Plant and Bird Presence Strongly Influences the Microbial Communities in Soils of Admiralty Bay, Maritime Antarctica

Lia C. R. S. Teixeira1, Etienne Yeargeau2, Fabiano C. Balieiro3, Marisa C. Piccolo4, Raquel S. Peixoto1, Charles W. Greer2, Alexandre S. Rosado1*

1 Laboratório de Ecologia Microbiana Molecular, Instituto de Microbiologia Paulo de Góes, Universidade Federal do Rio de Janeiro, Rio de Janeiro, RJ, Brasil, 2 Biotechnology Research Institute, National Research Council of Canada, Montréal, QC, Canada, 3 Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA) solos, Rio de Janeiro, RJ, Brasil, 4 Laboratório de Ciclagem de Nutrientes, Centro de Energia Nuclear na Agricultura, Universidade de São Paulo, SP, Brasil

Abstract

Understanding the environmental factors that shape microbial communities is crucial, especially in extreme environments, like Antarctica. Two main forces were reported to influence Antarctic soil microbes: birds and plants. Both birds and plants are currently undergoing relatively large changes in their distribution and abundance due to global warming. However, we need to clearly understand the relationship between plants, birds and soil microorganisms. We therefore collected rhizosphere and bulk soils from six different sampling sites subjected to different levels of bird influence and colonized by Colobanthus quitensis and Deschampsia antarctica in Admiralty Bay, King George Island, Maritime Antarctic. Microarray and qPCR assays targeting 16S rRNA genes of specific taxa were used to assess microbial community structure, composition and abundance and analyzed with a range of soil physico-chemical parameters. The results indicated significant rhizosphere effects in four out of the six sites, including areas with different levels of bird influence. Acidobacteria were significantly more abundant in soils with little bird influence (low nitrogen) and in bulk soil. In contrast, Actinobacteria were significantly more abundant in the rhizosphere of both plant species. At two of the sampling sites under strong bird influence (penguin colonies), Firmicutes were significantly more abundant in D. antarctica rhizosphere but not in C. quitensis rhizosphere. The Firmicutes were also positively and significantly correlated to the nitrogen concentrations in the soil. We conclude that the microbial communities in Antarctic soils are driven both by bird and plants, and that the effect is taxa-specific.

Introduction

Deschampsia antarctica Desv. (Poaceae) and Colobanthus quitensis (Kunth) Barhl. (Caryophyllaceae) are the only two native vascular plants in Antarctica. Both species are widespread, usually growing together and well adapted for life in the coastal Maritime Antarctic [1]. A considerable increase in distribution and abundance of D. antarctica and C. quitensis in the western Antarctic has been reported and interpreted as a response to more favorable growing and reproductive conditions [2]. In some locations, the annual average temperature has increased by more than 1°C in the last 30–50 years [3]. In the Maritime Antarctic region, this increase in temperature has led to the thaw of glaciers, that exposed new areas of land [3], which could further increase the distribution of vascular plants [4].

Through root exudation, plants produce a variety of chemical compounds that may be used by soil bacteria for energy and biomass production [5]. Several authors have reported that this interaction selects for specific microbial communities in the rhizosphere, the portion of soil that is directly influenced by roots, producing the “rhizosphere effect” [6–8]. However, there is also strong evidence that soil type could have a more determinant role in shaping the microbial communities than the plant [9,10]. Similarly, a recent study showed, using 16S rRNA gene pyrosequencing, that the microbial communities associated with the rhizospheres of D. antarctica and C. quitensis did not differ significantly [11]. However, this study did not compare bulk and rhizosphere soil, and it is thus still not known what level of influence vascular plants exert on Antarctic soil microorganisms.

