseate Tern (*Sterna dougallii*) (Miller, 1983; Ross, 1980; Gochfeld, 1983). Herring Gulls (*Larus argentatus*) also frequent this island, although they are not native (Miller, 1983). This island is an important breeding ground for grey seals (*Halichoerus grypus*) and harbour seals (*Phoca vitulina*) (Freedman et al. 2011). One of the most prominent species is the introduced feral horse (*Equus caballus*). There are also at least 573 documented invertebrates, of which 480 are native (Chow, 2020). Therefore, Sable Island is home to a diverse array of animal species, some of which are endemic and highly dependent on the island.

Vegetation on Sable Island covers 40% of the surface area with the unvegetated portion consisting of bare fine-medium textured sand (Byrne & McCann, 1995). The island was previously thought to have been mostly covered by vegetation, but that has decreased since the establishment of horses in the 18th century (Byrne & McCann, 1995). There are 158 native species and 82 introduced species of flora (Catling et al., 1984; Catling et al., 2009) forming communities of marram and shrub heathland which dominate the island, alongside sandwort and pond-edge vegetation (Catling et al., 1984; Eamer et al., 2022). Marram grass grows in wind-blown sandy substrate, shrub heathland is in protected inland sites, sandwort is found closer to the ocean where it is prone to inundation and sea spray during storms, and pond-edge vegetation is found surrounding brackish or freshwater ponds (Catling et al., 1984). The distribution of these communities on Sable Island is related to distance from shore and the slope of the dune which is associated with sand erosion or accumulation (Tissier et al., 2013).

In dunescapes in Nova Scotia, marram grass (e.g., *Calamagrostis breviligulata*) is responsible for the stabilization of the sand which leads to the formation of sand ridges (Davis, 1996). Heathland vegetation (e.g., *Juniperus horizontalis*) can then form communities in the stabilized substrate after there is an increase in organic matter (Davis, 1996). Vegetation types that are sensitive to sand accumulation, such as heathlands, are inland and away from potential sand burial sites, and plants with salt adaptations are near brackish water or by the shore (Tissier et al., 2013). Although marram grasslands are the most tolerant to sand accumulation, they are the most susceptible to horse damage (Freedman et al., 2011).

The horse population was introduced to this island by humans but has been feral for generations and is genetically distinct from other breeds, though they are not considered a distinct breed (Freedman et al., 2011; Plante et al., 2007). As of 2019, the population consisted of approximately 590 horses (Johnsen, 2022). Given the island's small size and vulnerability to erosion, having such a significant number of horses grazing and trampling the soil can cause substantial damage. These horses have been extensively studied in terms of their history, foraging habits, gut microbiome, population genetics, and negative effects on the vegetation communities, especially the marram grasslands (Christie, 1980; Johnsen, 2022; Stothart et al., 2020; Lucas et al., 2009; Plante et al., 2007; Freedman et al., 2011). However, the effects of the horses on the soil microbiome on Sable Island remain unclear due to a lack of research on the soil microbiome.

1.4 Objectives and Hypotheses

We used eDNA metabarcoding to assess the differences in the microbiomes of Sable Island. α-diversity and β-diversity were compared to assess differences in local species richness and the turnover in microbial communities across sites, respectively. Our objectives were to 1) conduct an

overall survey of bacteria and fungi, and 2) assess the effects of vegetation type (marram vs. heath), pH, organic matter, and phosphorous (P_2O_5) on microbial α-diversity and β-diversity.

Plant species richness positively affects microbial biomass, activity, and composition in other grasslands (Strecker et al., 2015; Chung et al., 2007). Therefore, we hypothesized that the α-diversity of the microbes would be lower in the marram grasslands than in the shrub heathlands due to the lower plant species richness, and the negative effects on marram by horses (Freedman et al., 2011). Similarly, as specific vegetation is expected to support different microbial taxa, and horse activity impacts the vegetation types differently, we hypothesized there would be more similarities in the microbial communities within the vegetation types than between them.

2. Materials and Methods

2.1 Site Design

In the spring of 2021, 16 sites were selected across Sable Island based on evidence of horse activity (e.g., grazing, trails, rubbing, or feces) (Figure 1). The plant communities and the geomorphology vary across sites, but each site was paired with a corresponding, similar site to create a total of eight pairs. The sites ranged in size from 0.25 ha to 2.36 ha, and five, 5 m x 5 m plots were evenly distributed within each site. The vegetation in these plots was categorized as marram grassland, heathland, intermediate, or unvegetated (marram n = 35, heath n = 31, intermediate n = 12, unvegetated n = 2). Plots dominated with marram grass (*Calamagrostis breviligulata*) or beach pea (*Lathyrus japonicus*) were categorized as marram, while plots with dominant species such as bayberry (*Morella pensylvanica*) or crowberry (*Empetrum nigrum*) were categorized as heath. Plots dominated by yarrow (*Achillea millefolium*) or Kentucky bluegrass (*Poa pratensis*) were categorized as intermediate, and unvegetated plots were categorized as

unvegetated. The plots were placed at least 5 m from the edge of the site to account for edge effects. In total, 80 plots representing five replicate plots for each of the 16 sites across Sable Island were used in this study.

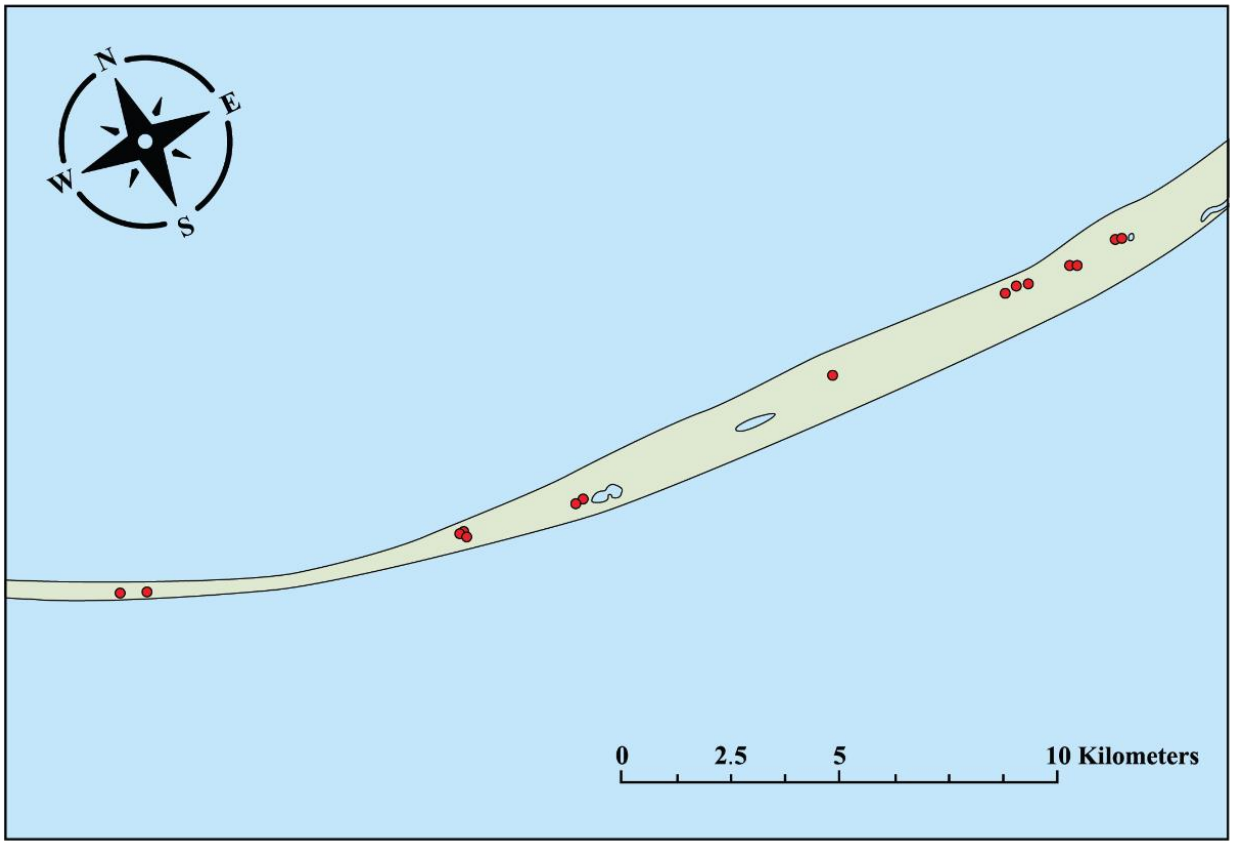

Figure 1. Locations of the 16 sites established on Sable Island, Nova Scotia in the spring of 2021. The size of each site ranged from 0.25 ha to 2.36 ha.

2.2 Soil Sampling and Analyses

2.2.1 eDNA

Vegetation was removed with pruning shears from a circular patch, 26 cm in diameter, near the centre of each plot (Figure 2). A bulb planter (12.7 cm width x 12.7 cm depth) was then used to take a soil sample for eDNA analysis. The bulb planter was cleaned between samples with a dilute, unscented soap solution and a rag to prevent cross-contamination. The samples were stored

individually in resealable plastic bags, kept in a cooler while in the field, and then stored at -20 °C for the duration of collection between mid-July and the end of August 2021. Samples were shipped to Dalhousie University and Saint Mary's University, NS where they were stored at -80 °C.

2.2.2 Soil Characteristics

Immediately outside the centre of the western edge of the plot, vegetation was removed from a 30 cm x 30 cm, 900 cm^2 area (Figure 2). A soil sample was taken with the same bulb planter (12.7 cm width x 12.7 cm depth) for pH, phosphorous concentration (kg/ha) and organic matter (%) analysis. The bulb planter was cleaned between samples with a dilute, unscented soap solution to prevent cross-contamination. The samples were stored individually in resealable plastic bags and kept in a cooler while in the field, and then stored at -20 °C for the duration of collection. Samples were shipped to the Department of Agriculture, Truro, NS for analysis. All soil samples were collected between mid-July and the end of August 2021.

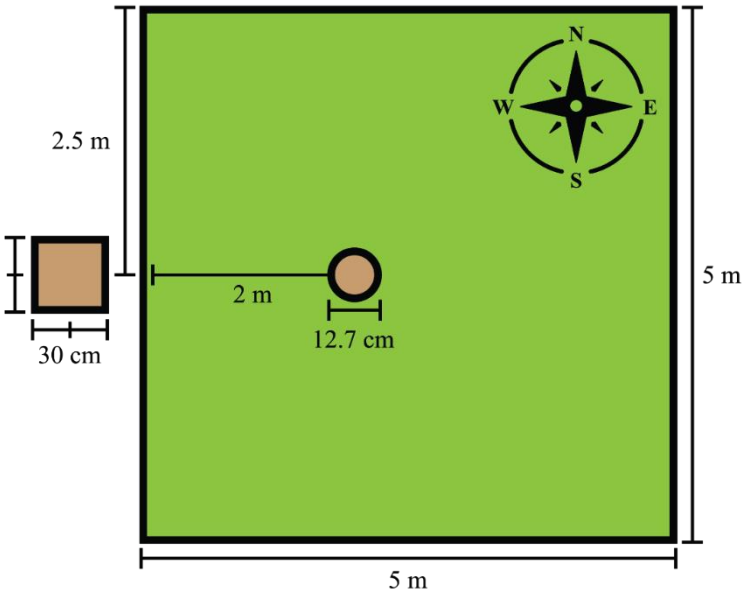

Figure 2. Plot placement set up for Sable Island soil sampling. The sample for soil eDNA came from the 12.7 cm diameter area inside the plot where vegetation was removed. The sample for soil characteristics (pH, phosphorous, and organic matter) came from the 30 cm x 30 cm area outside the west side of the plot where vegetation was removed. The measurements reported are accurate, but the figure is not to scale.

After the soil characteristics were analyzed, the samples were grouped into appropriately sized categories for analysis. For pH, the categories were 4.00-4.99 (n = 17), 5.00-5.99 (n = 33), and >6.00 (n = 28). For organic matter content (%) the categories were <1 (n = 48), 1-2 (n = 16), and >2 (n = 14). Finally, the phosphorous concentration (kg/ha) categories were 10-20 (n = 8), 21-30 (n = 53), and >30 (n = 17). One plot was not analyzed for any soil characteristics as no soil sample was taken. It was categorized as N/A (n = 1).

2.3 eDNA Extraction, Metabarcoding, and Bioinformatics Processing

The soil samples for eDNA were stored at -80 °C and were thawed and homogenized before DNA extraction. Environmental DNA was extracted from approximately 0.25 g of soil with a DNeasy® PowerSoil® Pro Kit (QIAGEN) following their recommended protocols and using a QIAGEN TissueLyser II at 25 Hz for 10 minutes for cell lysis as recommended. After the DNA was isolated and eluted, the samples were stored at -80 °C until sequencing.

The extracted eDNA was sent to the Integrated Microbiome Resource lab at Dalhousie University (Halifax, NS) for sequencing and bioinformatics processing (Comeau, 2022; Comeau et al., 2017). Briefly, the targeted DNA was PCR-amplified with the Phusion Plus polymerase and separate primers designed to amplify bacteria and fungi (Comeau, 2022). For bacteria, the 16S V4-V5 region was amplified (forward primer: 515FB = GTGYCAGCMGCCGCGGTAA, reverse primer: 926R = CCGYCAATTYMTTTRAGTTT (Quince et al., 2011)). For fungi, the ITS2 region was amplified (forward primer: ITS86(F) = GTGAATCATCGAATCTTTGAA (Turenne et al., 1999), reverse primer: ITS4(R) = TCCTCCGCTTATTGATATGC (White et al., 1990)). The PCR began with an initial denaturation at 98 °C for 30 seconds, followed by 25 cycles of 98 °C for 10 s, 55 °C for 30 s, 72 °C for 30 s, a final extension at 72 °C for 4 min 30 s and then held at 4 °C (Comeau, 2022). PCR products were verified by the Hamilton Nimbus Select robot using Coastal

Genomics Analytical Gels and normalized with the Charm Biotech Just-a-Plate 96-well Normalization Kit (Comeau, 2022). PCR products were quantified fluorometrically with the Invitrogen Qubit dsDNA HS assay before sequencing on an Illumina MiSeq (v3 2 x 300 bp paired-end reads) (Comeau et al., 2017).

After sequencing was completed, the sequence reads were processed according to Comeau et al. (2017). Briefly, the paired-end reads were merged using PEAR (v0.9.10) and any low-quality sequences (quality score <30 in 90% of bases) were identified by FastQC (v0.11.5) and removed by FASTX-Toolkit (v0.0.14). Any potentially chimeric reads were removed with VSEARCH (v1.11.1). Then, open-reference ASV (amplicon sequence variant) picking was done with QIIME wrapper scripts (v1.91) by comparing the sequence reads obtained to reference sequences to identify an ASV for each amplicon when possible. An ASV for bacteria (16S) includes reads that have 97% similar sequence identity. ASVs that were less than 0.1% of the total number of sequences were removed. Finally, QIIME2 (Bolyen et al., 2019) was used to compare the diversity of taxa found across samples.

2.4 Statistical Analyses

α-diversity of bacteria and fungi was determined using Shannon entropy which was performed using QIIME2 (Bolyen et al., 2019). Shannon entropy accounts for the evenness and abundance of taxa within a community by measuring the uncertainty and creating equivalencies which can be compared (Jost, 2006). Two communities which have the same entropy may differ in terms of evenness or abundance of taxa (Jost, 2006). The Shannon entropies were compared with a Kruskal-Wallis test to determine significance using QIIME2 (Bolyen et al., 2019).

The microbial community composition (β-diversity) of bacteria and fungi was determined by calculating Jaccard and Bray-Curtis distance matrixes and performing a Principal Coordinate Analysis (PCoA) using QIIME2 (Bolyen et al., 2019). Jaccard is based on presence/absence data and thus weights rare taxa equal to abundant taxa; Bray-Curtis is abundance-based and thus is less sensitive to changes in rare species (Jaccard, 1912; Bray & Curtis, 1957). The Jaccard index is the most robust to errors across indices, and Bray-Curtis is the most robust to errors for abundance-based indices (Schroeder & Jenkins, 2018). The variables' effects on the microbial communities were assessed with a permutational multivariate analysis of variance (PERMANOVA) using the Adonis2 function from the vegan package in R (Oksanen et al., 2022).

All data visualizations and the PERMANOVAs were performed in R v.4.3.2 (R Core Team, 2023) and R Studio v.2023.12.1+402 (Posit team, 2023). Packages not already stated are qiime2R (Bisanz, 2018) and phyloseq (McMurdie & Holmes, 2013) for reading qza files from QIIME2, tidyverse (Wickham et al., 2019) for data manipulation and visualizations, and RColorBrewer for colour-bind-friendly palettes (Neuwirth, 2022).

3. Results

3.1 Overview

Across all 80 samples from the 16 sites on Sable Island, there were a total of 3,057,553, and 2,282,503 raw DNA sequence reads for bacteria and fungi respectively. From those reads, we identified 37 bacterial and 12 fungal phyla with a total of 812 and 336 bacterial and fungal ASVs, respectively (Appendix Tables C1 & C2). Of the 80 samples, one unvegetated sample failed to amplify for bacteria and fungi, and one marram sample failed to be sequenced for fungi (bacteria n = 79, fungi n = 78). The bacterial communities had higher α-diversity than the fungal

communities. α-diversity of bacteria differed significantly ($p < 0.05$) across vegetation types and between most environmental factors, whereas α-diversity of fungi did not differ significantly. β-diversity in each vegetation type and across environmental factors were not significantly different for bacteria or fungi with the Jaccard distance. However, the β-diversity of bacterial taxa was significantly different across vegetation types with the Bray-Curtis distance.

