

1 Title: Biogeographical patterns in soil bacterial communities across the Arctic region

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28

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30 and laboratory work. MZA conducted bioinformatics processing and statistical analysis. LAM drafted  
31 the manuscript and MZA, DAP and CSJ revised and approved the final version.

32

## 33 **Abstract**

34 The considerable microbial diversity of soils, their variety and key role in biogeochemical cycling has  
35 led to growing interest in their global distribution and the impact that environmental change might  
36 have at the regional level. In the largest study of Arctic soil bacterial communities to date, we used  
37 high-throughput sequencing to investigate the bacterial diversity from 200 widely dispersed Arctic soil  
38 samples. We identified a core microbiome, composed of 13 OTUs present at over 95% of sites,  
39 regardless of geographical location and environmental conditions. pH was identified as the key  
40 environmental driver structuring Arctic soil communities, while total organic carbon, moisture and  
41 conductivity had little effect. We were able to identify specialist, generalist and indicator taxa. Only  
42 one core biogeographical region was apparent (East Greenland, Svalbard and Iceland), although strong  
43 similarities did exist between Arctic sites separated by substantial geographical distances. We suggest  
44 that while pH might appear as the primary factor structuring soil bacterial community composition,  
45 dispersal may drive community structure in some parts of the region. Overall, Arctic soil bacterial  
46 communities, while driven by the same environmental factors as those elsewhere, were  
47 fundamentally different from those of temperate and tropical soils.

## 48 **Introduction**

49 Biogeography, the study of biodiversity across space and time, gives insights into ecological  
50 mechanisms such as speciation, extinction, dispersal and species interactions (Martiny et al., 2006;  
51 Fierer, 2008). Theoretically, distant and isolated habitats are expected to present high endemism as  
52 a consequence of intrinsic dispersal limitations and environmental filtering (Mittelbach and Schemske,  
53 2015; Kleinteich et al., 2017; Bahram et al., 2018). Thus, isolated, pristine ecosystems with limited  
54 human presence, such as the Arctic region, should harbour endemic communities. However, microbial  
55 communities may be less constrained by geographical barriers and thus, have long been considered  
56 ubiquitous (Finlay, 2002; O'Malley, 2007). Yet, recent studies have uncovered patterns of microbial  
57 biogeography on global scales (Fierer and Jackson, 2006; Lauber et al., 2009; Tedersoo et al., 2014;  
58 Henschel et al., 2015; Bahram et al., 2018; Delgado-Baquerizo et al., 2018). The study by Delgado-

59 Baquerizo et al. (2018) illustrated the high number of OTU associations with soil pH and thus, the  
60 importance of pH in structuring bacterial communities globally. It followed a previous global study by  
61 Tedersoo et al. (2014) which identified pH as a major predictor of fungal richness and diversity  
62 worldwide. These studies, however, had a low number of Arctic samples despite the Arctic tundra  
63 covering over 5% of Earth land surface (Nemergut et al., 2005). Thus, the application of their  
64 predictions to the Arctic region is difficult to assess, especially considering that Arctic microbial  
65 communities generally cluster away from other terrestrial regions (Fierer et al., 2012; Tedersoo et al.,  
66 2014), suggesting a different character for these communities. Previous Arctic studies on various  
67 spatial scales have also identified pH as a primary factor structuring microbial communities (Chu et al.,  
68 2010; Siciliano et al., 2014). However, these studies generally have a low number of samples over  
69 restricted sampling areas. The study by Metcalfe et al. (2018) illustrated the sampling bias of Arctic  
70 studies, focused on Abisko, Sweden and Toolik lake, Alaska. This study identified large areas of  
71 Northern Canada and Siberia as being largely under-cited across all disciplines, including microbiology.  
72 The review by Malard and Pearce (2018) further illustrated this bias by identifying all studies  
73 investigating microbial diversity across the Arctic, and highlighting the need for increased research  
74 effort, sampling site number and standardized protocols.

75 Frozen soils in the Arctic region store over 1500 Pg of carbon (Koven et al., 2011; Mackelprang et al.,  
76 2011) and as Arctic warming is exacerbated and permafrost thaw accelerates, the depth of the active  
77 layer is increasing. As previously frozen carbon becomes available, it is expected that microbial activity  
78 will increase, which may lead to increased atmospheric release rates of climate active gases such as  
79 carbon dioxide (CO<sub>2</sub>), methane (CH<sub>4</sub>) and nitrous oxide (N<sub>2</sub>O) (Ma et al., 2007; Mackelprang et al.,  
80 2011). Carbon-climate feedback studies of permafrost affected regions use temperature, soil moisture  
81 and precipitation as the main drivers controlling decomposition rates (Koven et al., 2011; Schuur et  
82 al., 2015). While models are useful to gain a global understanding of the impact of climate change on  
83 permafrost thaw and greenhouse gas release, the accuracy of results obtained is highly variable when

84 compared with data collected in the field or laboratory (Schuur et al., 2015) due to empirical and  
85 modelling uncertainties still needing to be addressed (Bradford et al., 2016).