In the Maritime Antarctic, densely vegetated sites are often related to bird activities [12]. Organic matter rich in carbon, nitrogen and phosphorus is added to the soil in the form of guano, feathers, eggs and birds remains which leads to the formation of orthornogenic soils [4]. These soils can occur at active or abandoned penguin colonies, but also nearby rookeries of other large birds (e.g. skuas, petrels). Birds not only change soil conditions for microbial life, they also inoculate microorganisms through guano deposition, and the composition of this guano
seems to be influenced by penguin diet. Several studies reported *Firmicutes* 16S rRNA gene sequences related to ornithogenic soils [4,11,13] and, accordingly, Zdanowski and colleagues [14] isolated *Gammaproteobacteria*, *Firmicutes*, *Actinobacteria*, and *Bacteroidetes* from Adelie penguin guano.

Recent studies have provided a baseline knowledge of the microbial communities in terrestrial Antarctic environments [4,11,13,15–19]. For instance, the phylum-diversity in Admiralty Bay rhizosphere soils was much higher than previously reported, with the phyla *Firmicutes* and *Actinobacteria* representing more than 70% of the total community [11]. In contrast, along a latitudinal transect in the Maritime Antarctic, bacterial communities were dominated by the phyla *Proteobacteria*, *Actinobacteria*, *Bacteroidetes*, *Acidobacteria* and *Cyanobacteria*, with a strong influence of the vegetation cover, highlighting the potential for indirect effects of global warming on Antarctic soils [19]. In a recent report, *Acidobacteria*, *Bacteroidetes*, *Proteobacteria* and *Firmicutes* were the main phyla recovered in nine different soils of Livingston Island, Maritime Antarctic [20]. In soils from the Ross Sea region, Continental Antarctic, the dominant bacteria were related to the *Acidobacteria*, *Actinobacteria*, *Bacteroidetes*, *Proteobacteria* and *Firmicutes* [3].

Global warming is currently affecting both plant [2] and bird distribution and activity in Antarctica [21] and can also influence the activity of the microbial communities [18]. In view of the strong influence birds and vascular plants have on Antarctic soil microorganisms, it is crucial to understand this relationship in order to better predict any indirect effects global warming might have on soil microorganisms. In this paper we focus on the differences between community structure and composition at the phyla/class levels in *D. antarctica* and *C. quitensis* rhizosphere and in bulk soils from six different sampling sites around Admiralty Bay, King George Island, Maritime Antarctic. Soils with different levels of bird influence were compared to adjacent rhizosphere soils using 16S rRNA gene microarrays and phylum/class-specific quantitative PCR genes and the resulting patterns were analyzed together with soil physico-chemical parameters.

**Materials and Methods**

**Ethics Statement**

All necessary permits were obtained for the described field studies, from the Brazilian Antarctic Program, PROANTAR, as part of the IPY (International Polar Year) Activity # 403 and MMA (Brazilian Ministry of Environment).

**Sampling Site and DNA Extraction**

The study was carried out at the Brazilian Antarctic Station Comandante Ferraz (EACF, 62°04’S, 58°21’W), located in Martel Inlet, Admiralty Bay, King George Island, Antarctic Peninsula, which is part of the South Shetlands Archipelago in Maritime Antarctica. During the austral summers of 2006–2007 and 2008–2009, the vascular plants *D. antarctica* or *C. quitensis* were sampled, where both plants were found, in triplicate at six different sites: A – Arctowski (E: 423.807/N: 3.106.863–2006–2007), Q – Quimica (E: 427.335/N: 3.115.506–2006–2007), I – Ipanema (E: 426.570/N: 3.116.513–2006–2007), M – North Mountain (E: 426.63/N: 3.116.567–2008–2009), D – Demary Point (E: 425.102/N: 3.100.854–2008–2009), C – Copacobana (E: 424.706/N: 3.105.149–2008–2009). *Colobanthus quitensis* were not found at points C and M. Points A, C and D were located inside an environmental protected area. Point A is close to the Arctowski Polish Station and next to a colony of Adelie penguins (*Pygoscelis adeliae*), point C is next to the USA summer station Copacobana in a Gentoo penguin (*P. papua*) colony, and point D is near to a Polish refuge next to a colony of Chinstrap penguins (*P. antarcticus*). At point I, there were no penguin colonies present, but this section was used as a nesting site by local species of flying birds. Point Q was located in the vicinity of the EACF; thus there has been (and continues to be) an intense anthropogenic influence on this spot, which is not the case at the other sampling sites. Besides, there is a transient presence of birds. Point M was located at the top of North Mountain, around 200 m altitude. This site has no influence from penguin colonies and only a few nests of skua (Catharacta sp.) were observed.