3.2 Relative Abundance

Across vegetation types, the relative abundance of bacterial and fungal phyla differed, however, the dominant phyla were similar. The two most abundant bacterial phyla were the same across all three vegetation types (Table 1). Firmicutes was the most abundant bacterial phylum in all vegetation types and was more relatively abundant in heath than marram and intermediate (Table 1, Figure 3). Similarly, Basidiomycota was the most abundant fungal phylum across all vegetation types (Table 1). However, Basidiomycota were more relatively abundant in the intermediate sites than marram and heath (Table 1, Figure 3). The same bacterial and fungal phyla were in the top six most relatively abundant phyla across the vegetation types but differed in their abundance rank depending on the vegetation type (Table 1). There were fewer similarities in the phyla relative abundance rank in fungi between vegetation types compared to bacteria (Table 1).

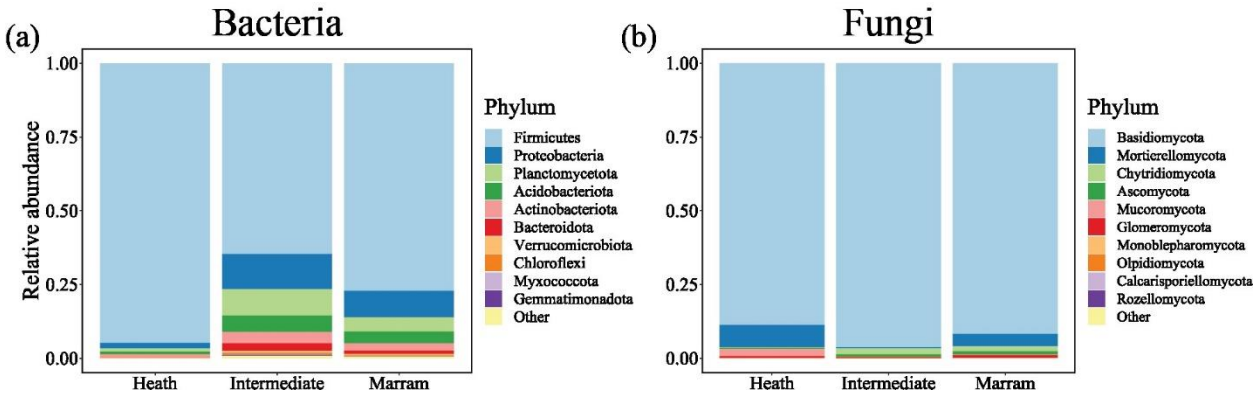

Figure 3. The relative abundances of taxa at the phylum classification in each vegetation type on Sable Island, NS. The most abundant 10 phyla are displayed, in order of decreasing relative abundance, with the remaining less abundant phyla grouped into the 'Other' category. **(a)** Bacterial taxa; **(b)** Fungal taxa.

Table 1. Ranking of the most relatively abundant bacteria and fungi phyla across the vegetation types on Sable Island, NS in 2021.

Abundance rank	Heath		Intermediate		Marram	
	Bacteria	**Fungi**	**Bacteria**	**Fungi**	**Bacteria**	**Fungi**
1	Firmicutes	Basidiomycota	Firmicutes	Basidiomycota	Firmicutes	Basidiomycota
2	Proteobacteria	Mortierellomycota	Proteobacteria	Chytridiomycota	Proteobacteria	Mortierellomycota
3	Acidobacteriota	Mucoromycota	Planctomycetota	Ascomycota	Planctomycetota	Chytridiomycota
4	Planctomycetota	Glomeromycota	Acidobacteriota	Mortierellomycota	Acidobacteriota	Ascomycota
5	Actinobacteriota	Ascomycota	Actinobacteriota	Glomeromycota	Actinobacteriota	Glomeromycota
6	Bacteroidota	Chytridiomycota	Bacteroidota	Mucoromycota	Bacteroidota	Mucoromycota
7	Verrucomicrobiota	Calcarisporiellomycota	Other	Olpidiomycota	Other	Monoblepharomycota
8	Other	Monoblepharomycota	Verrucomicrobiota	Monoblepharomycota	Verrucomicrobiota	Rozellomycota
9	Myxococcota	Other	Chloroflexi	Rozellomycota	Chloroflexi	Olpidiomycota
10	Chloroflexi	Olpidiomycota	Gemmatimonadota	Other	Myxococcota	Other
11	Gemmatimonadota	Rozellomycota	Myxococcota	Calcarisporiellomycota	Gemmatimonadota	Calcarisporiellomycota

3.3 α-Diversity

The intermediate vegetation type had the highest bacterial α-diversity, followed by the unvegetated, and then the marram (Figure 4a, Appendix Table A1). The heath bacterial diversity was significantly lower than the marram and the intermediate (p = 0.043, p = 0.006) (Figure 4a, Appendix Table A2). In fungi, the α-diversity was not significantly different across the vegetation types (p = 0.61) (Figure 4b, Appendix Table A1).

Bacterial α-diversity was similar in soil samples with pH 4.00-4.99 and >6, with 4.00-4.99 being slightly higher; the lowest diversity was in pH 5.00-5.99 (Figure 4c, Appendix Table A1). There was a significant difference from pH 4.00-4.99 to both pH 5.00-5.99 and >6 (p = 0.008, p = 0.004) (Appendix Table A2). In fungi, the α-diversity was not significantly affected by pH (p = 0.80) (Figure 4d, Appendix Table A1).

The bacterial α-diversity in soil samples with an organic matter content <1% and 1-2% was similar, with 1-2% being slightly higher (Figure 4e, Appendix Table A1). The bacterial diversity in organic matter >2% was significantly lower than <1% and 1-2% (p = 0.005, p = 0.011) (Figure 4e, Appendix Table A2). In fungi, the α-diversity was not significantly affected by organic matter content (p = 0.73) (Figure 4f, Appendix Table A1).

There were no significant differences in the α-diversity for bacteria or fungi across phosphorous concentrations (p = 0.44, p = 0.17) (Figure 4g, h, Appendix Table A1).

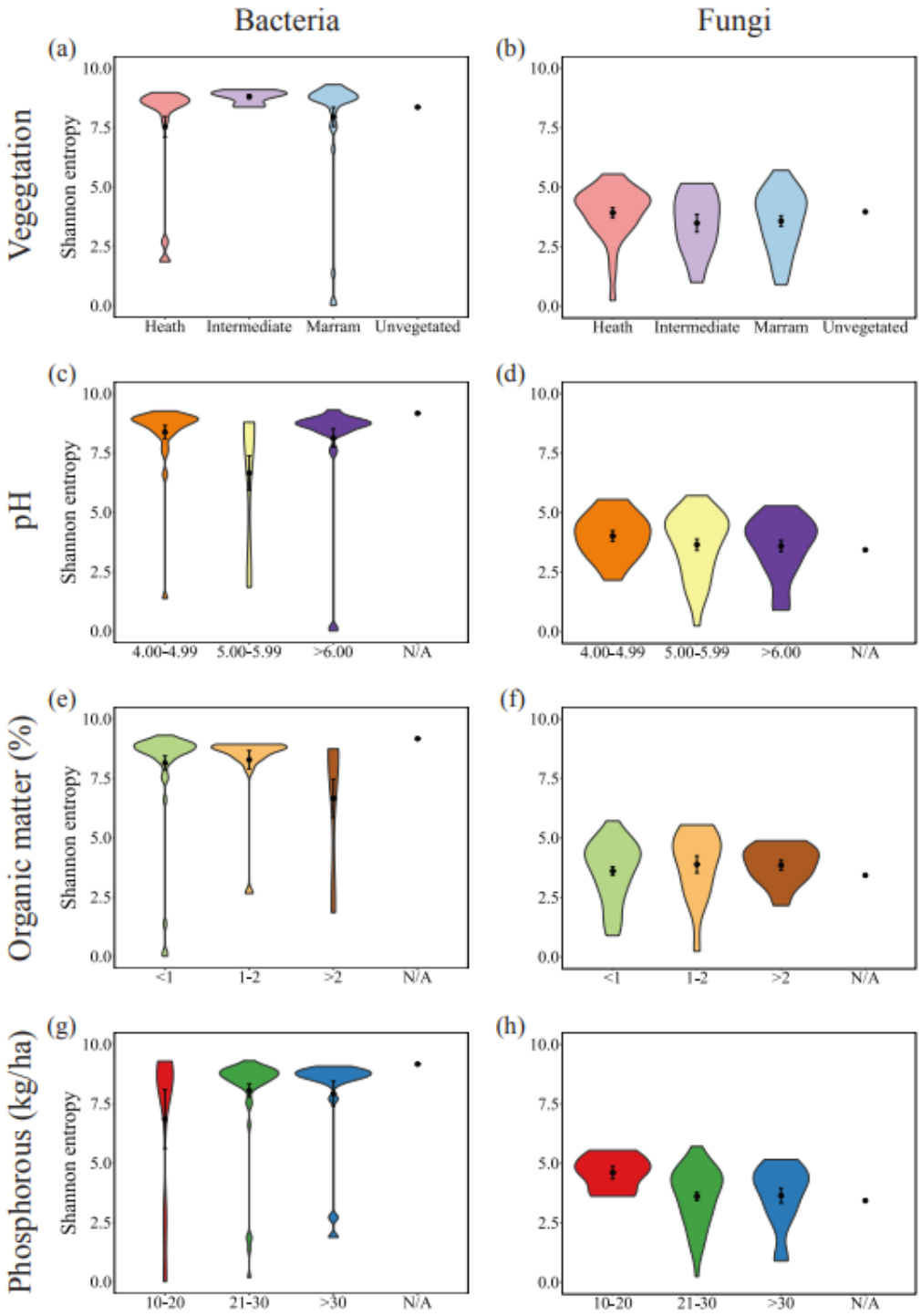

Figure 4. The mean Shannon entropy (α-diversity) of soil microbial communities in vegetation types and across environmental factors on Sable Island, NS. **(a, c, e, g)** Bacterial taxa; **(b, d, f, h)** Fungal taxa; **(a, b)** Vegetation types; **(c, d)** pH; **(e, f)** Organic matter content (%); **(g, h)** Phosphorous (P_2O_5) (kg/ha). N/A represents plots where soil analyses were not completed. Error bars represent standard error.

3.4 β-Diversity

β-diversity was compared using two different dissimilarity methods with a PCoA. When using the Jaccard distance on bacterial communities, the PC1 axis explained 14.28% of the variation, and PC2 explained 6.92%, compared to using the Bray-Curtis distance where the PC1 axis explained 17.43%, and PC2 explained 8.74%. When using the Jaccard distance on fungal communities, the PC1 axis explained 10.1% and PC2 explained 6.73%, whereas the Bray-Curtis distance PC1 axis explained 7.91% and, PC2 explained 6.84%. The microbial composition of vegetation types was not significantly different for either bacteria or fungi with the Jaccard distance ($p = 0.076$, $p = 0.85$) (Figure 5a, b, Appendix Table A3). However, with the Bray-Curtis distance, bacterial communities across vegetation types were significantly different, but not for fungi ($p = 0.038$, $p = 0.53$) (Figure 5c, d, Appendix Table A3). Both Jaccard and Bray-Curtis distances explained a low amount of variation (<5%) for bacteria and fungi (Appendix Table A3). The variance was not explained by the environmental factors (pH, organic matter, phosphorous) for Jaccard or Bray-Curtis distances for bacteria or fungi with all R^2 below 0.03, and all p-values >0.05 (Appendix Table A3, Appendix Figure B1, B2, B3).

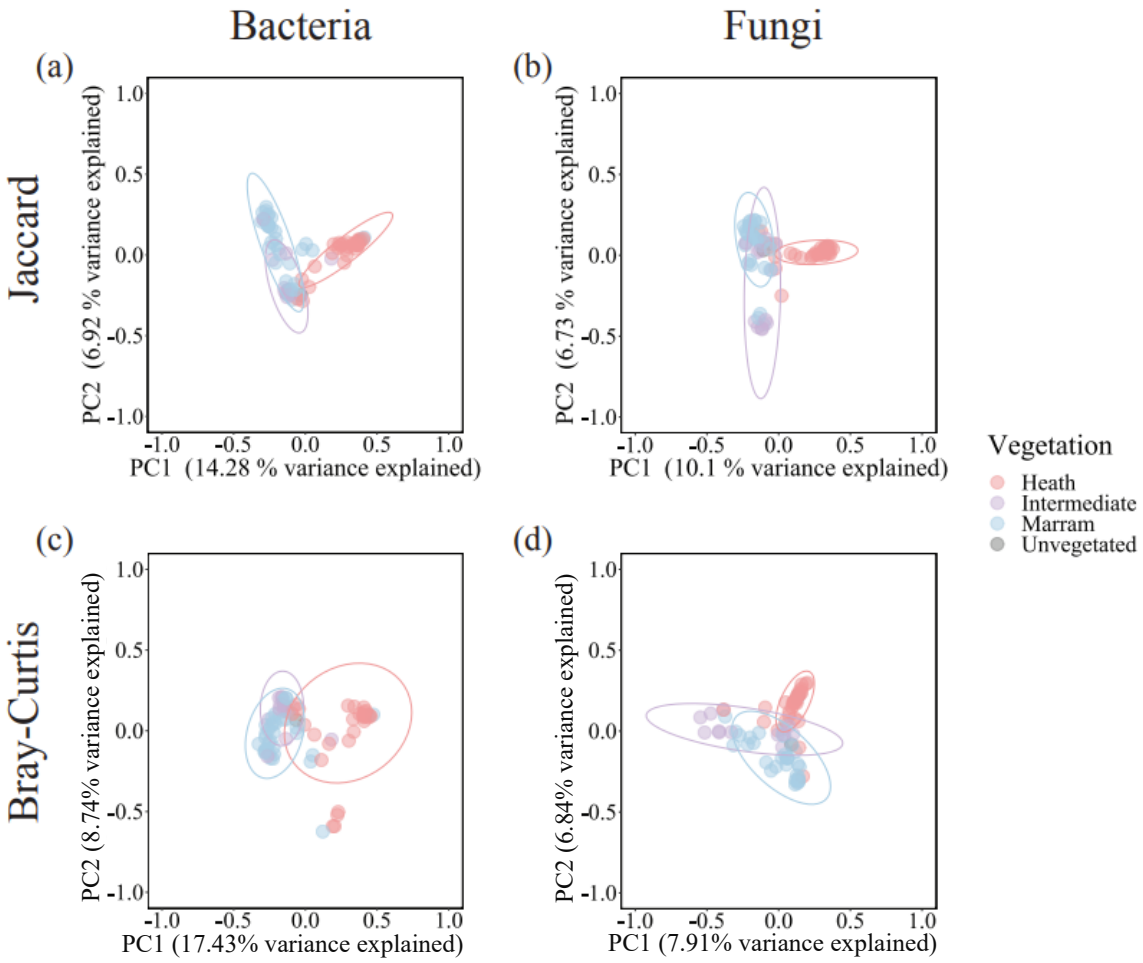

Figure 5. The beta diversity of soil microbes in vegetation types on Sable Island, NS with a principal coordinate analysis (PCoA) with a Jaccard **(a, b)**, and a Bray-Curtis distance matrix **(c, d)**. **(a, c)** Bacterial taxa; **(b, d)** Fungal taxa. N/A represents plots where soil analyses were not completed.

4. Discussion

Bacterial diversity differed based on several factors whereas fungal diversity did not change across any factor. We found significant effects of vegetation types, soil pH, and organic matter content, but not phosphorous concentration, on bacterial α-diversity. We found no significant effects of any factors on fungal α-diversity. Additionally, for β-diversity, the bacterial and fungal taxa in each vegetation type, soil pH, organic matter content, and phosphorous category

were not significantly different, and each factor explained less than 5% of the variation observed. Although the bacterial taxa abundances differed significantly across vegetation types, the vegetation still explains a low amount (3.7%) of the variation. The most relatively abundant phyla of bacteria and fungi were the same in each vegetation type further reflecting the lack of significant differences.

4.1 Effects of Vegetation Type on Microbial Diversity

4.1.1 Relative Abundance

Firmicutes had the highest bacterial relative abundance in all vegetation types, likely due to their close association with plant roots in the endorhizosphere and rhizosphere soil (Hashmi et al., 2020). The most abundant family of Firmicutes found was *Bacillaceae* in both marram grasslands and heathlands. This family is tolerant to a variety of conditions including drought, salinity and other extremes allowing them to survive in the different soils in the different vegetation types (Mandic-Mulec et al., 2016). Proteobacteria also had a high relative abundance in marram grasslands and intermediate vegetation. In another study, proteobacteria were also common in the soil with grasses (Qiao et al., 2022). Some classes of proteobacteria are copiotrophic and thus found in nutrient-rich soils, and copiotrophs are more abundant in herbs than shrubs (Ma et al., 2023). However, marram grass grows in a sandy substrate rather than soil which is typically nutrient-limited by nitrogen and phosphorous, which would not be preferable for copiotrophs. However, fecal excrement by horses along with nutrient transfer mediated by grey seal movements would enrich the soils facilitating copiotrophic bacteria such as proteobacteria to flourish (Read, 1989; McLoughlin et al., 2016).