86 Microorganisms drive biogeochemical cycling and participate in the uptake and release of CO<sub>2</sub>, CH<sub>4</sub>  
87 and N<sub>2</sub>O, so microbial data should be incorporated in climate models. Current models use soil  
88 properties to model changes in fluxes, without considering microbial communities and the changes in  
89 community composition induced by climate change (Bardgett et al., 2008; Nazaries et al., 2013).  
90 Adding microbial information into models will improve their predictions; however, detailed microbial  
91 data is still required, with a focus on microbial community, diversity, function and long-term changes  
92 in these communities (Graham et al., 2012; Nazaries et al., 2013). While global surveys of microbial  
93 diversity have already been conducted (Tedersoo et al., 2014; Delgado-Baquerizo et al., 2018), the  
94 number of Arctic samples is restricted (Malard and Pearce, 2018) and therefore, microbial data is still  
95 lacking for permafrost-affected regions.

96 Here, we conducted a Pan-Arctic survey of bacterial communities in Arctic soils to provide a baseline  
97 database, characterize Arctic soil bacterial communities and identify biogeographical patterns of  
98 diversity across the region. The most straightforward demonstration of biogeography is  
99 demonstrating that microbial composition across a landscape is non-random (Martiny et al., 2006). To  
100 do so, we evaluated the influence of environmental conditions, known to impact global microbial  
101 communities, on bacterial composition and diversity in the Arctic region. We identified specialist,  
102 generalist and indicator taxa to evaluate the impact of dispersal and environmental factors on the  
103 structure of these communities. We also characterized cosmopolitan OTUs representing the Arctic  
104 core microbiome. Our sample collection is widespread across 43 core sites and orders of magnitude  
105 larger than previous Arctic studies.

## 106 **Methods**

### 107 ***Sample collection***

108 Soil samples were collected at 43 sites across the Arctic region between April 2017 and September  
109 2017 [Fig. 1], the GPS coordinates of each site was recorded with a portable GPS and photographs  
110 were taken. At each site, 3 to 5 soil samples were collected within a 100 m<sup>2</sup> area under the most  
111 common vegetation, for a total of 200 unique Arctic samples. Approximately 150 g of soil per sample  
112 was collected in Whirl-Pak bags (Nasco, WI, USA), from the top 15 cm. Plant roots and rocks were  
113 removed, samples were homogenized thoroughly and frozen at -20 °C before transportation to the  
114 United Kingdom. Samples were conserved at – 20 °C until analysed.

### 115 ***Soil properties***

116 Moisture content was measured gravimetrically on soils after drying at 150 °C for 24 h and total  
117 organic content (TOC) was measured gravimetrically by heating previously dried soils to 550 °C for 4  
118 h. pH and conductivity were measured in the laboratory in a 1:5 freshly thawed soil to water ratio,  
119 using a Mettler-Toledo FE20 pH meter (Mettler-Toledo Instruments co., Shanghai, China) and a  
120 CMD500 conductivity meter (WPA, Cambridge, UK).

### 121 ***DNA extraction***

122 Soil DNA was extracted in duplicate for each sample using the PowerSoil kit (Qiagen, Hilden, Germany),  
123 for a total of 400 DNA extracts. Each sample was PCR amplified using the universal primers 515F-806R,  
124 as per the Schloss lab standard operating Procedure (Kozich et al., 2013) and the Earth Microbiome  
125 Project (Thompson et al., 2017), under the following conditions: initial denaturation at 95°C for 2 min  
126 then 30 cycles of 20 s denaturation at 95°C; primer annealing at 55°C for 15 s; elongation at 72°C for  
127 5 mn then a final elongation at 72°C for 10 min. Negative controls, DNA extraction kit controls and  
128 ZymoBIOMICS mock communities (Zymo Research, Irvine, CA, USA) were included alongside the soil  
129 DNA and sequenced. PCR amplicons were cleaned and normalized using SequalPrep Plate  
130 Normalization Kit (Invitrogen, Carlsbad, CA, USA) and combined into four pools. Each pool was  
131 quantified using fragment size determined by BioAnalyzer hsDNA assay (Agilent technologies, Santa

132 Clara, CA, USA) and concentration by Qubit hsDNA kit (Invitrogen). The library was supplemented with  
133 5% PhiX and loaded on an Illumina MiSeq V2 500 cycles cartridge.

#### 134 ***Illumina Sequencing and Data Processing***

135 Raw amplicon sequences were demultiplexed with the associated barcodes. Cutadapt (Martin, 2011)  
136 was used for adaptor and primer clipping. Forward and reverse reads that were long enough were  
137 merged (98 %  $\pm$  0.8 % / sample) using FLASH (fast length adjustment of short reads) (Magoč and  
138 Salzberg, 2011) for a total of 20 million reads ( $\sim$ 50,000  $\pm$  30000 reads/sample) initially. Vsearch  
139 (Rognes et al., 2016) was used for downstream analyses. Quality filtering was carried with an expected  
140 error > 1.5. Dereplication was performed to identify unique sequences. A two-step chimera detection  
141 method was used, first by aligning against ChimeraSlayer Gold database provided with SILVA (Pruesse  
142 et al., 2007), second by using the denovo detection module in Vsearch. An open-reference operational  
143 taxonomic unit (OTU) calling was performed on high-quality trimmed sequences at 97% similarity level  
144 using the USEARCH (Edgar, 2010) algorithm for clustering implemented in Vsearch to generate  
145 operational taxonomical units (OTUs). Unique chimera filtered sequences were aligned using the  
146 Python Nearest Alignment Space Termination (PyNASt) (Caporaso et al., 2009) tool with a relaxed  
147 neighbour-joining tree built using FastTree (Price et al., 2010). The taxonomy was determined using  
148 the Classification Resources for Environmental Sequence Tags (CREST) (Lanzén et al., 2012) classifier  
149 with a confidence threshold of 0.80 against SILVA release 128 as a reference database.