At each sampling site, triplicate soil samples (500 g of surface soil cores, 0–5 cm) were taken for chemical and biological analyses, with the exception of the Arctowski site (A) where we only take two replicates. Soil samples were preserved at 4 °C for chemical and at −20 °C for biological analyses. The plants occur in the same area, not necessarily growing one next to the other. Furthermore, we collected rhizosphere soil from isolated plant roots. Each vascular plant sample was frozen (−20 °C) at the EACF. To assess the bacterial communities associated with the rhizospheres of both vascular plants, 5 g of the roots with aggregated soil was shaken in a 45 mL of saline solution (NaCl 0.85%) for 2 hours. Then, the supernatant (without roots) was centrifuged for 10 minutes at 9,000 rpm, and 0.5 g of the pellet was used for DNA extraction using the Fast DNA Spin Kit for soil (QBiogene, Carlsbad, CA) following the manufacturer’s instructions. For the bulk soil, 0.5 g of each sample was used for the extractions also using the Fast DNA Spin Kit. The extracted DNA was quantified by fluorometric analysis and the integrity was assessed by gel electrophoresis. The DNA samples were used for the 16S rRNA gene-mediated phylogenetic analysis.
DNA was quantified using the PicoGreen® dsDNA quantitation assay (Invitrogen, Carlsbad, CA). The integrity of the DNA extracted from the soils was confirmed by electrophoresis on a 0.8% agarose gel in 0.5x TBE buffer (45 mM Tris–borate, 1 mM EDTA, pH 8.0).

### Soil Analysis

Chemical analyses on air dried, sieved (2 mm) subsamples of bulk soil samples were performed. A single subsample/replicate was used for the following analyses. Exchangeable cations: Ca$^{2+}$, Mg$^{2+}$ and Al$^{3+}$ extracted in 1 M KCl; P, Na and K by Mehlich-1 extractant (HCl 0.05 mol L$^{-1}$ and H2SO4 0.0125 mol L$^{-1}$) and pH (soil: water, 1:10); Potential acidity: H$^+$ extracted with 1 N calcium acetate (pH 7), titrated with 0.0125 N NaOH N, were analysed according to [22]. Inductively coupled Plasma apparatus for Ca$^{2+}$, Mg$^{2+}$ and Al$^{3+}$, flame emission (K and Na) and photocolometry (for P) were used for nutrient determinations. Total organic C was determined by wet combustion [23].

For the nitrogen quantification, all the bulk soils replicates were analyzed. Mineral nitrogen forms were first extracted from the soil samples with a KCl (2N) solution. The ammonium (NH$_4^+$) and nitrate (NO$_3^-$) contents in the extracts were determined by use of an automatic flow injection (FIA) analysis system. The ammonium (NH$_4^+$) was quantified colorimetrically using the Solorzano method [24], and the nitrate (NO$_3^-$) estimated by conductivity. The temperature profile included an initial denaturation step at 94°C for 5 min, 35 cycles of a denaturation step at 94°C for 30 s, a primer annealing step at 50°C for 30 s and an extension step at 72°C for 45 s, followed by a final step of 7 min at 72°C. PCR products were purified using the PureLink™ PCR purification Kit (Invitrogen Canada, Burlington, Ontario, CA), 1.5 mM MgCl$_2$, 2.5 U of Taq DNA polymerase (Fermentas), 0.2 mM of each dNTP and sterile filtered water to a final volume of 50 µl. The final volume included an initial denaturation step at 94°C for 5 min, 35 cycles of a denaturation step at 94°C for 30 s, a primer annealing step at 50°C for 30 s and an extension step at 72°C for 45 s, followed by a final step of 7 min at 72°C. PCR products were purified using the PureLink™ PCR purification Kit (Invitrogen Canada, Burlington, Ontario, CA). A microarray platform targeting the 16S rRNA genes of Bacteria and Archaea found in cold environments was used as previously described [31]. To summarize, the purified 16S rRNA genes were chemically labeled with Cy5 and hybridized overnight onto the microarray. Details about the microarray and probe design are available at the National Center for Biotechnology Information (NCBI) GEO database under the platform accession number GPL3953. The presence-absence of the different Bacteria and Archaea targeted by the microarray was used as community profile to evaluate the similarity between the bulk soil and rhizosphere samples from the six different sampling sites. Microarray data discussed here have been deposited in NCBI GEO and are accessible through GEO series accession no. GSE33847.