Basidiomycota had the highest relative abundance in all vegetation types by far. This may be due to their ability to form associations with plants and their saprotrophic ability allowing them to create symbioses with plants, and then continue to thrive after the plant has died (Watkinson, 2016). Arbuscular mycorrhizal fungi are from the phylum Glomeromycota and are associated with grasses often and trees, ectomycorrhizal fungi are from Basidiomycota and Ascomycota and are associated with trees, and ericoid mycorrhiza are from Ascomycota and are associated with heath plants (Watkinson, 2016). Based on those symbiotic relationships, we expected significant differences in the fungal phyla and their relative abundances between vegetation types; however, we found no significant differences. Though similar to our results, another study found a higher abundance of Ascomycota in grasslands and mixed vegetation sites (Qiao et al., 2022). Interestingly, there were no significant differences in fungal taxa turnover across vegetation types suggesting symbioses with plants may not be eliciting as much of an effect on fungi as previously expected.

4.1.2 α-Diversity

The vegetation type had significant effects on the bacterial α-diversity but not in the way we hypothesized. Instead, the intermediate vegetation had the highest α-diversity among the four vegetation types. One study also found that shrub-grass mixed communities had higher bacterial α-diversity than grass communities (Qiao et al., 2022). This is potentially due to having a variety of plant functional groups in this community (i.e., both grasses and shrubs), allowing for a higher variety of different plant-microbe associations. In contrast, the marram grass vegetation type mainly contained grasses, while the heath vegetation type mainly contained shrubs.

Aside from the symbioses occurring between the plant and microbes, the bacterial diversity results could be explained by the effects of horse activities. We initially hypothesized that marram

grasslands would have a decreased diversity due to horse activities such as frequent grazing, but our results show a lower diversity in heath than marram. The horses on Sable Island prefer to consume marram grass as it is a higher quality food, but when population density is high, heathlands are increasingly selected (Van Beest et al., 2014). This results in the horses foraging and thus trampling the soil and causing mechanical damage to the microbes in both marram and heathlands which was not accounted for previously. In unvegetated plots, there may be less trampling and damage which could contribute to the higher diversity in those plots.

4.1.3 β-Diversity

We hypothesized the microbial communities would differ between the vegetation types, which was partially supported. Bacteria in vegetation types were significantly different in abundance, but not in community composition. This indicates some vegetation types were more favourable for certain taxa allowing their dominance over other taxa. Other studies have also found significant differences in the microbial communities in different vegetation types (e.g., Ma et al., 2023), though we did not see the same differences in fungi. Many of the bacterial and fungal taxa in our samples inhabit a wide range of environments which is why we saw them in all vegetation types (Hashmi et al., 2020; Tedersoo et al., 2014; He et al., 2022). Our soil samples contained bulk and rhizospheric soil which means we were unable to detect microbial community differences at a finer scale. This could partially explain the overall microbial community homogeneity observed.

4.2 Effects of Soil Characteristics on Microbial Diversity

4.2.1 α-Diversity

Bacterial α-diversity was affected by the pH and organic matter content but not phosphorus. There were no significant effects of these factors on fungal α-diversity. There was a significantly

lower bacterial α-diversity in soil with a pH of 5-5.99 than in the lower and higher pH category, which is different from another study in which the bacterial α-diversity increased with pH from 3 to 9 (Griffiths et al., 2011). In other studies, fungal diversity also increased with increased pH from 3 to 6.5 (Liu et al., 2018). We also observed a lower bacterial α-diversity in organic matter >2%, which differs from other studies where more organic matter leads to an increase in microbial diversity (Sul et al., 2013). We found bacterial and fungal α-diversity were not affected by phosphorous, even though the taxa in our study were similar to a study which found an effect of phosphorus (Kuramae et al., 2011). Research has also shown that fungi tend to be more tolerant of environmental stressors than bacteria (Coleine et al., 2022). This could explain why there is a lack of significant effects on the fungal α-diversity.

4.2.2 β-Diversity

There were no significant differences in the turnover of bacteria or fungal communities across the various soil characteristics. Many of the bacterial and fungal taxa are ubiquitous in soil environments which is why we observed them across the full ranges of soil pH, organic matter content and phosphorous concentration (Hashmi et al., 2020; Ward et al., 2009; Tedersoo et al., 2014; He et al., 2022).

4.3 Ecosystem Management

Our research found bacteria to be more variable than fungi across the abiotic and biotic environment on Sable Island. Soil microbes influence the health of plants and may encourage growth through symbioses thus improving soil quality and reducing erosion (Clark, 2012; Money, 2016; Normaniza et al., 2018). As the vegetation on Sable Island is affected by the horses (Freedman et al., 2011), understanding how the microbes are affected and implementing protection for them is essential for ecosystem functionality. The microbial communities are important for

ecosystem management and can aid in the protection of vegetation, and resistance of the soil to erosion (Watkinson, 2016; Normaniza et al., 2018). The positive effects of microbes on vegetation and soil can also help vulnerable organisms such as the Roseate Terns, and the grey seals by protecting their nesting habitat from degradation.

4.4 Limitations and Future Research

This study was able to identify a wide variety of bacterial and fungal diversity by using eDNA. This methodology can identify taxa which are low in abundance or are unculturable giving us a deeper insight into the community (Torsvik & Øvreås, 2002). However, it does detect taxa which are inactive and in their dormant state, which means there may be more differentiation in active microbial communities between vegetation types and soil characteristics than we were able to detect (Locey et al., 2020). Accounting for microbial dormancy is a common issue when dealing with microorganisms which calls for different methods of analyzing microbial communities (Locey, 2010). Also, we sampled with a soil core and homogenized the soil samples, which makes identifying fine-scale relationships difficult as microbial communities can differ between soil aggregates and between bulk soil and the rhizosphere (Fierer, 2017; Philippot et al., 2013). It is important to keep in mind the complexity of the microbiome and that there are likely many interactions that were not identified.

Additionally, there may be more species that were not identified due to either sampling sites not encompassing enough areas to identify all taxa on Sable Island, or due to limitations of primers. Some taxa may not have been amplified consistently, or at all by the primers leading to a misrepresentation or a lack of representation overall. Even though some taxa may be left out or misrepresented, using DNA is still able to identify more than other methods such as culturing.

This study has resulted in a baseline survey of bacterial and fungal diversity across Sable Island, particularly on the microbiome diversity and composition between vegetation types. The next step for the microbiome on Sable Island is to investigate the direct and indirect effects the horses have on the microbiome and soil characteristics. As this study has found significant differences in the bacterial communities already, further determining the impacts of the horses on the microbiome will aid in ecosystem management to support the island's biodiversity.

5. Conclusion

The soil microbiome is responsible for driving many ecosystem functions, affecting above-ground organisms, and it is also affected by abiotic and biotic factors (Mishra et al., 2023; Van Der Heijden et al., 2008; Fierer, 2017). The microbiome taxa can adapt to changes in the abiotic and biotic environment by shifting to exploit new resources and by forming symbioses or other interactions (Li et al., 2022). Our results indicate bacterial α-diversity to be more variable than fungi due to environmental differences including vegetation types and soil characteristics. We found very few differences in the β-diversity of bacteria, and no differences in fungal diversity suggesting robust microbial communities or an indistinguishable variety of active and dormant taxa. Many of the taxa identified on Sable Island are common throughout the soil and occupy a wide range of environmental conditions. Some of our results are consistent with other studies, particularly regarding plant-microbe associations, while other results regarding soil characteristics found no significance or inconsistent patterns compared to other studies. Sable Island has allowed a unique study of a soil microbiome which is not affected by anthropogenic activity directly but rather by feral horses. Further research can identify the direct impacts of the horses on the microbiome. Identifying the key players of the microbiome along with what is driving the diversity

and composition is important for ecosystem management, especially in vulnerable ecosystems such as Sable Island (Fierer, 2017).

Acknowledgements

I would like to thank my supervisor, Dr. Erin Cameron for this opportunity, guidance, and feedback through this entire process. Also, a big thanks to all members of the CASE Lab for their feedback and support throughout the year. I would also like to thank my reader Dr. Ron Russell for the statistics help and input. Thank you to the Sable Island Institute for the funding and collections of samples and especially thanks to Ruth Greuel. Thank you to the IMR Lab for the eDNA sequencing and analysis, and to the Department of Agriculture for the soil characteristics analysis. Finally, I wish to thank my peers in the Honours 2024 class, the professors Dr. Anne Dalziel and Carla Crossman, and my friends and family for the support and feedback.

References

Amoo, A. E., Olanrewaju, O. S., Babalola, O. O., Ajilogba, C. F., Chukwuneme, C. F., Ojuederie, O. B., & Omomowo, O. I. (2023). The functionality of plant-microbe interactions in disease suppression. *Journal of King Saud University - Science*, *35*(8), 102893. https://doi.org/10.1016/j.jksus.2023.102893

Bahram, M., Hildebrand, F., Forslund, S. K., Anderson, J. L., Soudzilovskaia, N. A., Bodegom, P. M., Bengtsson-Palme, J., Anslan, S., Coelho, L. P., Harend, H., Huerta-Cepas, J., Medema, M. H., Maltz, M. R., Mundra, S., Olsson, P. A., Pent, M., Põlme, S., Sunagawa, S., Ryberg, M., … Bork, P. (2018). Structure and function of the global topsoil microbiome. *Nature*, *560*(7717), 233–237. https://doi.org/10.1038/s41586-018-0386-6

Bisanz, Jordan E. (2018). qiime2R: Importing QIIME2 artifacts and associated data into R sessions. https://github.com/jbisanz/qiime2R

Blagodatskaya, E., & Kuzyakov, Y. (2013). Active microorganisms in soil: Critical review of estimation criteria and approaches. *Soil Biology and Biochemistry*, *67*, 192–211. https://doi.org/10.1016/j.soilbio.2013.08.024

Bolyen, E., Rideout, J.R., Dillon, M.R., Bokulich, N.A., Abnet, C.C., Al-Ghalith, G.A., Alexander, H., Alm, E.J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J.E., Bittinger, K., Brejnrod, A., Brislawn, C.J., Brown, C.T., Callahan, B.J., Caraballo-Rodríguez, A.M., Chase, J., … Caporaso, J.G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, *37*, 852–857. https://doi.org/10.1038/s41587-019-0209-9

Bray, J. R., & Curtis, J. T. (1957). An ordination of the upland forest communities of Southern Wisconsin. *Ecological Monographs*, *27*(4), 325–349. https://doi.org/10.2307/1942268

Byrne, M.-L., & McCann, S. B. (1995). The dunescape of Sable Island. *The Canadian Geographer/Le Géographe Canadien*, *39*(4), 363–368. https://doi.org/10.1111/j.1541-0064.1995.tb00425.x

Catling, P. M., Freedman, B., & Lucas, Z. (1984). The vegetation and phytogeography of Sable Island, Nova Scotia. *Proceedings of the Nova Scotian Institute of Science*, *34*, 215-232.

Catling, P., Lucas, Z., & Freedman, B. (2009). Plants and insects new to Sable Island, Nova Scotia. *The Canadian Field-Naturalist*, *123*(2), 141. https://doi.org/10.22621/cfn.v123i2.692

Chow, H. E. (2020). *Examining diversity of ground dwelling terrestrial invertebrates on Sable Island*. [Honours thesis, Saint Mary's University]. Saint Mary's University | Patrick Power Library. https://library2.smu.ca/handle/01/29366

Christie, B. J. (1980). *The horses of Sable Island*. Petheric Press.

Chung, H., Zak, D. R., Reich, P. B., & Ellsworth, D. S. (2007). Plant species richness, elevated CO2, and atmospheric nitrogen deposition alter soil microbial community composition and function. *Global Change Biology*, *13*(5), 980–989. https://doi.org/10.1111/j.1365-2486.2007.01313.x

Clark, F. E. (2012). Bacteria in Soil. In A. Burgers & F. Raw (Eds.), *Soil Biology* (pp. 15–47). chapter, Academic Press.

Coleine, C., Stajich, J. E., & Selbmann, L. (2022). Fungi are key players in extreme ecosystems. *Trends in Ecology & Evolution*, *37*(6), 517–528. https://doi.org/10.1016/j.tree.2022.02.002

Comeau, A. M. (2022). Preparing Multiplexed 16S/18S/ITS amplicons for the Illumina MiSeq. *Protocols.Io*. https://doi.org/10.17504/protocols.io.4r3l277k3g1y/v1

Comeau, A. M., Douglas, G. M., & Langille, M. G. (2017). Microbiome helper: A custom and streamlined workflow for Microbiome Research. *mSystems*, *2*(1). https://doi.org/10.1128/msystems.00127-16

Davis, D. S. (1996). *The natural history of nova scotia topics & habitats* (Vol. 1). Nimbus Publishing.

Eamer, J. B. R., Didier, D., Kehler, D., Manning, I., Colville, D., Manson, G., Jagot, A., & Kostylev, V. E. (2022). Multi-decadal coastal evolution of a North Atlantic shelf-edge vegetated sand island — Sable Island, Canada. *Canadian Journal of Earth Sciences*, *59*(11), 812–825. https://doi.org/10.1139/cjes-2020-0194

Eldridge, D. J., Ding, J., & Travers, S. K. (2020). Feral horse activity reduces environmental quality in ecosystems globally. *Biological Conservation*, *241*, 108367. https://doi.org/10.1016/j.biocon.2019.108367

Fierer, N. (2017). Embracing the unknown: Disentangling the complexities of the soil microbiome. *Nature Reviews Microbiology*, *15*(10), 579–590. https://doi.org/10.1038/nrmicro.2017.87

Franche, C., Lindström, K., & Elmerich, C. (2009). Nitrogen-fixing bacteria associated with leguminous and non-leguminous plants. *Plant and Soil*, *321*(1–2), 35–59. https://doi.org/10.1007/s11104-008-9833-8

Freedman, B., Catling, P. M., & Lucas, Z. (2011). Effects of feral horses on vegetation of Sable Island, Nova Scotia. *The Canadian Field-Naturalist*, *125*(3), 200. https://doi.org/10.22621/cfn.v125i3.1222

Gochfeld, M. (1983). The roseate tern: World distribution and status of a threatened species. *Biological Conservation*, *25*(2), 103–125. https://doi.org/10.1016/0006-3207(83)90055-1

Griffiths, R. I., Thomson, B. C., James, P., Bell, T., Bailey, M., & Whiteley, A. S. (2011). The bacterial biogeography of British soils. *Environmental Microbiology*, *13*(6), 1642–1654. https://doi.org/10.1111/j.1462-2920.2011.02480.x

Hashmi, I., Bindschedler, S., & Junier, P. (2020). Firmicutes. *Beneficial Microbes in Agro-Ecology*, 363–396. https://doi.org/10.1016/b978-0-12-823414-3.00018-6

He, M.-Q., Zhao, R.-L., Liu, D.-M., Denchev, T. T., Begerow, D., Yurkov, A., Kemler, M., Millanes, A. M., Wedin, M., McTaggart, A. R., Shivas, R. G., Buyck, B., Chen, J., Vizzini, A., Papp, V., Zmitrovich, I. V., Davoodian, N., & Hyde, K. D. (2022). Species diversity of Basidiomycota. *Fungal Diversity*, *114*(1), 281–325. https://doi.org/10.1007/s13225-021-00497-3

Jaccard, P. (1912). The distribution of the flora in the alpine zone. *New Phytologist*, *11*(2), 37–50. https://doi.org/10.1111/j.1469-8137.1912.tb05611.x

Jansson, J. K., & Hofmockel, K. S. (2020). Soil Microbiomes and climate change. *Nature Reviews Microbiology*, *18*(1), 35–46. https://doi.org/10.1038/s41579-019-0265-7

Jiang, P., Xiao, L. Q., Wan, X., Yu, T., Liu, Y. F., & Liu, M. X. (2022). Research progress on microbial carbon sequestration in Soil: A Review. *Eurasian Soil Science*, *55*(10), 1395–1404. https://doi.org/10.1134/s1064229322100064

Johnsen, K. (2022). *Foraging Ecology of the Feral Horses of Sable Island* (Doctoral dissertation, University of Saskatchewan).