150 Samples less than at least 2000 reads/sample were filtered from the OTU table in order to have  
151 sufficient reads to capture the accurate relationships among samples as described in Caporaso et al.  
152 (2010a). After filtering, a total of 386 samples were used for the statistical analyses, corresponding to  
153 386 DNA extracts from 200 unique samples and  $\sim$ 19.5 million reads (50 609  $\pm$  26 700 reads/sample)  
154 assigned against 49 057 OTUs.

#### 155 ***Data Availability***

156 The dataset is deposited at European Nucleotide Archive / SRA under the accession number  
157 PRJEB29109.

## 158 ***Statistical Analysis***

159 All statistical analyses were performed with a combination of Qiime1 V 1.90 (Caporaso et al., 2010b)  
160 and R environment (Team, 2013) using phyloseq (McMurdie and Holmes, 2013), vegan (Dixon, 2003)  
161 and indicpecies (Cáceres and Legendre, 2009) packages. Alpha Diversity was calculated using  
162 matrices of richness (number of observed OTUs) and diversity (Shannon diversity) based on a rarefied  
163 OTU table to compensate for variation in sample depth. Multiple rarefaction was performed with the  
164 smallest sample size as maximum depth. The difference in alpha diversity indices was compared  
165 statistically using a non-parametric (Monte Carlo) test across different pH categories with Bonferroni  
166 correction. Beta Diversity using Bray-Curtis distance was calculated by normalizing the OTU table using  
167 cumulative-sum scaling (CSS) (Paulson et al., 2013). The dissimilarity matrix was plotted using principal  
168 coordinates analysis (PCoA). ANOSIM from vegan was used to analyze the similarities based on Bray-  
169 Curtis dissimilarity beta diversity matrix across pH categories with free permutations. Multivariate  
170 analysis by redundancy analysis (RDA) of bacterial communities and environmental variables was  
171 performed using Vegan (Dixon, 2003) to extract and summarize the variation in ordination explained  
172 by explanatory variables. Indicator species were determined by the Dufrene-Legendre indicator  
173 species analysis method (Cáceres and Legendre, 2009) to identify OTUs that were specifically  
174 associated with the different pH ranges. Spearman's correlation coefficient was used to identify the  
175 possible correlations between the environmental variables.

## 176 **Results**

### 177 ***Overall bacterial community composition and drivers of diversity***

178 We identified 48 147 bacterial taxa, of which 135 OTUs had abundances over 0.1% across all 386  
179 samples (defined as abundant taxa). Abundant taxa represented 32% of all the reads, illustrating the  
180 dominance of a few taxa over the rest of the community. Of the abundant taxa only, Acidobacteria

181 dominated the community at approximately 31% with Blastocatellia (12.8%) and Subgroup6 (7.2%) as  
182 abundant classes. Verrucomicrobia was the second most abundant phylum (23%), dominated by  
183 Spartobacteria (17.2%). Alphaproteobacteria (10.6%) and Betaproteobacteria (6.6%) were the most  
184 commonly identified Proteobacteria (20% overall). Actinobacteria (10.7%), Chloroflexi (7%) and  
185 Bacteroidetes (3.5%) were also among abundant phyla classified.

186 The Bray-Curtis dissimilarity heatmap and dendrogram [Fig. 2A] identified three main clusters  
187 illustrating community differences. The first cluster was composed of acidic samples in a gradient from  
188 Norwegian soils at pH = 4.07 ( $\pm$  0.35) to samples from Alaska (pH = 4.64  $\pm$  0.41) and West Greenland  
189 (pH = 4.90  $\pm$  0.85). The second cluster included the lower acidoneutral range of samples from East  
190 Greenland (pH = 5.96  $\pm$  0.69), Svalbard (pH = 5.65  $\pm$  0.53) and Iceland (pH = 5.84  $\pm$  0.46). Finally, the  
191 last cluster included the higher range of acidoneutral and alkaline soils from Russia (pH = 6.19  $\pm$  0.22)  
192 and Canada (pH = 7.94  $\pm$  0.67). The full spectrum of soil pH was covered from pH = 3.5 to pH = 9.0 and  
193 geographical locations often had samples from more than one pH category [Fig. S1].