### Statistical Analyses

All statistical analyses were performed in R (version 2.9.0, The R Foundation for Statistical Computing). For analysis of variance (ANOVA) of the qPCR data, normality was tested using the “shapiro.test” function and homoscedasticity was tested using the “bartlett.test” function. When necessary, data were log transformed to meet parametric ANOVA assumptions. ANOVA and post hoc Tukey HSD tests were then carried out using the “aov” and “TukeyHSD” functions, respectively. When transformations of the qPCR data were required, no-template controls were carried out and yielded no detectable signals. Lambda DNA was used to correct for potential PCR inhibitors present in soil extracts [29]. Equal volumes of 10-fold diluted soil DNA extract and of a cloned 500-bp fragment of bacteriophage lambda (10$^5$ copies per µl) were mixed. When the recovery of lambda was below 100%, quantification values for all other genes were corrected accordingly.
Figure 1. Rhizosphere effect on microbial community structure and relative abundance. Principal coordinate analysis calculated based on the microarray results for each sampling site separately. Only presence or absence of the probes was considered. All the replicates are represented in the figures. Red dots represent Colobanthus quitensis; Green dots represent Deschampsia antarctica; and yellow dots represent bulk soil samples. Insets: relative abundance of the main bacterial phyla quantified by qPCR. An average of the qPCR triplicates results of each sample is presented. doi:10.1371/journal.pone.0066109.g001
failed to normalize data, Kruskal-Wallis and associated multiple comparison tests were performed using “kruskal.test” and the “kruskalme” functions of the “pgirmess” library, respectively. Spearman linear correlation analyses (correlations on qPCR vs. soil data) were performed using the “cor.test” function. For the microarray analysis, distance matrices were calculated using the “vegas” function of the “vegan” library and principal coordinate analyses (PCoA) were carried out using the “cmdscale” function based on the square root of 1-Jaccard. PerMANOVA [32] of microarray data was carried out on Jaccard similarity, testing for significant differences between bulk soil and rhizosphere samples at each sampling site separately (Table 4). For each sampling site at least one phylum showed significantly different abundances between bulk soil and rhizosphere samples. For instance, the Firmicutes were significantly more abundant in the bulk soil samples than in the rhizosphere samples for the A, C, D and M sites (Fig. 1, Table 4). Similarly, the Acidobacteria were significantly more abundant in the bulk soil samples than in the rhizosphere samples for the Q, I and M sampling sites (Fig. 1, Table 4). The Actinobacteria showed an opposite trend, being significantly more abundant in the rhizosphere samples for the Q and M sites (Fig. 1, Table 4).

| Table 3. Test for significant difference between rhizosphere soils and bulk soil using PerMANOVA for all the different sites (microarray data). |
|---------------------------------------------------------------|
| **Arctowski** | **Copa Cabana** | **Demay Point** | **Ipanema** | **N. Mountain** | **Quimica** |
| **F** | 0.6335 | 0.7203 | 0.3024 | 0.4809 | 0.411 | 0.4224 |
| **P** | 1.00E-04 | 0.0465 | 0.2129 | 0.0095 | 0.0779 | 0.0325 |

Significant values (P<0.05) are in boldface.