Jost, L. (2006). Entropy and diversity. *Oikos*, *113*(2), 363–375. https://doi.org/10.1111/j.2006.0030-1299.14714.x

Kuramae, E., Gamper, H., Van Veen, J., & Kowalchuk, G. (2011). Soil and plant factors driving the community of soil-borne microorganisms across Chronosequences of secondary succession of chalk grasslands with a neutral ph. *FEMS Microbiology Ecology*, *77*(2), 285–294. https://doi.org/10.1111/j.1574-6941.2011.01110.x

Li, C., Liao, H., Xu, L., Wang, C., He, N., Wang, J., & Li, X. (2022). The adjustment of life history strategies drives the ecological adaptations of soil microbiota to aridity. *Molecular Ecology*, *31*(10), 2920–2934. https://doi.org/10.1111/mec.16445

Liang, C., & Balser, T. C. (2012). Warming and nitrogen deposition lessen microbial residue contribution to soil carbon pool. *Nature Communications*, *3*(1). https://doi.org/10.1038/ncomms2224

Liang, C., Schimel, J. P., & Jastrow, J. D. (2017). The importance of anabolism in microbial control over soil carbon storage. *Nature Microbiology*, *2*(8). https://doi.org/10.1038/nmicrobiol.2017.105

Liu, D., Liu, G., Chen, L., Wang, J., & Zhang, L. (2018). Soil ph determines fungal diversity along an elevation gradient in southwestern China. *Science China Life Sciences*, *61*(6), 718–726. https://doi.org/10.1007/s11427-017-9200-1

Locey, K. J. (2010). Synthesizing traditional biogeography with microbial ecology: The importance of dormancy. *Journal of Biogeography*, *37*(10), 1835–1841. https://doi.org/10.1111/j.1365-2699.2010.02357.x

Locey, K. J., Muscarella, M. E., Larsen, M. L., Bray, S. R., Jones, S. E., & Lennon, J. T. (2020). Dormancy dampens the microbial distance–decay relationship. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *375*(1798), 20190243. https://doi.org/10.1098/rstb.2019.0243

Lucas, Z. L., McLoughlin, P. D., Coltman, D. W., & Barber, C. (2009). Multiscale analysis reveals restricted gene flow and a linear gradient in heterozygosity for an island population of feral horses. *Canadian Journal of Zoology*, *87*(4), 310–316. https://doi.org/10.1139/z09-019

Ma, S., Zhu, W., Wang, W., Li, X., & Sheng, Z. (2023). Microbial assemblies with distinct trophic strategies drive changes in soil microbial carbon use efficiency along vegetation primary succession in a glacier retreat area of the southeastern Tibetan Plateau. *Science of The Total Environment*, *867*, 161587. https://doi.org/10.1016/j.scitotenv.2023.161587

Mandic-Mulec, I., Stefanic, P., & van Elsas, J. D. (2016). Ecology of *Bacillaceae*. *The Bacterial Spore*, 59–85. https://doi.org/10.1128/9781555819323.ch3

Marschner, H., & Dell, B. (1994). Nutrient uptake in mycorrhizal symbiosis. *Plant and Soil*, *159*(1), 89–102. https://doi.org/10.1007/bf00000098

McLoughlin, P. D., Lysak, K., Debeffe, L., Perry, T., & Hobson, K. A. (2016). Density-dependent resource selection by a terrestrial herbivore in response to sea-to-land nutrient transfer by seals. *Ecology*, *97*(8), 1929–1937. https://doi.org/10.1002/ecy.1451

McMurdie, Paul J., & Holmes, Susan. (2013) phyloseq: An R package for reproducible interactive analysis and graphics of microbiome census data. *PLoS ONE, 8*(4): e61217. https://doi.org/10.1371/journal.pone.0061217

McSherry, M. E., & Ritchie, M. E. (2013). Effects of grazing on grassland soil carbon: A global review. *Global Change Biology*, *19*(5), 1347–1357. https://doi.org/10.1111/gcb.12144

Mikola, J., Setälä, H., Virkajärvi, P., Saarijärvi, K., Ilmarinen, K., Voigt, W., & Vestberg, M. (2009). Defoliation and patchy nutrient return drive grazing effects on plant and soil properties in a dairy cow pasture. *Ecological Monographs*, *79*(2), 221–244. https://doi.org/10.1890/08-1846.1

Miller, E. H. (1983). Habitat and breeding cycle of the least sandpiper (*Calidris minutilla*) on Sable Island, Nova Scotia. *Canadian Journal of Zoology*, *61*(12), 2880–2898. https://doi.org/10.1139/z83-376

Mishra, A., Singh, L., & Singh, D. (2023). Unboxing the black box—one step forward to understand the soil microbiome: A systematic review. *Microbial Ecology*, *85*(2), 669–683. https://doi.org/10.1007/s00248-022-01962-5

Money, N. P. (2016). Chapter 1 - Fungal Diversity. In S. C. Watkinson, L. Boddy, & N. P. Money (Eds.), *The Fungi* (3rd ed., pp. 1–36). chapter, Academic Press.

Neuwirth, E. (2022). RColorBrewer: ColorBrewer Palettes. R package version 1.1-3, https://CRAN.R-project.org/package=RColorBrewer

Nolte, S., Van der Weyde, C., Esselink, P., Smit, C., Van Wieren, S. E., & Bakker, J. P. (2017). Behaviour of horses and cattle at two stocking densities in a coastal salt marsh. *Journal of Coastal Conservation*, *21*(3), 369–379. https://doi.org/10.1007/s11852-017-0515-7

Normaniza, O., Aimee, H., Ismail, Y., Tan, G. Y., & Rozainah, M. Z. (2018). Promoter effect of microbes in slope eco-engineering: Effects on plant growth, soil quality and erosion rate at different vegetation densities. *Applied Ecology and Environmental Research*, *16*(3), 2219–2232. https://doi.org/10.15666/aeer/1603_22192232

Oksanen J, Simpson G, Blanchet F, Kindt R, Legendre P, Minchin P, O'Hara R, Solymos P, Stevens M, Szoecs E, Wagner H, Barbour M, Bedward M, Bolker B, Borcard D, Carvalho G, Chirico M, De Caceres M, Durand S, … Weedon J (2022). vegan: Community Ecology Package. R package version 2.6-4. https://CRAN.R-project.org/package=vegan

Pearcy, R. W., & Ehleringer, J. (1984). Comparative ecophysiology of C_3 and C_4 plants. *Plant, Cell & Environment*, *7*(1), 1–13. https://doi.org/10.1111/j.1365-3040.1984.tb01194.x

Philippot, L., Raaijmakers, J. M., Lemanceau, P., & van der Putten, W. H. (2013). Going back to the roots: The microbial ecology of the rhizosphere. *Nature Reviews Microbiology*, *11*(11), 789–799. https://doi.org/10.1038/nrmicro3109

Plante, Y., Vega-Pla, J. L., Lucas, Z., Colling, D., de March, B., & Buchanan, F. (2007). Genetic diversity in a feral horse population from Sable Island, Canada. *Journal of Heredity*, *98*(6), 594–602. https://doi.org/10.1093/jhered/esm064

Posit team. (2023). RStudio: Integrated Development Environment for R. *Posit Software*, PBC, Boston, MA. http://www.posit.co/

Prell, J., & Poole, P. (2006). Metabolic changes of rhizobia in legume nodules. *Trends in Microbiology*, *14*(4), 161–168. https://doi.org/10.1016/j.tim.2006.02.005

Qiao, Y., Bai, Y., She, W., Liu, L., Miao, C., Zhu, G., Qin, S., & Zhang, Y. (2022). Arbuscular mycorrhizal fungi outcompete fine roots in determining soil multifunctionality and microbial diversity in a desert ecosystem. *Applied Soil Ecology*, *171*, 104323. https://doi.org/10.1016/j.apsoil.2021.104323

Quince, C., Lanzen, A., Davenport, R. J., & Turnbaugh, P. J. (2011). Removing noise from pyrosequenced amplicons. *BMC Bioinformatics*, *12*(1). https://doi.org/10.1186/1471-2105-12-38

R Core Team. (2023). R: A Language and Environment for Statistical Computing. *R Foundation for Statistical Computing,* Vienna, Austria. http://www.R-project.org

Read, D. J. (1989). Mycorrhizas and nutrient cycling in sand dune ecosystems. *Proceedings of the Royal Society of Edinburgh. Section B. Biological Sciences*, *96*, 89–110. https://doi.org/10.1017/s0269727000010873

Rickert, K. G. (1996). Stocking rate and sustainable grazing systems. *Wageningen Agricultural University Papers*, *96*(4), 29-66.

Ross, H. A. (1980). Growth of nestling Ipswich Sparrows in relation to season, habitat, brood size, and parental age. *The Auk*, *97*(4), 721-732.

Schroeder, P. J., & Jenkins, D. G. (2018). How robust are popular beta diversity indices to sampling error? *Ecosphere*, *9*(2). https://doi.org/10.1002/ecs2.2100

Stothart, M. R., Greuel, R. J., Gavriliuc, S., Henry, A., Wilson, A. J., McLoughlin, P. D., & Poissant, J. (2020). Bacterial dispersal and drift drive microbiome diversity patterns within a population of feral hindgut fermenters. *Molecular Ecology*, *30*(2), 555–571. https://doi.org/10.1111/mec.15747

Strecker, T., Barnard, R. L., Niklaus, P. A., Scherer-Lorenzen, M., Weigelt, A., Scheu, S., & Eisenhauer, N. (2015). Effects of plant diversity, functional group composition, and fertilization on soil microbial properties in experimental grassland. *PLOS ONE*, *10*(5). https://doi.org/10.1371/journal.pone.0125678

Strickland, M. S., & Rousk, J. (2010). Considering fungal:bacterial dominance in soils – methods, controls, and ecosystem implications. *Soil Biology and Biochemistry*, *42*(9), 1385–1395. https://doi.org/10.1016/j.soilbio.2010.05.007

Sul, W. J., Asuming-Brempong, S., Wang, Q., Tourlousse, D. M., Penton, C. R., Deng, Y., Rodrigues, J. L. M., Adiku, S. G. K., Jones, J. W., Zhou, J., Cole, J. R., & Tiedje, J. M. (2013). Tropical agricultural land management influences on soil microbial communities through its effect on Soil Organic Carbon. *Soil Biology and Biochemistry*, *65*, 33–38. https://doi.org/10.1016/j.soilbio.2013.05.007

Tedersoo, L., Bahram, M., Põlme, S., Kõljalg, U., Yorou, N. S., Wijesundera, R., Ruiz, L. V., Vasco-Palacios, A. M., Thu, P. Q., Suija, A., Smith, M. E., Sharp, C., Saluveer, E., Saitta, A., Rosas, M., Riit, T., Ratkowsky, D., Pritsch, K., Põldmaa, K., … Abarenkov, K. (2014). Global diversity and geography of soil fungi. *Science*, *346*(6213). https://doi.org/10.1126/science.1256688

Tissier, E. J., Mcloughlin, P. D., Sheard, J. W., & Johnstone, J. F. (2013). Distribution of vegetation along environmental gradients on Sable Island, Nova Scotia. *Écoscience*, *20*(4), 361–372. https://doi.org/10.2980/20-4-3616

Torsvik, V., & Øvreås, L. (2002). Microbial diversity and function in soil: From genes to ecosystems. *Current Opinion in Microbiology*, *5*(3), 240–245. https://doi.org/10.1016/s1369-5274(02)00324-7

Trillas, M. I., & Segarra, G. (2009). Chapter 8 interactions between nonpathogenic fungi and plants. *Advances in Botanical Research*, 321–359. https://doi.org/10.1016/s0065-2296(09)51008-7

Turenne, C. Y., Sanche, S. E., Hoban, D. J., Karlowsky, J. A., & Kabani, A. M. (1999). Rapid identification of fungi by using the ITS2 genetic region and an automated fluorescent capillary electrophoresis system. *Journal of Clinical Microbiology*, *37*(6), 1846–1851. https://doi.org/10.1128/jcm.37.6.1846-1851.1999

Van Beest, F. M., Uzal, A., Vander Wal, E., Laforge, M. P., Contasti, A. L., Colville, D., & McLoughlin, P. D. (2014). Increasing density leads to generalization in both coarse-grained habitat selection and fine-grained resource selection in a large mammal. *Journal of Animal Ecology*, *83*(1), 147–156. https://doi.org/10.1111/1365-2656.12115

Van Der Heijden, M. G., Bardgett, R. D., & Van Straalen, N. M. (2008). The unseen majority: Soil microbes as drivers of plant diversity and productivity in terrestrial ecosystems. *Ecology Letters*, *11*(3), 296–310. https://doi.org/10.1111/j.1461-0248.2007.01139.x

Vessey, J. K., Pawlowski, K., & Bergman, B. (2004). Root-based N2-fixing symbioses: Legumes, actinorhizal plants, *Parasponia* sp. and cycads. *Plant and Soil*, *266*(1–2), 205–230. https://doi.org/10.1007/s11104-005-0871-1

Ward, N. L., Challacombe, J. F., Janssen, P. H., Henrissat, B., Coutinho, P. M., Wu, M., Xie, G., Haft, D. H., Sait, M., Badger, J., Barabote, R. D., Bradley, B., Brettin, T. S., Brinkac, L. M., Bruce, D., Creasy, T., Daugherty, S. C., Davidsen, T. M., DeBoy, R. T., … Kuske, C. R. (2009). Three genomes from the phylum *Acidobacteria* provide insight into the lifestyles of these microorganisms in Soils. *Applied and Environmental Microbiology*, *75*(7), 2046–2056. https://doi.org/10.1128/aem.02294-08

Watkinson, S. C. (2016). Mutualistic symbiosis between fungi and autotrophs. *The Fungi*, 205–243. https://doi.org/10.1016/b978-0-12-382034-1.00007-4

White, T. J., Bruns, T., Lee, S., & Taylor, J. (1990). Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *PCR Protocols*, 315–322. https://doi.org/10.1016/b978-0-12-372180-8.50042-1

Wickham, H., Averick, M., Bryan, J., Chang, W., McGowan, L.D., François, R., Grolemund, G., Hayes, A., Henry, L., Hester, J., Kuhn, M., Pedersen, T.L., Miller, E., Bache, S.M., Müller, K., Ooms, J., Robinson, D., Seidel, D.P., Spinu, V., ... Yutani, H. (2019). Welcome to the tidyverse. *Journal of Open Source Software, 4*(43), 1686. https://doi.org/10.21105/joss.01686

Young, I. M., & Crawford, J. W. (2004). Interactions and self-organization in the soil-microbe complex. *Science*, *304*(5677), 1634–1637. https://doi.org/10.1126/science.1097394

Appendix

Appendix A

Table A1. Shannon entropy mean values for the vegetation types and environmental factors for each microbe. The *H* and *p* values are reported for each variable for bacteria and fungi. Significant *p* values are in bold ($p<0.05$).

Microbe	Variable	Shannon entropy	Standard error	*H*	*p* value
	Vegetation type				
Bacteria	*Heath*	7.536	0.432		
	Intermediate	8.803	0.075	9.140	**0.027**
	Marram	7.949	0.403		
	Unvegetated	8.357			
Fungi	*Heath*	3.926	0.205		
	Intermediate	3.488	0.367	1.836	0.607
	Marram	3.576	0.216		
	Unvegetated	3.965			
	pH				
Bacteria	*4.00-4.99*	8.374	0.281		
	5.00-5.99	6.652	0.725	12.240	**0.007**
	>6	8.130	0.378		
Fungi	*4.00-4.99*	4.019	0.226		
	5.00-5.99	3.648	0.236	1.027	0.795
	>6	3.594	0.233		
	Organic matter content (%)				
Bacteria	*<1*	8.147	0.297		
	1-2	8.280	0.382	11.300	**0.010**
	>2	6.652	0.808		
Fungi	*<1*	3.607	0.183		
	1-2	3.888	0.355	1.314	0.726
	>2	3.855	0.210		
	Phosphorous (P_2O_5) (kg/ha)				
Bacteria	*10-20*	6.850	1.238		
	21-30	8.058	0.276	2.690	0.442
	>30	7.927	0.521		
Fungi	*10-20*	4.616	0.269		
	21-30	3.612	0.167	4.992	0.172
	>30	3.644	0.310		

Table A2. Pair-wise Kruskal Wallis (post hoc) test results to determine significant differences within variables. The *H*, *p* values, and *q* values (adjusted *p* value for false discovery rate) are reported for interactions within bacterial variables which were significant. Significant *p* values are in bold ($p<0.05$).

Variable		*H*	*p* value	*q* value
Group 1	**Group 2**			
Vegetation type				
Unvegetated	*Heath*	0.355	0.551	0.551
	Intermediate	2.570	0.109	0.218
	Marram	0.669	0.413	0.496
Heath	*Intermediate*	7.628	**0.006**	0.034
	Marram	4.100	**0.043**	0.129
Intermediate	*Marram*	1.101	0.294	0.441
pH				
4.00-4.99	*5.00-5.99*	7.030	**0.008**	0.024
	>6.00	8.427	**0.004**	0.022
5.00-5.99	*>6.00*	0.681	0.409	0.409
Organic matter content (%)				
<1	*>2*	7.901	**0.005**	0.030
	1-2	0.312	0.577	0.577
>2	*1-2*	6.430	**0.011**	0.034

Table A3. Permutational multivariate analysis of variance results of *F*, variance explained (R^2), and *p* value for each variable, each microbe and with Jaccard or Bray-Curtis distances. Significant *p* values are in bold ($p<0.05$).