194 The clustering of samples by pH range was clearly observed on the principal coordinate analysis (PCoA)  
195 of bacterial communities [Fig. 2B]. The overlapping acidoneutral and alkaline samples in the PCoA  
196 illustrate the third cluster of samples, which is composed of the higher range of acidoneutral and  
197 alkaline samples. The multivariate analysis [table 1] further indicated that pH explained the largest  
198 variability ( $R^2=0.789$ ,  $p<0.001$ ) while site location accounted for only 5% ( $R^2=0.063$ ,  $p=0.001$ ) of the  
199 variance. Pearson's correlation coefficients identified positive and negative correlations between  
200 environmental variables [table S1]. The redundancy analysis [Fig. S2] also suggested that pH, amongst  
201 all explanatory variables, can most significantly explain the variation of bacterial communities'  
202 ordination and composition. This trend was consistent in pH binned samples (ANOSIM:  $|R| = 0.748$ ,  
203  $P < 0.001$ ; table S2); further confirming pH accounted for the observed variations in community  
204 composition.



205 In the literature, alkaline soils are consistently identified as pH>7 (Clark and Baligar, 2000; Rousk et al.,  
206 2010) while the differentiation between acidoneutral and acidic soils is less distinct, and as such, we  
207 based the cut-off on the study by Gubry-Rangin et al. (2011), which showed ecological clustering of  
208 archaeal ammonia oxidizers within these pH categories.

### 209 ***Abundant taxa diversity by pH range***

210 The characterisation of bacterial communities across pH ranges identified clear differences. The  
211 observed richness and Shannon diversity index were significantly lower in acidic samples than in  
212 acidoneutral and alkaline soils [Fig. S3], which were not significantly different from each other [table  
213 S3]. At the phylum level [Fig. 3A], the main differences observed were the increase in Acidobacteria  
214 from 22% in acidic to 33% in acidoneutral and 42% in alkaline soils, along with a decrease in  
215 Actinobacteria, from 17% in acidic soils, to 8% in acidoneutral and less than 5% in alkaline samples.  
216 We also observed a drop in Verrucomicrobia from 25% in acidic and acidoneutral soils, to 16% in  
217 alkaline samples, along with changes in Chloroflexi, Bacteroidetes, Gemmatimonadetes and  
218 Planctomycetes. The abundance of Proteobacteria remained relatively stable across the gradient, with  
219 a slight drop from 21% to 18% in acidoneutral soils. At the class level [Fig. 3B], the differences in  
220 bacterial communities appeared more clearly, with large differences in presence, absence and relative  
221 abundance of certain classes [Fig. 3B]. For instance, acidoneutral and alkaline soils harboured high  
222 proportions of *Blastocatellaceae* (17% and 27% respectively) while they represented 1.39% in acidic  
223 soils. Acidic soils had a higher diversity of Acidobacteria, which were dominated by Acidobacteria  
224 group 1 (8%) and Acidobacteria group 2 (5.7%). We could also observe the decrease in Acidobacteria  
225 group 6 from alkaline (10%) to acidic (2.3%) soils. A decrease in Actinobacteria (12% to 3%) and  
226 Thermoleophilia (4% to 1%) could be observed from acidic to alkaline soils. Similarly,  
227 Alphaproteobacteria and Gammaproteobacteria were identified in higher abundance in acidic soils,  
228 while Betaproteobacteria were more abundant in alkaline soils. Acidic soils also harboured some  
229 classes that could not be identified or only in very low abundances in other pH ranges. Notably, the

230 candidate *Methylacidiphilum* which composed over 7% of the acidic bacterial communities but was  
231 present in <0.5% in acidoneutral and <0.005% in alkaline soils. Overall, acidoneutral and alkaline soil  
232 bacterial communities showed similarities when considering OTUs with over 0.1% abundance.

### 233 ***Generalist vs specialist taxa***

234 The differentiation of specialist from generalist taxa associated with pH range was conducted by  
235 considering all phylotypes identified in this study and present in a minimum 95% of all samples from  
236 each pH category [Fig. 4]. 125 acidic specialist OTUs were identified and unique to acidic soil samples.  
237 Of these 125 unique OTUs, most belonged to the Acidobacteria (27%), Verrucomicrobia (20%),  
238 Actinobacteria (14%), Planctomycetes (14%) and Proteobacteria (14%). At the class level,  
239 Acidobacteria group 1 dominated at 14%, while the rest of the identified classes had balanced relative  
240 abundances oscillating between 5 and 8%. Shared OTUs, or generalists were present in low numbers  
241 in acidic soils. Only 12 OTUs were shared with acidoneutral soils only, which were dominated by  
242 Alphaproteobacteria (65%), mainly Rhizobiales, while 3 OTUs were shared with alkaline only,  
243 belonging to the Spartobacteria (Verrucomicrobia), Phycisphaerae (Planctomycetes) and  
244 Chitinophagia (Bacteroidetes). In comparison, acidoneutral soils had 76 shared taxa with alkaline soils,  
245 against 12 shared OTUs with acidic. Taxa shared with alkaline soils mainly identified as Blastocatellia  
246 (Acidobacteria), Spartobacteria and Acidobacteria subgroup 6. Taxa exclusively found in acidoneutral  
247 soils belonged mainly to Actinobacteria (20%), Verrucomicrobia (20%) and Acidobacteria (19%). At the  
248 class level, unique taxa living in acidoneutral soils were dominated by Spartobacteria,  
249 Alphaproteobacteria and Holophagae. Alkaline soils presented a combination of both, a high number  
250 of shared (79 OTUs in total) and 125 exclusive taxa. Alkaline unique taxa were mostly composed of  
251 Acidobacteria (36%) and Proteobacteria (22%). From these unique taxa, the Acidobacteria subgroup  
252 6 (20%), *Blastocatellia* (12%) and Alphaproteobacteria (12%) dominated the community.