Results

Soil Characteristics

The three sites located in penguin colonies (A, C and D) had similar soil chemical characteristics, with low pH and high bioavailability of P (Table 2). The two other sites under the influence of birds (Q and I) also had high values of organic C and P, but only a moderate pH. The site, which was not directly under the influence of birds, had the highest pH value (8.2), exchangeable Ca and S, but the lowest value for P. The nitrogen concentrations (NH₄⁺ and NO₃⁻) were very high for the sites under the influence of penguins, very low in the sites under the influence of other birds (Q and I) and below the detection limit for the M site. For all sampling sites NH₄⁺ values were higher than NO₃⁻ values. Site C had nitrogen values similar to the other sites under the influence of penguins, but lower values of exchangeable Ca and Mg.

Rhizosphere vs. Bulk Soil

A microarray targeting the 16S rRNA genes of microorganisms frequently found in cold environments consisting of 525 25-mer oligonucleotides targeting 159 bacterial and archaeal taxa was used to compare bulk soil and rhizosphere samples. Out of these 159 taxa, 13 to 41 taxa were detected per sample. Principal coordinate analyses of the microarray results for bulk soil and rhizosphere samples were made separately for each sampling site (Fig. 1). Figure 1 shows a clear separation of the bacterial communities from bulk soil and rhizosphere at most sites with the exception of the D and M sites. This visual interpretation was confirmed by PerMANOVA analyses that tested for significant differences between bulk soil and rhizosphere samples at each sampling site separately (Table 3). No clear differences between the microbial communities of the rhizosphere of C. quitensis and D. antarctica were detected for most sampling sites, with the exception of the A site where it was possible to see a clear segregation between the microbial communities associated with the rhizosphere of the two plant species (Fig. 1).

The microbial communities of different sites around Admiralty Bay were compared (Figs 2a and 2b). According to the qPCR results, Actinobacteria was the most abundant phylum, followed by the Proteobacteria (Epsilon-, Gamma-, Beta- and Alpha) and the Firmicutes when considering all samples together. In the bulk soils from sites I, Q and M, Acidobacteria was also abundant (Fig. 2b). ANOVA analyses of the qPCR results were also made in order to compare rhizosphere and bulk soil samples at each of the six sampling sites separately (Table 4). For each sampling site at least one phylum showed significantly different abundances between bulk soil and rhizosphere samples. For instance, the Firmicutes were significantly more abundant in the bulk soil samples than in the rhizosphere samples for the A, C, D and M sites (Fig. 1, Table 4). Similarly, the Acidobacteria were significantly more abundant in the bulk soil than in the rhizosphere samples for the Q, I and M sampling sites (Fig. 1, Table 4). The Actinobacteria showed an opposite trend, being significantly more abundant in the rhizosphere samples for the Q and M sites (Fig. 1, Table 4).

Differences between Sites

A PCoA analysis was also carried out using only the microarray profiles of bulk soils in order to compare the general microbial community at different sites around Admiralty Bay (Fig. 2a). Replicate samples from a site clustered together in most cases, and differences were seen between most of the sites. PerMANOVA analyses confirmed that there were significant differences between the microbial community structures of different sites (F = 6.87, P = 0.0001). Samples from sites A and D grouped together (with the exception of one site D replicate), while samples from sites Q and I also grouped together. Samples from sites C and M were unusual and did not clearly group with any samples from the other sites. According to ANOVA analyses (Table 5), Acidobacteria abundance was significantly higher at the M site and significantly lower at the C site. In contrast, the M site showed significantly lower abundance of Actinobacteria compared to all other sites (Fig. 2b). The Bacteroidetes phyla were significantly more abundant at the C site compared to most other sites. The Alphaproteobacteria were significantly more abundant at the I site and the Gammaproteobacteria were significantly less abundant in the Q site compared to the C and D sites. Epsilonproteobacteria had no difference among the bulk soils samples. Betaproteobacteria seems to vary among samples, especially comparing sampling points A and M to the other sampling points (D, C, Q and I), where this group was more representative.