Dissimilarity Measure	Microbe	Variable	*F*	R^2	*p* value
Jaccard	Bacteria	Vegetation type	1.260	0.033	0.076
		pH	1.062	0.028	0.284
		Organic matter content	1.070	0.028	0.275
		Phosphorous	0.888	0.023	0.739
	Fungi	Vegetation type	0.880	0.023	0.851
		pH	0.866	0.023	0.890
		Organic matter content	1.066	0.028	0.252
		Phosphorous	1.085	0.029	0.208
Bray-Curtis	Bacteria	Vegetation type	1.454	0.037	**0.038**
		pH	1.036	0.027	0.366
		Organic matter content	0.986	0.026	0.459
		Phosphorous	0.657	0.017	0.988
	Fungi	Vegetation type	0.977	0.026	0.531
		pH	0.833	0.022	0.925
		Organic matter content	1.035	0.027	0.346
		Phosphorous	1.097	0.029	0.195

Appendix B

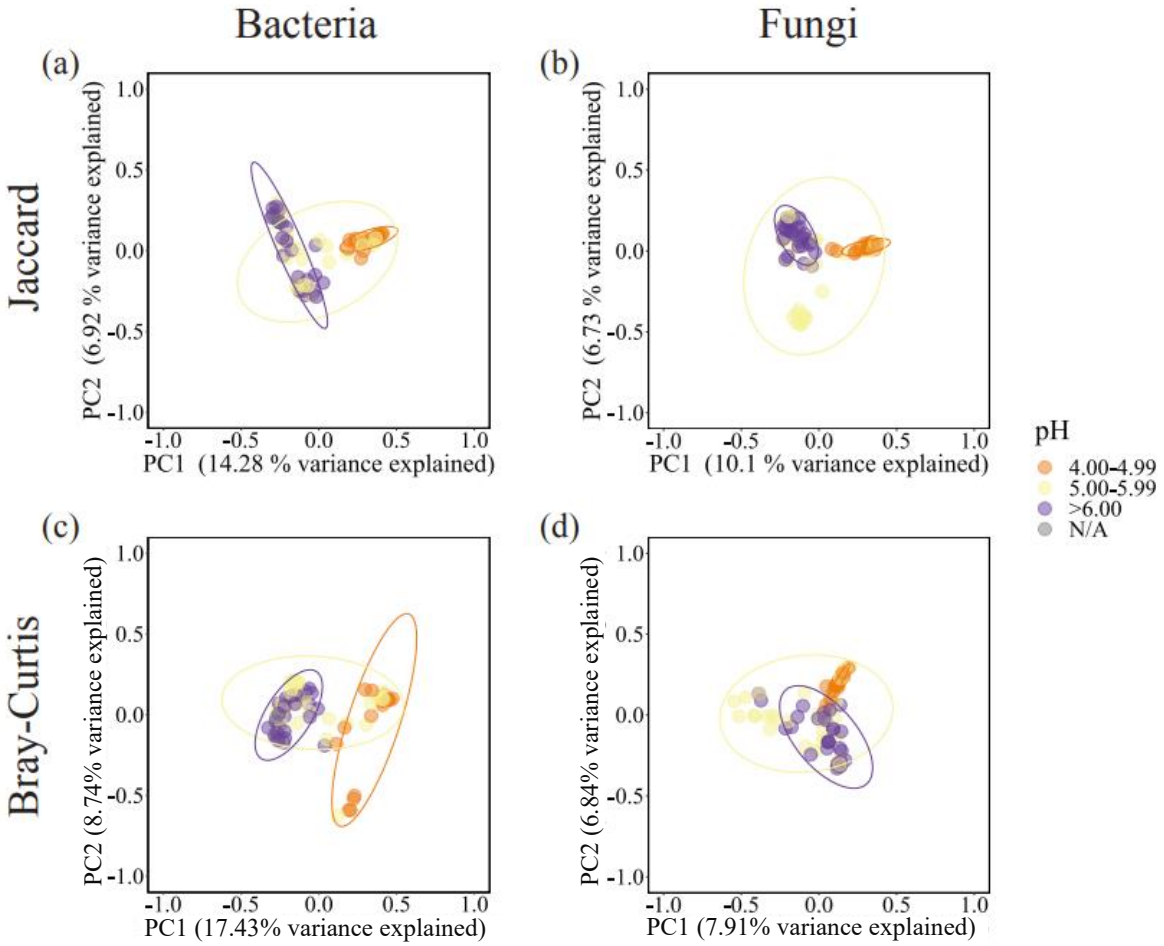

Figure B1. The beta diversity of soil microbes in different soil pH on Sable Island, NS with a principal coordinate analysis (PCoA) with a Jaccard **(a, b)**, and a Bray-Curtis distance matrix **(c, d)** for **(a, c)** Bacterial taxa and **(b, d)** Fungal taxa. N/A represents plots where soil analyses were not completed.

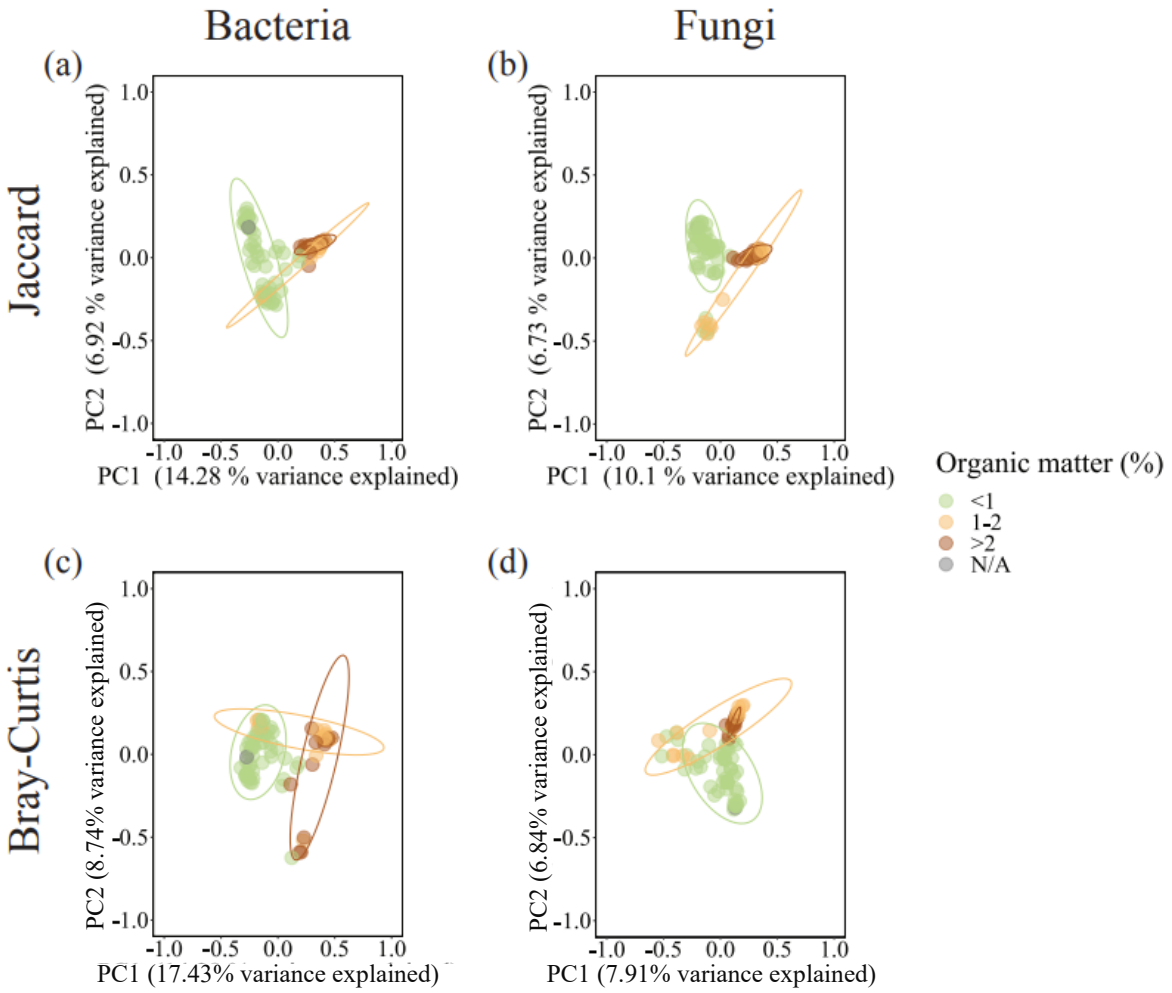

Figure B2. The beta diversity of soil microbes in different soil organic matter contents on Sable Island, NS with a principal coordinate analysis (PCoA) with a Jaccard **(a, b)**, and a Bray-Curtis distance matrix **(c, d)** for **(a, c)** Bacterial taxa and **(b, d)** Fungal taxa. N/A represents plots where soil analyses were not completed.

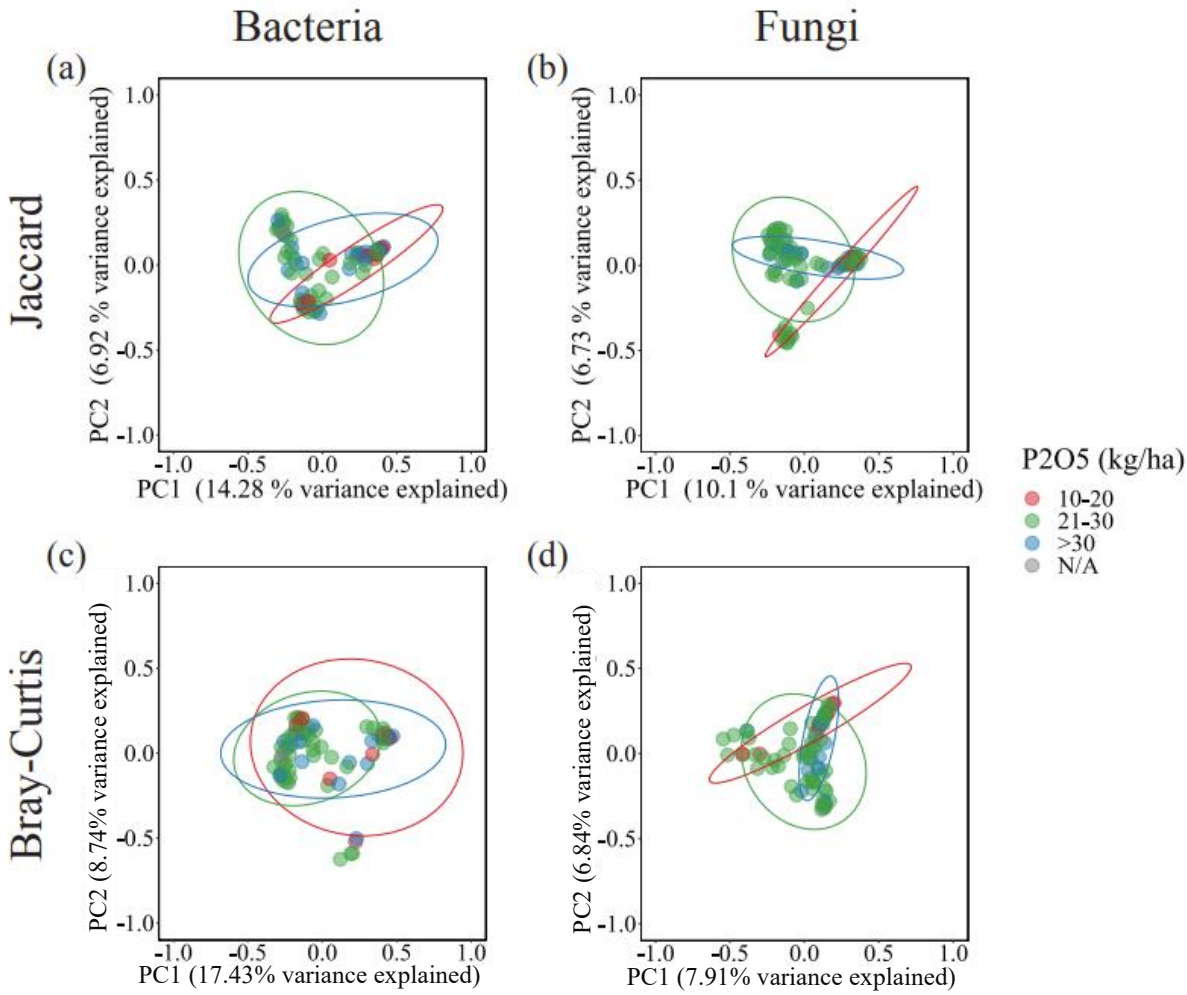

Figure B3. The beta diversity of soil microbes in different soil phosphorous (P_2O_5) concentrations on Sable Island, NS with a principle coordinate analysis (PCoA) with a Jaccard **(a, b)**, and a Bray-Curtis distance matrix **(c, d)** for **(a, c)** Bacterial taxa and **(b, d)** Fungal taxa. N/A represents plots where soil analyses were not completed.

Appendix C

C.1. Bacteria and Archaea

Table C1. All archaeal and bacterial ASVs identified on Sable Island, NS in 2021 in alphabetical order.

Kingdom	Phylum	Family	Genus	Species
Archaea	Crenarchaeota	*Bathyarchaeia*	*Bathyarchaeia*	*uncultured_methanogenic*
		Group_1.1c	*Group_1.1c*	*uncultured_crenarchaeote*
		Nitrosotaleaceae	*Candidatus_Nitrosotalea*	*uncultured_archaeon*
		Nitrososphaeraceae	*Candidatus_Nitrocosmicus*	*uncultured_archaeon*
Bacteria	Abditibacteriota	*Abditibacteriaceae*	*Abditibacterium*	*utsteinense*
				bacterium
				bacterium_LY17
				metagenome
				uncultured_actinobacterium
				uncultured_bacterium
Bacteria	Acidobacteriota	*Acidobacteriaceae_(Subgroup_1)*	*Acidicapsa*	*acidisoli*
				borealis
				Acidicapsa_sp.
			Acidipila	*Acidobacteria_bacterium*
				metagenome
				uncultured_bacterium
			Bryocella	*elongata*
				uncultured_Acidobacteria
				uncultured_bacterium
			Edaphobacter	*Edaphobacter_sp.*
				uncultured_Acidobacterium
			Granulicella	*bacterium_enrichment*
				paludicola
				Granulicella_sp.
			Occallatibacter	*bacterium_enrichment*
				uncultured_bacterium
				uncultured_forest
			uncultured	*Acidobacteria_bacterium*
				uncultured_Acidobacterium
				uncultured_forest
		Acidobacteriae	*Paludibaculum*	*metagenome*
				uncultured_Acidobacteria
				uncultured_bacterium
		AKIW659	*AKIW659*	*uncultured_bacterium*
		Blastocatellaceae	*Aridibacter*	*uncultured_bacterium*
			Blastocatella	*uncultured_organism*
		Bryobacteraceae	*Bryobacter*	*Acidobacteria_bacterium*
				Acidobacteriaceae_bacterium
				metagenome
				uncultured_eubacterium
				uncultured_Holophaga
				uncultured_Solibacteraceae

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
		DS-100	*DS-100*	*uncultured_bacterium*
		Holophagaceae	*Holophagaceae*	*uncultured_bacterium*
		Koribacteraceae	*Candidatus_Koribacter*	*uncultured_Acidobacteria*
				uncultured_bacterium
				uncultured_eubacterium
		Solibacteraceae	*Candidatus_Solibacter*	*bacterium_Ellin7504*
				uncultured_Acidobacteriaceae
				uncultured_bacterium
				uncultured_forest
				uncultured_Holophaga
		Subgroup_12	*Subgroup_12*	*uncultured_bacterium*
		Subgroup_13	*Subgroup_13*	*uncultured_bacterium*
				uncultured_Holophaga
		Subgroup_17	*Subgroup_17*	*metagenome*
		Subgroup_2	*Subgroup_2*	*bacterium_enrichment*
				metagenome
				uncultured_Acidobacteria
				uncultured_bacterium
				uncultured_eubacterium
				uncultured_forest
				uncultured_Holophaga
		Subgroup_5	*Subgroup_5*	*uncultured_bacterium*
		Subgroup_7	*Subgroup_7*	*uncultured_Desulfovirga*
				uncultured_proteobacterium
		Thermoanaerobaculaceae	*Subgroup_10*	*Acidobacteria_bacterium*
				Holophaga_sp.
				uncultured_soil
			Thermoanaerobaculum	*uncultured_bacterium*
		uncultured	*uncultured*	*metagenome*
				metagenome
				uncultured_Acidobacteriaceae
				uncultured_Acidobacteriales
				uncultured_Acidobacteriales
				uncultured_bacterium
				uncultured_Candidatus
				uncultured_forest
				uncultured_Holophaga
		Vicinamibacteraceae	*Vicinamibacteraceae*	*Acidobacteria_bacterium*
Bacteria	Actinobacteriota	*67-14*	*67-14*	*bacterium_enrichment*
				metagenome
				Solirubrobacterales_bacterium
				uncultured_bacterium
				uncultured_Conexibacteraceae
		Acidothermaceae	*Acidothermus*	*Actinomycetales_bacterium*
				metagenome
				uncultured_Actinoallomurus
				uncultured_actinobacterium
				uncultured_bacterium
				uncultured_soil
				uncultured_Thermomonosporaceae

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
		Actinospicaceae	*Actinospica*	*Actinospica_sp.*
				Persicaria_minor
				uncultured_actinobacterium
				uncultured_bacterium
		Catenulisporaceae	*Catenulispora*	*Catenulispora_acidiphila*
				Catenulispora_sp.
		Demequinaceae	*Demequina*	*globuliformis*
		Dermabacteraceae	*Brachybacterium*	*tyrofermentans*
		Dermacoccaceae	*Flexivirga*	*alba*
		Frankiaceae	*Jatrophihabitans*	*bacterium_Ellin6090*
				Jatrophihabitans_sp.
				metagenome
				uncultured_actinobacterium
				uncultured_bacterium
		Gaiellaceae	*Gaiella*	*metagenome*
		Iamiaceae	*Iamia*	*uncultured_Acidimicrobiales*
				Aquihabitans_daechungensis
		Ilumatobacteraceae	*CL500-29_marine_group*	*Hevea_brasiliensis*
				metagenome
			Ilumatobacter	*nonamiensis*
			uncultured	*uncultured_Actinomycetales*
				uncultured_bacterium
		IMCC26256	*IMCC26256*	*actinobacterium_BGR*
				bacterium_enrichment
				uncultured_Acidimicrobiia
				uncultured_Acidothermaceae
				uncultured_actinobacterium
				uncultured_Ferrimicrobium
		Kineosporiaceae	*Kineosporia*	*Kineosporia_aurantiaca*
				uncultured_Kineosporiaceae
			Quadrisphaera	*granulorum*
		MB-A2-108	*MB-A2-108*	*metagenome*
		Microbacteriaceae	*Agrococcus*	*jejuensis*
			Amnibacterium	*uncultured_bacterium*
		Micromonosporaceae	*Actinocatenispora*	*Actinocatenispora_rupis*
			Dactylosporangium	*uncultured_bacterium*
			Luedemannella	*metagenome*
		Microtrichaceae	*uncultured*	*uncultured_Acidimicrobiia*
		Microtrichales	*Microtrichales*	*metagenome*
		Nakamurellaceae	*Nakamurella*	*uncultured_Nakamurellaceae*
				uncultured_organism
		Nocardiaceae	*Rhodococcus*	*aerolatus*
		Nocardioidaceae	*Marmoricola*	*uncultured_bacterium*
			Nocardioides	*Kribbella_sp.*
				dilutus
				halotolerans
				uncultured_organism
		Propionibacteriaceae	*Aestuariimicrobium*	*actinobacterium_MH3-4*
			Friedmanniella	*uncultured_bacterium*
			uncultured	*uncultured_endolithic*
		Pseudonocardiaceae	*Amycolatopsis*	*balhimycina*