### 253 ***Indicator species***

254 The indicator species analysis of dominant taxa (abundance > 0.1%) identified 17 taxon-habitat  
255 patterns of associations [table S4]. In acidic soils, 10 indicator species were identified, mainly  
256 Acidobacteria group 1 and 2 and the candidate Methyacidiphilum. The 6 OTUs associated with  
257 Acidoneutral soils were mainly Acidobacteria group 4 (Blastocatellia) and Spartobacteria  
258 (Verrucomicrobia). Finally, only 1 OTU was identified as indicator species for alkaline soils and  
259 belonged to the Holophagae. We also conducted the indicator species analysis of abundant taxa to  
260 combine pH ranges and identified 84 OTUs. 21 were identified as indicator species of acidic and  
261 acidoneutral soils combined, and mainly belonged to the Verrucomicrobia. Only 2 OTUs were  
262 associated with acidic and alkaline soils, Acidothermus (Actinobacteria) and Candidatus  
263 Xiphinematobacter (Verrucomicrobia), further illustrating the low overlap of taxa between these  
264 ecosystems. Finally, 61 OTUs were associated with acidoneutral and alkaline soils, mainly belonging  
265 to the Acidobacteria and Proteobacteria phyla.

#### 266 ***The Arctic soil core microbiome***

267 While some taxa displayed unique patterns of distribution, others were cosmopolitan and identified  
268 in over 95% of all sequenced samples. The core Arctic microbiome represented 0.026 % of bacterial  
269 communities and accounted for 2.77 % of all reads. It was composed of 13 OTUs, mainly  
270 Alphaproteobacteria and Acidobacteria, notably belonging to the *Rhizobiales* and *Acidobacteria* SD6  
271 orders (Fig. S4).

## 272 **Discussion**

### 273 ***The importance of pH***

274 The characterisation of soil bacterial communities on the Pan-Arctic scale and the investigation of the  
275 impact of environmental factors identified pH as explaining the most variation across bacterial  
276 communities. While TOC and moisture also explained some variation [table 1], Pearson's correlations  
277 of the physicochemical properties [table S2] indicated that both, moisture and TOC, were negatively  
278 correlated with pH and positively correlated with each other and thus, could not be used as sole

279 predictors of microbial communities. Furthermore, soil moisture is largely dependent on seasonal  
280 variations as soil moisture increases during snow melt, active layer thaw and precipitation events  
281 (Godin et al., 2016).

282 The identification of pH as the main factor influencing Arctic soil bacterial community composition is  
283 in line with previous Arctic studies, over both, small and large scales (Männistö et al., 2006; Ganzert  
284 et al., 2014; Siciliano et al., 2014; Schostag et al., 2015), including the study by Chu et al. (2010) which  
285 also investigated Pan-Arctic diversity by analysing 47 samples. While pH has been identified globally  
286 as a major factor influencing microbial diversity and community structure (Fierer and Jackson, 2006;  
287 Lauber et al., 2009; Tedersoo et al., 2014; Delgado-Baquerizo et al., 2018), the underlying processes  
288 and mechanisms by which it does remain unclear.

289 Studies have demonstrated that the soil pH is correlated with other elements of the geochemistry and  
290 has a strong impact on nutrient and water availability as well as solubility and adsorption. (Gray et al.,  
291 2014) For instance, acidic pH increases aluminium, hydrogen and manganese solubility, retarding  
292 plant root growth due to high toxicity (Clark and Baligar, 2000; Singh et al., 2017). Acidic soils also have  
293 nutrient deficiencies such as calcium, magnesium and potassium but also decreased phosphorus and  
294 molybdenum solubilities (Clark and Baligar, 2000; Gray et al., 2014). Alkaline soils are generally the  
295 result of low precipitation and high evapotranspiration, leading to low water availability and in  
296 common with acidic soils, nutrient deficiencies are found with, for instance, decreased phosphorus,  
297 iron, copper or zinc (Clark and Baligar, 2000). In similar ways, acidic and alkaline soils are generally  
298 considered harsh environments requiring a wide range of adaptations from microorganisms while  
299 acidoneutral soils are considered the optimum environment for microbial life (Fierer and Jackson,  
300 2006; Rousk et al., 2010); such differences in soil composition are likely responsible for the observed  
301 differences in microbial community composition by pH range.

302 We investigated soil bacterial communities (abundant and rare taxa) but focused descriptions and bar  
303 charts on the abundant bacterial taxa, which includes taxa with abundance > 0.1 % for ease of

304 visualisation. Rare taxa (< 0.1%) are characterized by Lynch and Neufeld (2015) as the rare biosphere  
305 and represent a large and diverse pool of taxa across the Arctic region. Rare microbes are a vast  
306 functional gene pool, which may be used by other microbes as a resource to respond to disturbance  
307 events or harsh environmental conditions and may play essential roles in ecosystem functioning,  
308 disproportionate to their abundance (Lynch and Neufeld, 2015; Jousset et al., 2017).