The statistical correlations between the soil physical and chemical composition and measured microbial communities were performed, but gave no significant result for most soil abiotic characteristics (data not shown). Only NH₄ and NO₃ presented some correlation. In order to check the relationship between...
nitrogen and soil bacterial communities in Admiralty Bay, correlation analyses were carried out (Fig. 3). Using the Spearman coefficient, we found a significantly positive correlation between the Actinobacteria and the Firmicutes and the ammonia concentrations in soil (Fig. 3). A significantly negative correlation was found between the Acidobacteria and the Alphaproteobacteria and ammonia concentration. Acidobacteria and Alphaproteobacteria were also significantly and negatively correlated with nitrate concentration. For all the other bacterial groups-nitrogen concentration combinations, no significant correlations were found. We also carried out PermANOVA analyses on the microarray dataset using NH$_4^+$ and NO$_3^-$ as explanatory variables and found that the microbial community structure in bulk soil was significantly influenced by NH$_4^+$ (F = 4.04, P = 0.0009) and NO$_3^-$ (F = 3.30, P = 0.0064).

**Discussion**

Our results showed that both plant and bird presence had significant influences on microbial community structure and on the relative abundance of several major bacterial taxa. The presence of birds was related to higher soil nitrogen concentra-
tions, which was identified as significantly correlated with the abundance of several bacterial groups and as significantly influencing the microbial community structure. In the case of plants, it appeared that the effect observed was a general rhizosphere effect, as very little difference was seen between the rhizosphere of the two vascular plants sampled, in line with previous reports [11].

Influence of Birds
As expected, we observed a strong relationship between microbial communities and soil characteristics, but we could not disentangle the effect of nutrient availability from any pH-related effect, as the sites with high nitrogen and phosphorus concentrations had also the lowest pH values. These characteristics are typical of ornithogenic soils as bird guano, feathers, eggshells and remains are rich in nitrogen and phosphorus [4]. In the Maritime Antarctic, densely vegetated sites covered by lichens, mosses and vascular plants are often related to bird activity [12]. The influence of birds in the development of Antarctic soils can occur at different levels. According to Simas and colleagues [34] the presence of flying birds, such as skuas (Catharacta sp), giant-petrels (Macronectes sp) and seagulls (Larus sp), leads to the development of weakly ornithogenic soils (moderately high N and P concentrations, slightly acidic pH) while the presence of penguin colonies leads to highly ornithogenic soils (very high N and P concentrations and acidic pH). Based on the results from our soil analyses and from previous studies of Admiralty Bay soils [12,34,35], we can roughly classified the soils from our sampling sites as follows: soils from sites A, C and D would be highly ornithogenic soils, soils from sites I and Q would be weakly ornithogenic soils and soil from site M