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
				saalfeldensis
			Pseudonocardia	*spinosispora*
		Solirubrobacteraceae	*Conexibacter*	*uncultured_bacterium* *woesei*
				Rubrobacterineae_bacterium
				uncultured_bacterium
				uncultured_Conexibacteraceae
			JCM_18997	*Conexibacter_sp.*
			uncultured	*Phytoplasma_sp.*
		Sporichthyaceae *uncultured*	*uncultured* *uncultured*	*Solirubrobacterales_bacterium* *uncultured_bacterium* *bacterium_Ellin6515*
				bacterium_Ellin6517
				Gaiella_sp.
				metagenome
				uncultured_Conexibacter
				uncultured_forest
Bacteria	Armatimonadota	*Armatimonadales*	*Armatimonadales*	*uncultured_Pseudonocardiaceae* *uncultured_Armatimonadetes*
				uncultured_bacterium
				uncultured_Chloroflexi
				uncultured_eubacterium
		Chthonomonadaceae	*Chthonomonas*	*uncultured_soil* *uncultured_Armatimonadetes*
				uncultured_bacterium
		Chthonomonadales *Fimbriimonadaceae*	*Chthonomonadales* *Fimbriimonadaceae*	*unidentified_marine* *uncultured_bacterium* *metagenome*
		uncultured	*uncultured*	*uncultured_bacterium* *metagenome*
				uncultured_actinobacterium
Bacteria	Bacteroidota	*37-13* *AKYH767*	*37-13* *AKYH767*	*uncultured_bacterium* *uncultured_Chitinophagaceae* *metagenome*
		Chitinophagaceae	*Arachidicoccus*	*uncultured_Bacteroidetes* *Arachidicoccus_sp.*
			Aurantisolimonas	*uncultured_bacterium*
				uncultured_soil
			Chitinophaga	*metagenome*
			Dinghuibacter	*silviterrae*
			Edaphobaculum	*uncultured_bacterium*
				uncultured_Bacteroidetes
				uncultured_Chitinophaga
				uncultured_Chitinophagaceae
			Filimonas	*Filimonas_sp.*
			Heliimonas	*uncultured_bacterium*
			Niabella	*hibiscisoli*
			Niastella	*koreensis*
				metagenome

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
			Parafilimonas	*metagenome*
				uncultured_bacterium
				uncultured_Bacteroidetes
			Pseudoflavitalea	*metagenome*
				uncultured_bacterium
			Puia	*metagenome*
			Rurimicrobium	*uncultured_bacterium*
			Segetibacter	*aerophilus*
				uncultured_bacterium
				uncultured_Chitinophagaceae
			Taibaiella	*smilacinae*
			Terrimonas	*metagenome*
			uncultured	*Panacibacter_ginsenosidivorans*
				Panacibacter_sp.
				uncultured_Chitinophaga
				uncultured_Ferruginibacter
			UTBCD1	*uncultured_bacterium*
		Crocinitomicaceae	*Fluviicola*	*Fluviicola_sp.*
				uncultured_bacterium
		CWT_CU03-E12	*CWT_CU03-E12*	*bacterium_enrichment*
				uncultured_bacterium
				uncultured_Bacteroidetes
		Cytophagaceae	*Cytophaga*	*metagenome*
				uncultured_bacterium
			Cytophagaceae	*uncultured_bacterium*
			Sporocytophaga	*myxococcoides*
		env.OPS_17	*env.OPS_17*	*metagenome*
		FFCH9454	*FFCH9454*	*uncultured_bacterium*
		Flavobacteriaceae	*Flavobacterium*	*hauense*
				ceti
			Sediminicola	*uncultured_Flavobacteriaceae*
			Vitellibacter	*uncultured_Aequorivita*
		Hymenobacteraceae	*Adhaeribacter*	*uncultured_bacterium*
			Hymenobacter	*algoricola*
				metagenome
				psychrophilus
				Siccationidurans_ginsengisoli
				uncultured_bacterium
		Ignavibacteriaceae	*Ignavibacterium*	*uncultured_Chlorobi*
		Kapabacteriales	*Kapabacteriales*	*uncultured_bacterium*
				uncultured_soil
		KD3-93	*KD3-93*	*metagenome*
		Microscillaceae	*Chryseolinea*	*metagenome*
				uncultured_bacterium
			Ohtaekwangia	*metagenome*
			OLB12	*uncultured_bacterium*
			uncultured	*Algoriphagus_sp.*
				Cytophagales_bacterium
				Musa_ABB

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
				uncultured_Flammeovirgaceae
				uncultured_Flexibacter
				uncultured_Flexibacteraceae
		NS9_marine_group	*NS9_marine_group*	*metagenome*
		Paludibacteraceae	*Paludibacter*	*uncultured_bacterium*
		Rhodothermaceae	*Rubrivirga*	*uncultured_bacterium*
			uncultured	*uncultured_bacterium*
		S15-21	*S15-21*	*uncultured_bacterium*
		Saprospiraceae	*uncultured*	*wastewater_metagenome*
		SB-5	*SB-5*	*uncultured_soil*
		SJA-28	*SJA-28*	*uncultured_bacterium*
				uncultured_Ignavibacterium
		Sphingobacteriaceae	*Mucilaginibacter*	*calamicampi*
			Olivibacter	*soli*
			Pedobacter	*arcticus*
				heparinus
				Sphingobacteriia_bacterium
		Spirosomaceae	*Dyadobacter*	*fermentans*
				Dyadobacter_sp.
			Persicitalea	*uncultured_bacterium*
			Spirosoma	*fluminis*
				horti
				jeollabukense
				linguale
				luteum
				spitsbergense
				uncultured_bacterium
				unidentified
			uncultured	*uncultured_Bacteroidetes*
		uncultured	*uncultured*	*uncultured_bacterium*
				uncultured_Bacteroidetes
				uncultured_Cyclobacteriaceae
		Weeksellaceae	*Chryseobacterium*	*piscium*
Bacteria	Bdellovibrionota	*Bdellovibrionaceae*	*OM27_clade*	*uncultured_bacterium*
		0319-6G20	*0319-6G20*	*marine_metagenome*
				uncultured_gamma
				uncultured_Syntrophobacteraceae
		Bdellovibrionaceae	*Bdellovibrio*	*uncultured_bacterium*
				unidentified
		Silvanigrellaceae	*Silvanigrella*	*metagenome*
		Oligoflexales	*Oligoflexus*	*Thymallus_thymallus*
				uncultured_bacterium
Bacteria	Chloroflexi	*A4b*	*A4b*	*metagenome*
				uncultured_bacterium
				uncultured_soil
				wastewater_metagenome
		AD3	*AD3*	*uncultured_Chloroflexi*
				uncultured_soil
		AKIW781	*AKIW781*	*uncultured_bacterium*
				uncultured_Kouleothrix
		Anaerolineaceae	*Leptolinea*	*uncultured_soil*

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
		Anaerolineae	*Anaerolineae*	*uncultured_Bellilinea*
		C0119	*C0119*	*uncultured_bacterium*
				uncultured_Chloroflexi
		Elev-1554	*Elev-1554*	*uncultured_bacterium*
		JG30-KF-AS9	*JG30-KF-AS9*	*Chloroflexi_bacterium*
				uncultured_bacterium
		JG30-KF-CM45	*JG30-KF-CM45*	*metagenome*
				uncultured_bacterium
				uncultured_soil
				uncultured_Sphaerobacter
				uncultured_Thermomicrobium
		JG30-KF-CM66	*JG30-KF-CM66*	*uncultured_Caldilinea*
		Ktedonobacteraceae	*1959-1*	*uncultured_bacterium*
			Ktedonobacter	*uncultured_Chloroflexi*
			Thermosporothrix	*uncultured_bacterium*
			uncultured	*uncultured_bacterium*
				uncultured_soil
		Roseiflexaceae	*uncultured*	*uncultured_bacterium*
		S085	*S085*	*metagenome*
		TK10	*TK10*	*metagenome*
Bacteria	Cloacimonadota	*PBS-18*	*PBS-18*	*uncultured_bacterium*
Bacteria	Cyanobacteria	*Gastranaerophilales*	*Gastranaerophilales*	*uncultured_bacterium*
		Leptolyngbyaceae	*Leptolyngbya_PCC-6306*	*Plectolyngbya_hodgsonii*
		Nostocaceae	*Anabaena_PCC-7122*	*Anabaena_sp.*
		Obscuribacteraceae	*Candidatus_Obscuribacter*	*uncultured_bacterium*
			Obscuribacteraceae	*metagenome*
				uncultured_bacterium
		Sericytochromatia	*Sericytochromatia*	*metagenome*
				uncultured_bacterium
		Vampirovibrionaceae	*Vampirovibrio*	*metagenome*
				uncultured_bacterium
			Vampirovibrionaceae	*uncultured_bacterium*
Bacteria	Deinococcota	*Deinococcaceae*	*Deinococcus*	*bacterium_Ellin510*
				aerolatus
				aerophilus
				alpinitundrae
				irradiatisoli
				persicinus
				radiomollis
				radioresistens
				ruber
				swuensis
Bacteria	Dependentiae	*Babeliaceae*	*Babeliaceae*	*uncultured_bacterium*
		Babeliales	*Babeliales*	*uncultured_bacterium*
		UBA12409	*UBA12409*	*uncultured_bacterium*
		Vermiphilaceae	*Vermiphilaceae*	*uncultured_bacterium*
				uncultured_Candidatus
Bacteria	Desulfobacterota	*Desulfobulbaceae*	*uncultured*	*uncultured_bacterium*
		Desulfosarcinaceae	*Desulfatirhabdium*	*uncultured_bacterium*
		Syntrophorhabdaceae	*Syntrophorhabdus*	*uncultured_bacterium*
				uncultured_delta
		uncultured	*uncultured*	*uncultured_Dongia*
Bacteria	Elusimicrobiota	*Endomicrobiaceae*	*Endomicrobium*	*uncultured_bacterium*

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
		Lineage_IIa	*Lineage_IIa*	*uncultured_actinobacterium*
				uncultured_bacterium
				uncultured_soil
		Lineage_IIb	*Lineage_IIb*	*uncultured_bacterium*
		Lineage_IV	*Lineage_IV*	*uncultured_Termite*
Bacteria	FCPU426	*FCPU426*	*FCPU426*	*uncultured_bacterium*
Bacteria	Fibrobacterota	*B122*	*B122*	*uncultured_bacterium*
		Fibrobacteraceae	*uncultured*	*bacterium_enrichment*
				metagenome
			possible_genus_04	*Juncus_effusus*
				metagenome
				uncultured_bacterium
		uncultured	*uncultured*	*uncultured_bacterium*
Bacteria	Firmicutes	*Alicyclobacillaceae*	*Tumebacillus*	*avium*
				Tumebacillus_sp.
		Bacillaceae	*Bacillus*	*murimartini*
				psychrosaccharolyticus
				thermoamylovorans
		Caloramatoraceae	*Fonticella*	*uncultured_bacterium*
		Clostridia_vadinBB60_group	*Clostridia_vadinBB60_group*	*uncultured_bacterium*
		Clostridiaceae	*Clostridium_sensu_stricto_12*	*Clostridium_akagii*
			Clostridium_sensu_stricto_9	*uncultured_Clostridium*
			uncultured	*uncultured_bacterium*
		Erysipelotrichaceae	*Turicibacter*	*uncultured_bacterium*
			ZOR0006	*uncultured_organism*
		Ethanoligenenaceae	*Incertae_Sedis*	*uncultured_bacterium*
		Hungateiclostridiaceae	*uncultured*	*uncultured_Ruminococcaceae*
		Lachnospiraceae	*Tyzzerella*	*uncultured_Clostridium*
		Paenibacillaceae	*Paenibacillus*	*alvei*
				daejeonensis
				kobensis
				lautus
				oryzae
				pectinilyticus
				populi
				turicensis
				uliginis
				xylanilyticus
				uncultured_actinobacterium
		Planococcaceae	*Domibacillus*	*metagenome*
		Sporomusaceae	*Dendrosporobacter*	*unidentified_eubacterium*
			Pelosinus	*uncultured_bacterium*
		Thermoactinomycetaceae	*Pasteuria*	*uncultured_Firmicutes*
		type_III	*type_III*	*uncultured_Mollicutes*
		uncultured	*uncultured*	*low_GC*
Bacteria	GAL15	*GAL15*	*GAL15*	*uncultured_Firmicutes*
Bacteria	Gemmatimonadota	*Gemmatimonadaceae*	*Gemmatimonas*	*bacterium_Ellin5290*
				Gemmatimonadetes_bacterium
				uncultured_Gemmatimonadaceae
				uncultured_soil
			Roseisolibacter	*Gemmatirosa_kalamazoonesis*
				agri

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
				uncultured_bacterium
				uncultured_forest
			uncultured	*Gemmatimonadetes_bacterium*
				metagenome
				uncultured_Alphaproteobacteria
				uncultured_proteobacterium
		Longimicrobiaceae	*Longimicrobiaceae*	*uncultured_bacterium*
Bacteria	Methylomirabilota	*Methylomirabilaceae*	*Sh765B-TzT-35*	*uncultured_bacterium*
Bacteria	Myxococcota	*Amb-16S-1034*	*Amb-16S-1034*	*uncultured_Polyangiaceae*
		BIrii41	*BIrii41*	*metagenome*
		Haliangiaceae	*Haliangium*	*myxobacterium_AT3-03*
				uncultured_Myxococcales
				uncultured_Nannocystineae
				uncultured_proteobacterium
		mle1-27	*mle1-27*	*uncultured_Polyangiaceae*
		Myxococcaceae	*KD3-10*	*metagenome*
				uncultured_bacterium
			uncultured	*metagenome*
				uncultured_delta
		Nannocystaceae	*Nannocystis*	*unidentified*
		Phaselicystidaceae	*Phaselicystis*	*uncultured_bacterium*
		Polyangiaceae	*Aetherobacter*	*uncultured_bacterium*
			Minicystis	*uncultured_bacterium*
			Pajaroellobacter	*Sorangiineae_bacterium*
				uncultured_bacterium
				uncultured_Polyangiaceae
				uncultured_proteobacterium
		Sandaracinaceae	*uncultured*	*delta_proteobacterium*
				metagenome
				uncultured_soil
Bacteria	Nitrospirota	*Nitrospiraceae*	*Nitrospira*	*moscoviensis*
				uncultured_Green
				uncultured_Nitrospirales
		uncultured	*uncultured*	*uncultured_bacterium*
Bacteria	Patescibacteria	*Parcubacteria*	*Parcubacteria*	*uncultured_bacterium*
		Saccharimonadales	*Saccharimonadales*	*uncultured_bacterium*
Bacteria	Planctomycetota	*BD7-11*	*BD7-11*	*uncultured_bacterium*
		CPla-3_termite_group	*CPla-3_termite_group*	*metagenome*
				uncultured_bacterium
				uncultured_planctomycete
		Gemmataceae	*Fimbriiglobus*	*Gemmata_sp.*
				metagenome
				uncultured_bacterium
				uncultured_Gemmata
			Gemmata	*bacterium_enrichment*
				Gemmata_sp.
				metagenome
				uncultured_bacterium
				uncultured_Planctomycetaceae
				uncultured_Planctomycetales

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
				uncultured_planctomycete
				uncultured_soil
			uncultured	*bacterium_enrichment*
				metagenome
				Planctomycetaceae_bacterium
				planctomycete_WY69
				uncultured_bacterium
				uncultured_planctomycete
				uncultured_Planctomycetia
				uncultured_sludge
				uncultured_thermal
				uncultured_Zavarzinella
			Zavarzinella	*uncultured_bacterium*
				Zavarzinella_formosa
		Gimesiaceae	*uncultured*	*uncultured_bacterium*
		Isosphaeraceae	*Aquisphaera*	*uncultured_bacterium*
				uncultured_planctomycete
			Candidatus_Nostocoida	*Candidatus_Nostocoida*
				uncultured_bacterium
			Paludisphaera	*metagenome*
				Paludisphaera_borealis
				uncultured_bacterium
			Singulisphaera	*Isosphaera_sp.*
				acidiphila
				rosea
				uncultured_Planctomycetales
				uncultured_planctomycete
			Tundrisphaera	*metagenome*
				lichenicola
				uncultured_bacterium
				uncultured_eubacterium
				uncultured_Planctomycetaceae
				uncultured_planctomycete
			uncultured	*Isosphaera_sp.*
				metagenome
				uncultured_bacterium
				uncultured_Planctomycetaceae
				uncultured_Planctomycetales
				uncultured_Singulisphaera
		OM190	*OM190*	*uncultured_bacterium*
				uncultured_soil
		Phycisphaeraceae	*I-8*	*uncultured_bacterium*
			Phycisphaera	*uncultured_bacterium*
			SM1A02	*metagenome*
			uncultured	*metagenome*
		Pirellulaceae	*Blastopirellula*	*marina*
			Pir4_lineage	*metagenome*