309 Dominant Arctic soil bacterial taxa appeared generally different from global diversity, as seen in  
310 Delgado-Baquerizo et al. (2018). Specifically, Verrucomicrobia were not clearly identified in the low  
311 pH cluster, and present in low abundance in the high pH cluster of global soils. In Arctic soils, they  
312 appeared dominant [Fig. 3A], with up to 25% in acidic soils. Proteobacteria consistently represented  
313 approximately 20% of communities, against almost 40% in global soils. Similarly, Acidobacteria  
314 comprised between 22% to 42% of Arctic soil communities, while only up to 15% in global soils. While  
315 there is likely an overlap of taxa between global and polar soils, Arctic bacterial communities seem to  
316 be dominated by different taxa than other biomes, likely reflecting the impact of polar environmental  
317 conditions on microbial communities. However, it should be noted that the differences of methods  
318 likely accounts for some of these differences, highlighting the need to include more Arctic samples in  
319 global studies to capture the full extent of worldwide soil microbial diversity.

### 320 ***Distribution of generalist and specialist taxa***

321 Microbial communities are assembled by deterministic (selection) and stochastic (dispersal)  
322 processes. It has been hypothesized that communities primarily structured by deterministic processes  
323 will host more specialist taxa, highly adapted to the ecosystem, while communities influenced by  
324 dispersal will harbour primarily generalist taxa, more resilient to change (Pandit et al., 2009; Graham  
325 and Stegen, 2017; Sriswasdi et al., 2017). While specialist taxa are restricted to certain habitats, they  
326 can be locally abundant; shared taxa, or generalists, are distributed across many habitats (Barberán  
327 et al., 2012). In most cases specialist are more abundant because generalists rapidly become  
328 specialists to adapt to their ecosystems, despite generalists having evolutionary advantages (Sriswasdi

329 et al., 2017). By identifying specialist and generalist taxa, we can speculate about the dominant  
330 processes structuring microbial communities, providing hypotheses for future studies.

331 In this study, bacterial communities changed from specialist-dominated in acidic soils, to generalist-  
332 dominated in acidoneutral, to a mixed community in alkaline samples. The higher abundance of  
333 specialists in acidic soils (considered the harshest systems) illustrates the need for environmental  
334 adaptations to survive in these ecosystems and suggests that deterministic processes likely structure  
335 microbial communities. Geographically, the first cluster identified by the Bray-Curtis dissimilarity  
336 matrix [Fig. 2] grouped all acidic samples from northern Norway, western Greenland and Alaska,  
337 illustrating the similarities of their bacterial communities despite the large distances separating these  
338 locations, further suggesting the strong influence of selection over dispersal. The dominance of  
339 generalists in acidoneutral soils illustrates the lower environmental pressure to have specific survival  
340 adaptations and infers the dominance of stochastic processes in community structuring. Eastern  
341 Greenland, Svalbard and Iceland were grouped together by the Bray-Curtis dissimilarity matrix.  
342 Geographically, these locations are influenced by the East Greenland current, East Icelandic current,  
343 Jan Mayen current, and West Spitzbergen currents, all connected through the Greenland sea and  
344 possible routes of dispersal, in addition to possible Aeolian dispersal. Finally, alkaline soils hosted a  
345 mixed-community of specialists and generalists, suggesting the combination of both, selection and  
346 dispersal, in community structuring. The abundance of generalist taxa in alkaline soils, generally  
347 considered a harsh system in many ways similar to acidic soils, highlights the adaptability of generalists  
348 to a wide range of environmental conditions. Interestingly, the Bray-Curtis dissimilarity matrix  
349 clustered the Canadian (alkaline) and Russian (acidoneutral) samples together. The Russian samples  
350 were on the higher end of the acidoneutral pH scale and the grouping of these samples illustrates the  
351 blurred boundary between acidoneutral and alkaline pH categories. While environmental selection  
352 may be driven by many variables, dispersal could occur via the Yukon current, the Beaufort gyre,  
353 aeolian dispersal and possibly winter sea ice.

354 ***Identification of indicator species***

355 The indicator species analysis determined OTU-pH range associations identifying different classes of  
356 Acidobacteria and Verrucomicrobia, primarily, characteristic of each pH range. The identification of  
357 abundant indicator species with strong habitat associations opens the possibility of predicting the  
358 presence and relative abundance of these taxa across the Arctic region. This is especially important  
359 for taxa such as *Ca. Methylacidiphilum*, a known methanotroph unlike others as it belongs to the  
360 Verrucomicrobia phylum instead of the Proteobacteria (Dunfield et al., 2007; Khadem et al., 2010).  
361 The high abundance of these phylotypes in acidic soils suggest that they may might play major roles  
362 in CH<sub>4</sub> uptake, thus limiting methane release to the atmosphere. While natural CH<sub>4</sub> emissions come  
363 primarily from wetlands, the identification of these phylotypes in acidic soils suggests wetland may  
364 not be the only major source of northern methane emissions. Northern latitudes are estimated to  
365 support over 53% of all wetlands (Aselmann and Crutzen, 1989) but estimations of CH<sub>4</sub> emissions from  
366 northern wetlands can vary drastically, from 18 to 120 Tg CH<sub>4</sub> yr<sup>-1</sup> (Petrescu et al., 2010) and the rates  
367 and impact of methanotrophy on CH<sub>4</sub> emissions are difficult to assess (Jørgensen et al., 2015).  
368 Understanding the distribution and abundance of such taxa, combined with field gas measurements  
369 may allow large-scale estimates of methanotrophic rates in the region, from soils and wetlands  
370 (Wartiainen et al., 2006; Jørgensen et al., 2015). In addition to the uptake of CH<sub>4</sub>, *Ca.*  
371 *Methylacidiphilum* is also able to fix N<sub>2</sub>, illustrating the essential role of this class not only in the carbon  
372 cycle but also in the nitrogen cycle (Khadem et al., 2010).

373 ***Arctic soil core microbiome***

374 The scale of this study led to the identification of the Arctic core microbiome, composed of 13 OTUs  
375 only. The most abundant of these taxa belonged to the *Bradyrhizobiaceae* family. This is one of the  
376 most common families worldwide, as identified by Delgado-Baquerizo et al. (2018), for which most  
377 species are plant-associated bacteria. The identification of a core Arctic soil microbiome is novel and  
378 this low number of cosmopolitan OTUs illustrates the low microbial ubiquity in the region.

379 **Concluding remarks**

380 To our knowledge, this is the first Pan-Arctic soil study with this scale and diversity of samples. Here,  
381 we focused on bacterial communities but there is a lack of understanding for archaeal, fungal, viral  
382 and eukaryotic communities in the region as well. We also focused our investigations on variables  
383 known to influence global bacterial communities, however, it is likely that nutrient concentration,  
384 metal content and other factors participate in the structuring of microbial assemblages in the region,  
385 on different scales and magnitudes. By conducting a large Pan-Arctic survey of bacterial communities  
386 of Arctic soils and associated environmental variables, we identified pH as the main factor structuring  
387 these communities, emphasising the need to investigate the underlying mechanisms and processes  
388 by which pH directly or indirectly influences microbial communities. We also highlighted differences  
389 between Arctic soil communities and global communities, further suggesting the impact of Polar  
390 environmental conditions on prokaryotes. The investigation of specialist and generalist taxa  
391 highlighted the possible role of geographical dispersal across the region, which may be more  
392 important in acidoneutral soils dominated by generalist taxa. Finally, we identified the Arctic core  
393 microbiome, composed of only 13 OTUs across the entire region. While this study brings a deeper  
394 understanding of Arctic bacterial community assemblages, this is also a baseline for future functional  
395 studies in the region, which will be critical to forecast the ecological consequences of environmental  
396 change.

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402 sequencing service (Northumbria University).

403 **Conflict of interest**



404 The authors report no conflict of interests.

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559 **Figures and tables**

560



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562 Figure 1: Map of sampling sites. A total of 200 soil samples in 43 different sites were collected for  
563 this study.

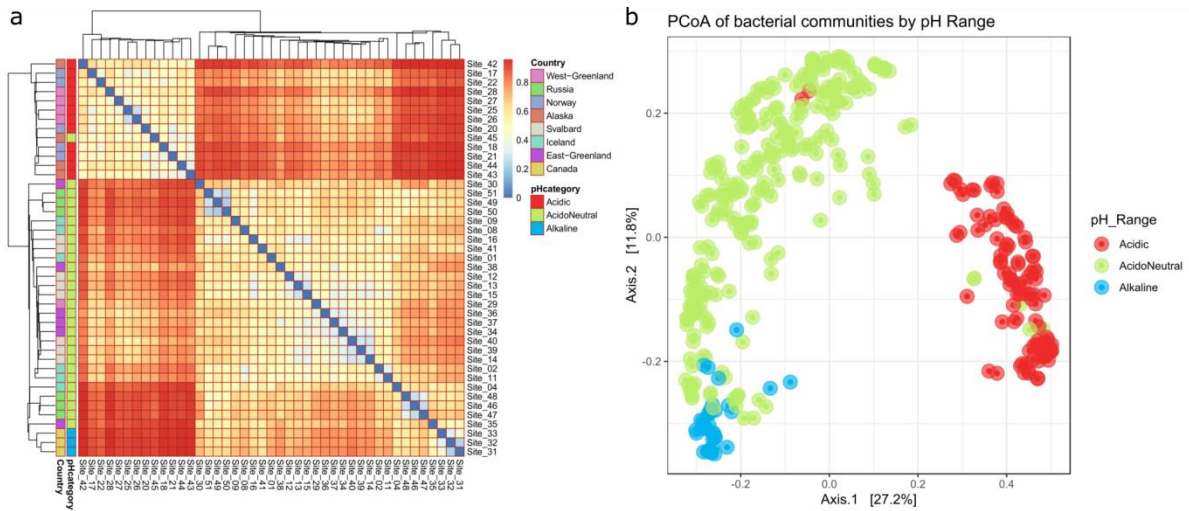
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570 Figure 2A: Bray-Curtis dissimilarity matrix by sampling site. Each site was composed of 3 to 5 soil  
 571 samples for which DNA extracted and sequenced in duplicates. In this analysis, all sequenced samples  
 572 within a site were combined for ease of visualisation, and only the dominant pH category was  
 573 displayed. Figure 2B: PCoA of microbial communities. Samples were individually considered to  
 574 conserve accurate clustering.