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
				uncultured_bacterium
				uncultured_Planctomycetaceae
				uncultured_Planctomycetales
				uncultured_soil
			Pirellula	*agricultural_soil*
				metagenome
				Pirellula_sp.
				Planctomycetes_bacterium
				uncultured_bacterium
				uncultured_Pasteuria
				uncultured_Planctomycetaceae
				uncultured_Planctomycetales
			Rhodopirellula	*planctomycete_str.*
				uncultured_Planctomycetaceae
			uncultured	*bacterium_enrichment*
				metagenome
				uncultured_bacterium
				uncultured_Firmicutes
				uncultured_Planctomycetaceae
				uncultured_Planctomycetales
				uncultured_sludge
		Rubinisphaeraceae	*Planctomicrobium*	*uncultured_bacterium*
			SH-PL14	*metagenome*
				uncultured_bacterium
				uncultured_Planctomycetaceae
				uncultured_planctomycete
		Schlesneriaceae	*Planctopirus*	*metagenome*
				uncultured_bacterium
			Schlesneria	*metagenome*
				uncultured_bacterium
				uncultured_planctomycete
				uncultured_Schlesneria
		Tepidisphaeraceae	*Tepidisphaeraceae*	*uncultured_bacterium*
				uncultured_planctomycete
		uncultured	*uncultured*	*agricultural_soil*
				metagenome
				uncultured_bacterium
				uncultured_bacterium
				uncultured_Planctomyces
				uncultured_soil
		vadinHA49	*vadinHA49*	*uncultured_bacterium*
		WD2101_soil_group	*WD2101_soil_group*	*Planctomycetales_bacterium*
				uncultured_bacterium
				uncultured_eubacterium
				uncultured_Planctomycetaceae
				uncultured_Planctomycetales
				uncultured_planctomycete

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
				uncultured_soil
Bacteria	Proteobacteria	*A0839*	*A0839*	*metagenome*
				uncultured_Phyllobacteriaceae
				uncultured_proteobacterium
		A21b	*A21b*	*uncultured_bacterium*
				uncultured_soil
		Acetobacteraceae	*Acetobacteraceae*	*Acidisphaera_sp.*
			Acidicaldus	*uncultured_forest*
			Acidiphilium	*metagenome*
				uncultured_bacterium
				uncultured_eubacterium
				uncultured_soil
			Acidisoma	*tundrae*
				uncultured_bacterium
			Acidisphaera	*metagenome*
				uncultured_soil
			Acidocella	*uncultured_bacterium*
			Belnapia	*uncultured_bacterium*
			Rhodopila	*uncultured_bacterium*
			Rhodovastum	*Acetobacteraceae_bacterium*
				metagenome
				uncultured_bacterium
			Roseomonas	*arctica*
				lacus
				ludipueritiae
				uncultured_organism
			uncultured	*metagenome*
				uncultured_soil
		Amb-16S-1323	*Amb-16S-1323*	*uncultured_bacterium*
		Beijerinckiaceae	*1174-901-12*	*Methyloferula_sp.*
				Rhizobiales_bacterium
				uncultured_Alphaproteobacteria
				uncultured_bacterium
				uncultured_Rhizobiales
				uncultured_soil
			alphaI_cluster	*Alsobacter_sp.*
			Beijerinckiaceae	*Chelatococcus_asaccharovorans*
			Camelimonas	*uncultured_bacterium*
			Methylobacterium-Methylorubrum	*Methylobacterium_adhaesivum*
				Methylobacterium_aerolatum
				Methylobacterium_cerastii
				Methylobacterium_komagatae
				uncultured_organism
			Methylocapsa	*uncultured_bacterium*
			Methylocella	*Methylocella_palustris*
			Methylocystis	*uncultured_bacterium*
			Methylorosula	*Beijerinckia_sp.*

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
				uncultured_bacterium
			Methylovirgula	*uncultured_bacterium*
			Psychroglaciecola	*Psychroglaciecola_arctica*
				uncultured_bacterium
			Rhodoblastus	*uncultured_bacterium*
			Roseiarcus	*uncultured_Alphaproteobacteria*
				uncultured_bacterium
			uncultured	*Methylobacterium_sp.*
				uncultured_bacterium
		Burkholderiaceae	*Limnobacter*	*uncultured_forest metagenome*
			Pandoraea	*Burkholderia_sp.*
		Caulobacteraceae	*Asticcacaulis*	*uncultured_bacterium*
			Brevundimonas	*abyssalis*
			Caulobacter	*uncultured_soil*
			Phenylobacterium	*Afipia_genosp.*
			uncultured	*uncultured_Alphaproteobacteria*
				uncultured_bacterium
		CCD24	*CCD24*	*uncultured_Caulobacteraceae metagenome*
		Cellvibrionaceae	*Cellvibrio*	*uncultured_bacterium*
		Comamonadaceae	*Aquabacterium*	*citratiphilum*
			Variovorax	*soli*
		Coxiellaceae	*Coxiella*	*uncultured_bacterium*
		Devosiaceae	*Devosia*	*uncultured_Coxiellaceae neptuniae*
		Diplorickettsiaceae	*Aquicella*	*metagenome*
				uncultured_bacterium
			uncultured	*metagenome*
				Rickettsiella_sp.
				uncultured_bacterium
		Dongiaceae	*Dongia*	*uncultured_Coxiellaceae metagenome*
		Elsteraceae	*Aliidongia*	*uncultured_Rhodospirillaceae dinghuensis*
			uncultured	*uncultured_bacterium*
		Geminicoccaceae	*Candidatus_Alysiosphaera*	*metagenome*
			Candidatus_Alysiosphaera	*uncultured_bacterium*
			Geminicoccus	*uncultured_bacterium*
		Granulosicoccaceae	*Granulosicoccus*	*marinus*
		Holosporaceae	*uncultured*	*uncultured_bacterium*
		Hyphomicrobiaceae	*Hyphomicrobium*	*methylovorum*
		Hyphomonadaceae	*Hirschia*	*Hyphomicrobium_sp. metagenome*
			SWB02	*metagenome*
		Inquilinaceae	*Inquilinus*	*uncultured_Alphaproteobacteria*
		JG36-TzT-191	*JG36-TzT-191*	*uncultured_eubacterium uncultured_bacterium*
		KF-JG30-C25	*KF-JG30-C25*	*uncultured_proteobacterium uncultured_gamma*

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
				uncultured_soil
		Labraceae	*Labrys*	*methylaminiphilus*
				uncultured_Phyllobacteriaceae
				Xanthobacteraceae_bacterium
		Legionellaceae	*Legionella*	*uncultured_bacterium*
		Magnetospirillaceae	*uncultured*	*uncultured_bacterium*
		Methyloligellaceae	*uncultured*	*metagenome*
		Methylomonadaceae	*Crenothrix*	*uncultured_bacterium*
		Methylophilaceae	*uncultured*	*metagenome*
			Methylotenera	*uncultured_bacterium*
		Methylopilaceae	*Albibacter*	*Methylopila_sp.*
		Micropepsaceae	*Micropepsaceae*	*uncultured_Hyphomicrobiaceae*
				uncultured_proteobacterium
			Micropepsis	*uncultured_bacterium*
			Rhizomicrobium	*uncultured_bacterium*
			uncultured	*bacterium_enrichment*
				metagenome
				uncultured_Acidobacterium
				uncultured_bacterium
				uncultured_Hyphomicrobiaceae
				uncultured_proteobacterium
		Moraxellaceae	*Psychrobacter*	*alimentarius*
			uncultured	*metagenome*
		Nitrosomonadaceae	*Ellin6067*	*alpha_proteobacterium*
			GOUTA6	*uncultured_bacterium*
			IS-44	*metagenome*
			mle1-7	*uncultured_Rhodocyclaceae*
			MND1	*metagenome*
			uncultured	*metagenome*
		Oxalobacteraceae	*Massilia*	*albidiflava*
		Paracaedibacteraceae	*Candidatus_Paracaedibacter*	*uncultured_bacterium*
		Pleomorphomonadaceae	*uncultured*	*uncultured_Rhizobiales*
		Pseudomonadaceae	*Pseudomonas*	*marincola*
		R7C24	*R7C24*	*metagenome*
				uncultured_bacterium
		Reyranellaceae	*Reyranella*	*metagenome*
			uncultured	*uncultured_Alphaproteobacteria*
		Rhizobiaceae	*Mesorhizobium*	*thiogangeticum*
				Phyllobacteriaceae_bacterium
				Rhodospirillales_bacterium
			Tianweitania	*uncultured_bacterium*
		Rhizobiales_Incertae_Sedis	*Alsobacter*	*metallidurans*
			Bauldia	*metagenome*
				uncultured_bacterium
				uncultured_Methylocystaceae
				uncultured_proteobacterium
			Nordella	*uncultured_bacterium*
			uncultured	*metagenome*
				uncultured_Alphaproteobacteria
		Rhodanobacteraceae	*Dokdonella*	*uncultured_Dokdonella*
			Dyella	*uncultured_Dyella*

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
			Luteibacter	*Luteibacter_sp.*
			Mizugakiibacter	*uncultured_Xanthomonadaceae*
			Rhodanobacter	*uncultured_Dokdonella*
				uncultured_Rudaea
				uncultured_Xanthomonadaceae
			Rudaea	*uncultured_gamma*
		Rhodobacteraceae	*Amaricoccus*	*tamworthensis*
				uncultured_bacterium
		Rhodocyclaceae	*Uliginosibacterium*	*metagenome*
		Rhodomicrobiaceae	*Rhodomicrobium*	*uncultured_Hyphomicrobiaceae*
		Rhodospirillaceae	*uncultured*	*uncultured_bacterium*
		SC-I-84	*SC-I-84*	*metagenome*
				uncultured_Nitrosomonadaceae
				uncultured_soil
		Solimonadaceae	*Alkanibacter*	*gamma_proteobacterium*
				metagenome
			Nevskia	*Persicaria_minor*
				uncultured_bacterium
			Polycyclovorans	*uncultured_bacterium*
				uncultured_Xanthomonadaceae
			uncultured	*uncultured_bacterium*
		Sphingomonadaceae	*Altererythrobacter*	*bacterium*
				Porphyrobacter_mercurialis
				uncultured_Altererythrobacter
			Hephaestia	*uncultured_bacterium*
			Novosphingobium	*rosa*
				uncultured_soil
			Parablastomonas	*uncultured_bacterium*
			Plot4-2H12	*uncultured_Sphingomonadaceae*
			Polymorphobacter	*uncultured_Sphingomonas*
			Qipengyuania	*uncultured_bacterium*
			Rhizorhapis	*Sphingomonas_gotjawalisoli*
			Sphingobium	*Sphingomonas_azotofornans*
				sufflavum
			Sphingomonas	*Afipia_sp.*
				crusticola
				ginsengisoli
				oligoaromativorans
				panacis
				phyllosphaerae
				polyaromaticivorans
				uncultured_eubacterium
			Sphingopyxis	*baekryungensis*
				taejonensis
		Steroidobacteraceae	*Steroidobacter*	*bacterium_MI-37*
				bacterium_MI-8
			uncultured	*Hypsibius_dujardini*
				metagenome

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
		Sutterellaceae	*AAP99*	*metagenome*
			uncultured	*uncultured_bacterium*
		uncultured	*uncultured*	*metagenome*
				metagenome
				Rhodospirillaceae_bacterium
				uncultured_Alphaproteobacteria
				uncultured_bacterium
				uncultured_Bradyrhizobiaceae
				uncultured_forest
				uncultured_Hyphomicrobiaceae
				uncultured_proteobacterium
				uncultured_Rhizobiales
				uncultured_Rhodospirillaceae
				uncultured_soil
		Unknown_Family	*Acidibacter*	*metagenome*
				Steroidobacter_sp.
				uncultured_bacterium
				uncultured_gamma
				uncultured_proteobacterium
				uncultured_Steroidobacter
				uncultured_Xanthomonadales
			Candidatus_Berkiella	*uncultured_Thiotrichales*
				uncultured_bacterium
			Candidatus_Ovatusbacter	*uncultured_bacterium*
			Unknown_Family	*uncultured_soil*
		WD260	*WD260*	*uncultured_bacterium*
		Xanthobacteraceae	*Afipia*	*uncultured_Rhodopseudomonas*
			Rhodoplanes	*uncultured_Hyphomicrobiaceae*
			uncultured	*uncultured_Bradyrhizobiaceae*
				uncultured_forest
			Xanthobacteraceae	*Rhizobiales_bacterium*
		Xanthomonadaceae	*Pseudoxanthomonas*	*Pseudomonas_sp.*
			Stenotrophomonas	*rhizophila*
			uncultured	*uncultured_bacterium*
		Yersiniaceae	*Serratia*	*symbiotica*
Bacteria	RCP2-54	*RCP2-54*	*RCP2-54*	*uncultured_bacterium*
				uncultured_Syntrophobacterales
Bacteria	Spirochaetota	*Spirochaetaceae*	*Spirochaeta*	*Spirochaeta_sp.*
			Spirochaeta_2	*metagenome*
			uncultured	*uncultured_soil*
		V2072-189E03	*V2072-189E03*	*uncultured_Spirochaetales*
Bacteria	Sumerlaeota	*Sumerlaeaceae*	*Sumerlaea*	*uncultured_Acidobacteria*
				uncultured_bacterium
				uncultured_Desulfocaldus
Bacteria	Verrucomicrobiota	*Chthoniobacteraceae*	*Candidatus_Udaeobacter*	*uncultured_Verrucomicrobia*
			Chthoniobacter	*bacterium_Ellin506*
				bacterium_Ellin507
				uncultured_bacterium
				uncultured_soil

Table C1. *(Continued)*

Kingdom	Phylum	Family	Genus	Species
				Verrucomicrobia_bacterium
			Chthoniobacteraceae	*uncultured_bacterium*
			LD29	*uncultured_bacterium*
		Methylacidiphilaceae	*uncultured*	*uncultured_bacterium*
		Omnitrophaceae	*Candidatus_Omnitrophus*	*uncultured_planctomycete*
		Omnitrophales	*Omnitrophales*	*uncultured_planctomycete*
		Opitutaceae	*uncultured*	*uncultured_bacterium*
		Pedosphaeraceae	*ADurb.Bin063-1*	*uncultured_bacterium*
			Ellin516	*metagenome*
				uncultured_bacterium
			Pedosphaera	*uncultured_bacterium*
			Pedosphaeraceae	*bacterium_enrichment*
			uncultured	*bacterium_enrichment*
				uncultured_bacterium
		Puniceicoccaceae	*Cerasicoccus*	*uncultured_organism*
		S-BQ2-57_soil_group	*S-BQ2-57_soil_group*	*uncultured_Verrucomicrobia*
		Verrucomicrobiaceae	*Roseimicrobium*	*metagenome*
			uncultured	*uncultured_soil*
		Xiphinematobacteraceae	*Candidatus_Xiphinematobacter*	*uncultured_Verrucomicrobia*
				uncultured_Xiphinematobacteriaceae
Bacteria	WPS-2	*WPS-2*	*WPS-2*	*hydrothermal_vent*
				metagenome
				uncultured_bacterium
				uncultured_Firmicutes
				uncultured_forest
Bacteria	WS2	*WS2*	*WS2*	*uncultured_soil*

C.2 Fungi

Table C2. All fungal ASVs identified on Sable Island, NS in 2021 in alphabetical order.