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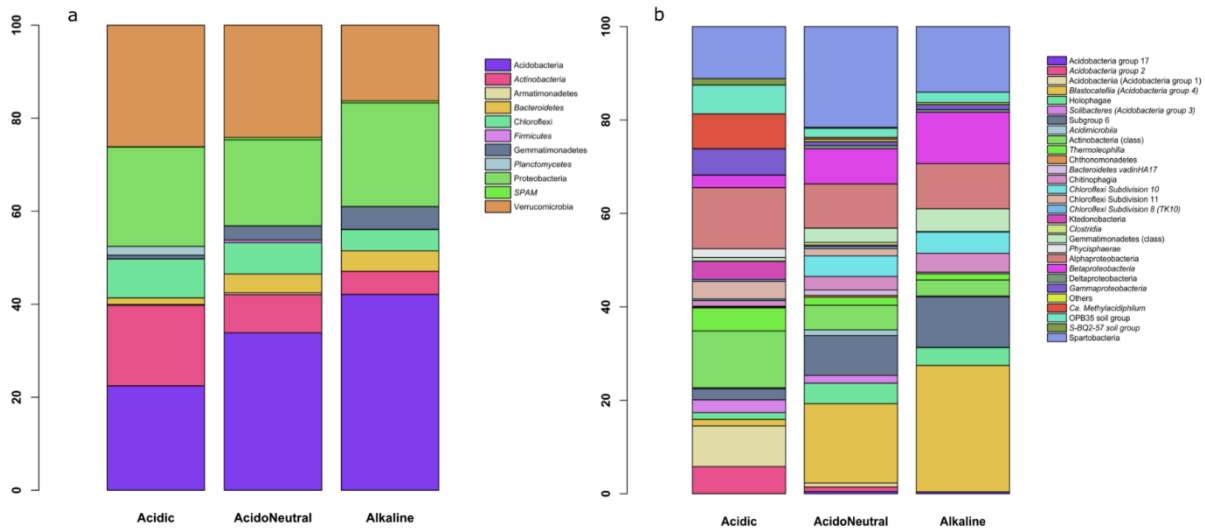
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584 Figure 3A: Relative abundance of bacterial phyla with abundances over 0.1%, by pH range. Figure 3B:

585 Relative abundance of bacterial classes with abundances over 0.1%, by pH range.

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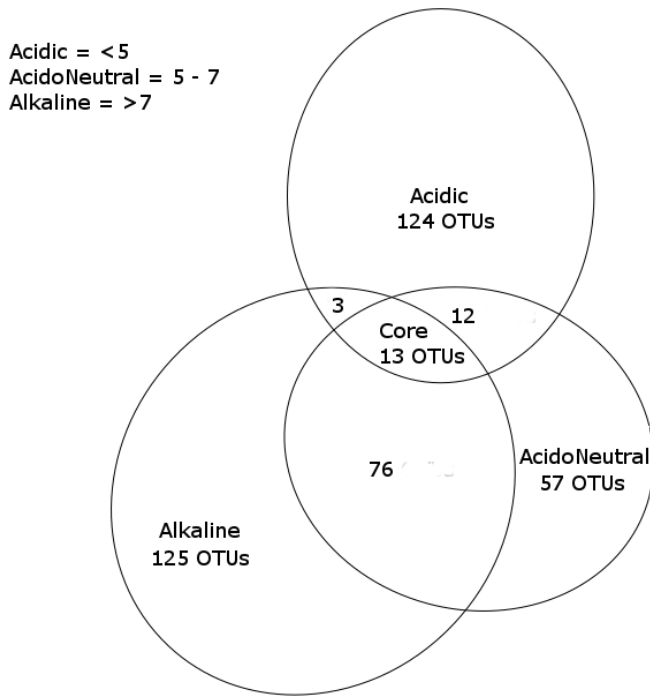
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596 Figure 4: Venn diagram of unique (specialists) and shared (generalists) OTUs by pH range. Only OTUs  
597 present in at least 95% of samples for each category are taken into account.

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600 Table 1: MetaMDS results of the influence of environmental variables on bacterial communities.  
601 NMDS1 and NMDS2 illustrate the nature of the correlation between environmental variables and  
602 bacterial communities. R<sup>2</sup> indicates the percentage of variance explained by each variable and Pr  
603 indicates the significance of the results.

Explanatory variable	NMDS1	NMDS2	r <sup>2</sup>	Pr(>r)
Site	-0.180	0.984	0.063	0.001***
pH	-0.883	-0.470	0.789	0.001***
Conductivity	-0.825	-0.565	0.080	0.001***
Moisture	0.452	0.892	0.384	0.001***
TOC	0.840	0.542	0.469	0.001***

604 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

605 Permutation: free

606 Number of permutations: 999

607