Phylum	Family	Genus	Species
Ascomycota	*Celotheliaceae*	*Celotheliaceae_gen_Incertae_sedis*	*Celotheliaceae_sp*
	Clavicipitaceae	*Clavicipitaceae_gen_Incertae_sedis*	*Clavicipitaceae_sp*
		Metapochonia	*suchlasporia*
	Cyphellophoraceae	*Cyphellophoraceae_gen_Incertae_sedis*	*Cyphellophoraceae_sp*
	Herpotrichiellaceae	*Exophiala*	*moniliae*
			opportunistica
			quercina
	Hypocreaceae	*Hypocreaceae_gen_Incertae_sedis*	*Hypocreaceae_sp*
	Hypocreales_fam_Incertae_sedis	*Hypocreales_gen_Incertae_sedis*	*Hypocreales_sp*
	Ophiocordycipitaceae	*Drechmeria*	*campanulata*
		Hirsutella	*rostrata*
		Perennicordyceps	*paracuboidea*
	Orbiliales_fam_Incertae_sedis	*Orbiliales_gen_Incertae_sedis*	*Orbiliales_sp*
	Pezizales_fam_Incertae_sedis	*Pezizales_gen_Incertae_sedis*	*Pezizales_sp*

Table C2. *(Continued)*

Phylum	Family	Genus	Species
		Coprotus	*Coprotus_sp*
	Pezizomycotina_fam_Incertae_sedis	*Cytosporella*	*Cytosporella_sp*
	Saccharomycetales_fam_Incertae_sedis	*Candida*	*Candida_fluviatilis*
	Taphrinaceae	*Taphrina*	*inositophila*
			Taphrina_sp
Basidiobolomycota	*Basidiobolaceae*	*Basidiobolus*	*Basidiobolus_sp*
Basidiomycota	*Agaricaceae*	*Coprinus*	*foetidellus*
			vosoustii
	Agaricales_fam_Incertae_sedis	*Agaricales_gen_Incertae_sedis*	*Agaricales_sp*
	Agaricomycetes_fam_Incertae_sedis	*Agaricomycetes_gen_Incertae_sedis*	*Agaricomycetes_sp*
	Agaricostilbales_fam_Incertae_sedis	*Agaricostilbales_gen_Incertae_sedis*	*Agaricostilbales_sp*
	Atheliaceae	*Athelia*	*acrospora*
			Athelia_sp
	Auriculariales_fam_Incertae_sedis	*Auriculariales_gen_Incertae_sedis*	*Auriculariales_sp*
		Oliveonia	*Oliveonia_pauxilla*
	Bolbitiaceae	*Panaeolus*	*fimiputris*
			papilionaceus
	Boletales_fam_Incertae_sedis	*Hydnomerulius*	*pinastri*
		Leucogyrophana	*olivascens*
	Buckleyzymaceae	*Buckleyzyma*	*aurantiaca*
	Byssocorticiaceae	*Athelopsis*	*lembospora*
	Camptobasidiaceae	*Camptobasidium*	*Camptobasidium_sp*
	Cantharellales_fam_Incertae_sedis	*Cantharellales_gen_Incertae_sedis*	*Cantharellales_sp*
	Ceratobasidiaceae	*Ceratobasidiaceae_gen_Incertae_sedis*	*Ceratobasidiaceae_sp*
		Ceratobasidium	*Ceratobasidium_sp*
		Ceratorhiza	*rhizodes*
		Thanatephorus	*cucumeris*
		Thanatephorus	*Thanatephorus_sp*
	Chionosphaeraceae	*Ballistosporomyces*	*sasicola*
		Kurtzmanomyces	*Kurtzmanomyces_sp*
	Chrysozymaceae	*Bannozyma*	*yamatoana*
		Chrysozyma	*Chrysozyma_sp*
		Chrysozymaceae_gen_Incertae_sedis	*Chrysozymaceae_sp*
		Oberwinklerozyma	*silvestris*
		Pseudohyphozyma	*bogoriensis*
		Slooffia	*cresolica*
		Slooffia	*tsugae*
	Classiculaceae	*Classicula*	*sinensis*
	Clathraceae	*Camarophyllopsis*	*Camarophyllopsis_sp*
		Clathrus	*Clathrus_sp*
		Clavaria	*argillacea*
			falcata

Table C2. *(Continued)*

Phylum	Family	Genus	Species
			griseolilacina
			Clavaria_sp
			sphagnicola
		Clavariaceae_gen_Incertae_sedis	*Clavariaceae_sp*
		Clavulinopsis	*corniculata*
			fusiformis
			helvola
			laeticolor
			luteoalba
			Clavulinopsis_sp
		Ramariopsis	*crocea*
			flavescens
			Ramariopsis_sp
	Colacogloeaceae	*Colacogloea*	*Colacogloea_sp*
		Coleosporium	*solidaginis*
	Coniophoraceae	*Coniophora*	*Coniophora_sp*
	Corticiaceae	*Laetisaria*	*Laetisaria_fuciformis*
		Limonomyces	*roseipellis*
			Limonomyces_sp
	Cortinariaceae	*Cortinarius*	*spilomeus*
	Cryptococcaceae	*Cryptococcus*	*watticus*
	Cyphellaceae	*Rectipilus*	*Rectipilus_sp*
	Cystobasidiaceae	*Cystobasidium*	*fimetarium*
			minuta
			slooffiae
		Occultifur	*externus*
			kilbournensis
			mephitis
			Occultifur_sp
	Cystobasidiomycetes_fam_Incertae_sedis	*Cystobasidiomycetes_gen_Incertae_sedis*	*Cystobasidiomycetes_sp*
	Cystofilobasidiaceae	*Cystofilobasidium*	*capitatum*
	Entolomataceae	*Clitopilus*	*baronii*
			passeckerianus
			Clitopilus_sp
		Entocybe	*nitida*
		Entoloma	*brunneosericeum*
			conferendum
			cuspidiferum
			foliomarginatum
			lampropus
			longistriatum
			paraconferendum

Table C2. *(Continued)*

Phylum	Family	Genus	Species
			pleopodium
			porphyrogriseum
			Entoloma_sp
		Inocephalus	*murrayi*
		Rhodocybe	*cistetorum*
	Entylomataceae	*Entyloma*	*magnusii*
	Eocronartiaceae	*Eocronartium*	*Eocronartium_sp*
	Erythrobasidiaceae	*Erythrobasidium*	*hasegawae*
	Erythrobasidiales_fam_Incertae_sedis	*Erythrobasidiales_gen_Incertae_sedis*	*Erythrobasidiales_sp*
	Exobasidiaceae	*Exobasidium*	*rostrupii*
	Filobasidiaceae	*Filobasidium*	*globosum*
			magnum
			Filobasidium_sp
			wieringae
		Goffeauzyma	*agrionensis*
		Goffeauzyma	*gastrica*
		Heterocephalacria	*Heterocephalacria_sp*
		Naganishia	*diffluens*
	Filobasidiales_fam_Incertae_sedis	*Filobasidiales_gen_Incertae_sedis*	*Filobasidiales_sp*
	Ganodermataceae	*Ganoderma*	*applanatum*
	Geastraceae	*Nidulariopsis*	*iowensis*
	Glomosporiaceae	*Thecaphora*	*Thecaphora_sp*
	GS29_fam_Incertae_sedis	*GS29_gen_Incertae_sedis*	*GS29_sp*
	Hydnaceae	*Sistotrema*	*oblongisporum*
			Sistotrema_sp
	Hydnodontaceae	*Brevicellicium*	*Brevicellicium_sp*
		Gliophorus	*Gliophorus_sp*
			irrigatus
			laetus
		Humidicutis	*marginata*
		Hygrocybe	*cantharellus*
			chlorophana
			flavescens
			helobia
			insipida
			miniata
			turunda
		Luellia	*cystidiata*
		Trechispora	*caucasica*
			invisitata
			Trechispora_sp
			stellulata

Table C2. *(Continued)*

Phylum	Family	Genus	Species
			stevensonii
			verruculosa
	Hygrophoropsidaceae	*Hygrophoropsis*	*aurantiaca*
			Hygrophoropsis_sp
	Hymenochaetales_fam_Incertae_sedis	*Hymenochaetales_gen_Incertae_sedis*	*Hymenochaetales_sp*
	Hyphodermataceae	*Hyphoderma*	*Hyphoderma_sp*
	Kriegeriaceae	*Phenoliferia*	*Phenoliferia_sp*
	Kriegeriales_fam_Incertae_sedis	*Kriegeriales_gen_Incertae_sedis*	*Kriegeriales_sp*
	Leucosporidiaceae	*Leucosporidium*	*creatinivorum*
			fragarium
			golubevii
			Leucosporidium_sp
	Leucosporidiales_fam_Incertae_sedis	*Leucosporidiales_gen_Incertae_sedis*	*Leucosporidiales_sp*
	Lyophyllaceae	*Sagaranella*	*Sagaranella_sp*
	Marasmiaceae	*Marasmius*	*curreyi*
	Microbotryales_fam_Incertae_sedis	*Microbotryales_gen_Incertae_sedis*	*Microbotryales_sp*
	Microbotryomycetes_fam_Incertae_sedis	*Curvibasidium*	*cygneicollum*
		Microbotryomycetes_gen_Incertae_sedis	*Microbotryomycetes_sp*
	Microsporomycetaceae	*Microsporomycetaceae_gen_Incertae_sedis*	*Microsporomycetaceae_sp*
	Microstromatales_fam_Incertae_sedis	*Pseudomicrostroma*	*phylloplanum*
	Mrakiaceae	*Mrakia*	*aquatica*
			Mrakia_sp
	Mycenaceae	*Mycena*	*abramsii*
			albidolilacea
			filopes
			galericulata
			griseoviridis
			leptocephala
			metata
			pura
			rubromarginata
			sanguinolenta
			Mycena_sp
			stylobates
	Omphalotaceae	*Collybiopsis*	*hasanskyensis*
		Gymnopus	*earleae*
			impudicus
		Marasmiellus	*paspali*
		Mycetinis	*scorodonius*
		Rhodocollybia	*Rhodocollybia_butyracea_f._asema*
	Phallaceae	*Mutinus*	*ravenelii*
			Mutinus_sp

Table C2. *(Continued)*

Phylum	Family	Genus	Species
	Phallales_fam_Incertae_sedis	*Phallales_gen_Incertae_sedis*	*Phallales_sp*
	Piskurozymaceae	*Piskurozyma*	*fildesensis*
			silvicola
			Piskurozyma_sp
			taiwanensis
		Solicoccozyma	*terricola*
			zizaniae
	Platygloeales_fam_Incertae_sedis	*Platygloeales_gen_Incertae_sedis*	*Platygloeales_sp*
	Podoscyphaceae	*Hypochnicium*	*Hypochnicium_sp*
	Polyporales_fam_Incertae_sedis	*Polyporales_gen_Incertae_sedis*	*Polyporales_sp*
	Psathyrellaceae	*Coprinellus*	*brevisetulosus*
			curtus
		Coprinopsis	*babosiae*
			filamentifera
			pseudofriesii
			radiata
			Coprinopsis_sp
			villosa
		Parasola	*misera*
		Psathyrella	*fimiseda*
	Pucciniaceae	*Puccinia*	*graminis*
			striiformis
	Pucciniastraceae	*Pucciniastraceae_gen_Incertae_sedis*	*Pucciniastraceae_sp*
	Rhynchogastremataceae	*Papiliotrema*	*fusca*
	Rickenellaceae	*Peniophorella*	*pallida*
	Russulales_fam_Incertae_sedis	*Russulales_gen_Incertae_sedis*	*Russulales_sp*
	Sakaguchiaceae	*Sakaguchia*	*dacryoidea*
			Sakaguchia_sp
	Schizoporaceae	*Lyomyces*	*Lyomyces_sp*
	Serendipitaceae	*Serendipita*	*Serendipita_sp*
		Serendipita	*herbamans*
		Serendipita	*vermifera*
		Serendipitaceae_gen_Incertae_sedis	*Serendipitaceae_sp*
	Sphaerobolaceae	*Sphaerobolus*	*ingoldii*
			Sphaerobolus_sp
	Spiculogloeales_fam_Incertae_sedis	*Meniscomyces*	*layueensis*
	Sporidiobolaceae	*Rhodotorula*	*graminis*
			kratochvilovae
			mucilaginosa
			sphaerocarpa
		Sporidiobolaceae_gen_Incertae_sedis	*Sporidiobolaceae_sp*
		Sporidiobolus	*salmonicolor*

Table C2. *(Continued)*

Phylum	Family	Genus	Species
		Sporobolomyces	*roseus*
	Sporidiobolales_fam_Incertae_sedis	*Sporidiobolales_gen_Incertae_sedis*	*Sporidiobolales_sp*
	Stephanosporaceae	*Cristinia*	*helvetica*
			Cristinia_sp
		Lindtneria	*Lindtneria_sp*
	Strophariaceae	*Agrocybe*	*pediades*
		Deconica	*phillipsii*
		Galerina	*marginata*
			Galerina_sp
			venenata
		Hypholoma	*capnoides*
			lateritium
		Protostropharia	*semiglobata*
		Psilocybe	*semilanceata*
	Symmetrosporaceae	*Symmetrospora*	*symmetrica*
			gracilis
	Thelephorales_fam_Incertae_sedis	*Thelephorales_gen_Incertae_sedis*	*Thelephorales_sp*
	Tilletiariaceae	*Tilletiaria*	*anomala*
	Trechisporales_fam_Incertae_sedis	*Trechisporales_gen_Incertae_sedis*	*Trechisporales_sp*
	Tremellales_fam_Incertae_sedis	*Tremellales_gen_Incertae_sedis*	*Tremellales_sp*
	Tremellodendropsidales_fam_Incertae_sedis	*Tremellodendropsidales_gen_Incertae_sedis*	*Tremellodendropsidales_sp*
	Tremellomycetes_fam_Incertae_sedis	*Tremellomycetes_gen_Incertae_sedis*	*Tremellomycetes_sp*
	Tricholomataceae	*Ampulloclitocybe*	*clavipes*
		Clitocybe	*dealbata*
		Delicatula	*integrella*
		Flagelloscypha	*minutissima*
			Flagelloscypha_sp
		Lachnella	*Lachnella_sp*
		Leucoinocybe	*Leucoinocybe_sp*
		Ripartites	*Ripartites_sp*
	Tubulicrinaceae	*Butlerelfia*	*eustacei*
	Typhulaceae	*Typhula*	*Typhula_sp*
	Ustilaginaceae	*Farysia*	*Farysia_acheniorum*
		Kalmanozyma	*Kalmanozyma_fusiformata*
		Moesziomyces	*aphidis*
			bullatus
		Sporisorium	*graminicola*
			Sporisorium_sp
		Tranzscheliella	*yupeitaniae*
		Ustilago	*kummeri*
			Ustilago_sp
	Ustilentylomataceae	*Bauerago*	*Bauerago_sp*

Table C2. *(Continued)*

Phylum	Family	Genus	Species
		Ustilentyloma	*graminis*
			Ustilentyloma_sp
Calcarisporiellomycota	*Calcarisporiellaceae*	*Calcarisporiella*	*Calcarisporiella_sp*
Chytridiomycota	*Alphamycetaceae*	*Betamyces*	*Betamyces_sp*
	Chytridiomycota_fam_Incertae_sedis	*Chytridiomycota_gen_Incertae_sedis*	*Chytridiomycota_sp*
	Chytriomycetaceae	*Rhizidium*	*Rhizidium_sp*
	GS13_fam_Incertae_sedis	*GS13_gen_Incertae_sedis*	*GS13_sp*
	Powellomycetaceae	*Fimicolochytrium*	*jonesii*
			Fimicolochytrium_sp
		Geranomyces	*variabilis*
		Powellomyces	*Powellomyces_sp*
		Powellomycetaceae_gen_Incertae_sedis	*Powellomycetaceae_sp*
	Rhizophlyctidaceae	*Rhizophlyctis*	*rosea*
			Rhizophlyctis_sp
	Rhizophlyctidales_fam_Incertae_sedis	*Rhizophlyctidales_gen_Incertae_sedis*	*Rhizophlyctidales_sp*
	Rhizophydiaceae	*Rhizophydiaceae_gen_Incertae_sedis*	*Rhizophydiaceae_sp*
	Rhizophydiales_fam_Incertae_sedis	*Rhizophydiales_gen_Incertae_sedis*	*Rhizophydiales_sp*
	Sonoraphlyctidaceae	*Sonoraphlyctis*	*ranzonii*
			Sonoraphlyctis_sp
	Spizellomycetaceae	*Spizellomyces*	*pseudodichotomus*
	Spizellomycetales_fam_Incertae_sedis	*Spizellomycetales_gen_Incertae_sedis*	*Spizellomycetales_sp*
Fungi_phy_Incertae_sedis	*Fungi_fam_Incertae_sedis*	*Fungi_gen_Incertae_sedis*	*Fungi_sp*
Glomeromycota	*Acaulosporaceae*	*Acaulospora*	*lacunosa*
	Archaeosporaceae	*Archaeospora*	*ecuadoriana*
			trappei
	Archaeosporales_fam_Incertae_sedis	*Archaeosporales_gen_Incertae_sedis*	*Archaeosporales_sp*
	Claroideoglomeraceae	*Claroideoglomus*	*Claroideoglomus_sp*
	Glomeraceae	*Glomeraceae_gen_Incertae_sedis*	*Glomeraceae_sp*
		Rhizoglomus	*vesiculiferum*
		Rhizophagus	*intraradices*
			irregularis
			Rhizophagus_sp
	Glomeromycota_fam_Incertae_sedis	*Glomeromycota_gen_Incertae_sedis*	*Glomeromycota_sp*
Monoblepharomycota	*Harpochytriaceae*	*Harpochytrium*	*Harpochytrium_sp*
	Monoblepharidales_fam_Incertae_sedis	*Monoblepharidales_gen_Incertae_sedis*	*Monoblepharidales_sp*
Mortierellomycota	*Mortierellaceae*	*Dissophora*	*globulifera*
		Entomortierella	*beljakovae*
		Gryganskiella	*cystojenkinii*
		Linnemannia	*amoeboidea*
			hyalina
			zychae
		Mortierella	*alliacea*

Table C2. *(Continued)*

Phylum	Family	Genus	Species
			alpina
			angusta
			basiparvispora
			echinula
			elongatula
			exigua
			fluviae
			formicae
			gemmifera
			macrocystis
			pulchella
			sarnyensis
			Mortierella_sp
			tsukubaensis
			turficola
		Mortierellaceae_gen_Incertae_sedis	*Mortierellaceae_sp*
		Podila	*humilis*
			minutissima
	Mortierellales_fam_Incertae_sedis	*Mortierellales_gen_Incertae_sedis*	*Mortierellales_sp*
Mucoromycota	*Cunninghamellaceae*	*Absidia*	*glauca*
			Absidia_sp
		Cunninghamella	*elegans*
	Endogonales_fam_Incertae_sedis	*Endogonales_gen_Incertae_sedis*	*Endogonales_sp*
	GS22_fam_Incertae_sedis	*GS22_gen_Incertae_sedis*	*GS22_sp*
	Umbelopsidaceae	*Umbelopsis*	*isabellina*
			ramanniana
Olpidiomycota	*Olpidiomycota_fam_Incertae_sedis*	*Olpidiomycota_gen_Incertae_sedis*	*Olpidiomycota_sp*
Rozellomycota	*GS05_fam_Incertae_sedis*	*GS05_gen_Incertae_sedis*	*GS05_sp*