| Table 4. Anova analysis to test the differences in the phyla abundance (qPCR) between bulk soils and rhizospheres from the same sampling site. |
|---------------------------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|
| Quimica                                     | Groups          | Gamma           | Firm            | Alpha           | Acido           | Actino          | Bacteroi        | Beta            | Epsilon         |
| P-value                                     | 0.718           | 0.075           | 0.504           | 0.002           | 0.013           | 0.288           | 0.064           | 0.216           |
| Soil                                        | a               | a               | a               | b               | b               | a               | a               | a               | a               |
| Colobanthus                                 | a               | a               | a               | a               | a               | a               | a               | a               | a               |
| Deschampsia                                 | a               | a               | a               | a               | a               | a               | a               | a               | a               |
| Demay                                       | Groups          | Gamma           | Firm            | Alpha           | Acido           | Actino          | Bacteroi        | Beta            | Epsilon         |
| P-value                                     | 0.803           | 0.035           | 0.101           | 0.070           | 0.242           | 0.945           | 0.750           | 0.398           |
| Soil                                        | a               | b               | a               | a               | a               | a               | a               | a               | a               |
| Colobanthus                                 | a               | a               | a               | a               | a               | a               | a               | a               | a               |
| Deschampsia                                 | a               | ab              | a               | a               | a               | a               | a               | a               | a               |
| Copacabana                                  | Groups          | Gamma           | Firm            | Alpha           | Acido           | Actino          | Bacteroi        | Beta            | Epsilon         |
| P-value                                     | 0.510           | 0.014           | 0.100           | 0.011           | 0.099           | 0.001           | 0.567           | 0.022           |
| Soil                                        | a               | a               | a               | a               | a               | a               | a               | a               | a               |
| Deschampsia                                 | a               | b               | a               | b               | a               | b               | a               | b               | a               |
| N. Mountain                                 | Groups          | Gamma           | Firm            | Alpha           | Acido           | Actino          | Bacteroi        | Beta            | Epsilon         |
| P-value                                     | 0.0007          | 0.002           | 0.523           | 0.0004          | 0.003           | 0.203           | 0.179           | 0.373           |
| Soil                                        | a               | a               | a               | a               | a               | a               | a               | a               | a               |
| Deschampsia                                 | b               | b               | a               | b               | b               | a               | a               | a               | a               |
| Ipanema                                     | Groups          | Gamma           | Firm            | Alpha           | Acido           | Actino          | Bacteroi        | Beta            | Epsilon         |
| P-value                                     | 0.151           | 0.716           | 0.723           | 0.0007          | 0.117           | 0.013           | 0.660           | 0.428           |
| Soil                                        | a               | a               | a               | b               | a               | b               | a               | a               | a               |
| Colobanthus                                 | a               | a               | a               | a               | a               | a               | a               | a               | a               |
| Deschampsia                                 | a               | a               | a               | a               | a               | a               | a               | a               | a               |
| Arctowski                                   | Groups          | Gamma           | Firm            | Alpha           | Acido           | Actino          | Bacteroi        | Beta            | Epsilon         |
| P-value                                     | 0.235           | 0.005           | 0.012           | 0.223           | 0.003           | 0.081           | 0.001           | 0.181           |
| Soil                                        | a               | b               | b               | a               | b               | a               | b               | a               | a               |
| Colobanthus                                 | a               | a               | a               | a               | a               | a               | a               | a               | a               |
| Deschampsia                                 | a               | ab              | a               | a               | a               | a               | a               | a               | a               |

Different letters within a column represent significant difference between samples. Significant values (P<0.05) are in boldface.
doi:10.1371/journal.pone.0066109.t004
would not be ornithogenic soil. According to [12], which used a comprehensive sampling, the amount of sand, silt and clay in ornithogenic soils are about 73% ± 10, 15% ± 7 and 11% ± 4%, respectively, and 41% ± 18, 32% ± 4 and 21% ± 8% to weakly ornithogenic soils. Soil from the M site, with high pH, high concentration of exchangeable Ca and low concentrations of organic C and total nitrogen could be classified as basaltic/andesitic soil according to [12], and presents about 38% ± 16, 32% ± 7 and 25% ± 5% of sand, silt and clay respectively. The high S concentration found for this site could be attributed to the sulfide bearing andesites and related tills present in the region [12].

According to PCoA generated from the microarray data, the bacterial communities were strongly shaped by the nitrogen level in the soil, and consequently, to the bird influence. Samples of weakly ornithogenic soils generally grouped together (sites Q and I), while the non-ornithogenic soils (site M) formed a separate group. However, for the highly ornithogenic soils (sites A, D and C) two separate groups could be observed: one comprising samples from sites D and A, and another comprising only samples from site C. Interestingly, each of these sites is occupied by different penguin species which have different diets. Studies on penguin diet showed that *Pygoscelis adeliae* and *P. antarctica* (the species found in sites A and D, respectively) feed on krill, mainly *Euphrasia superba*, while *P. papua* (the species found in site C) eats krill but also fish, particularly *Notothenia* species [36–38]. The diet of the penguin could influence soil microbial communities in two ways: through modification of the penguin’s gut microbiota and thus in the microbial inputs to soil through guano deposition [4], and through modification of the physico-chemical composition (N, P and pH) of the penguin’s guano. We hypothesize that the diet of *P. papua*, which colonizes site C, is at least partially responsible for the different microbial community patterns observed at this site.
Influence of Plants

C. quitensis of [43]. However, in the present study, we did not find any clear compounds, the rhizosphere effect is thought to be plant-specific exudation [46] and since different plants exude different specific microbial community in their rhizosphere through root different microbial communities [5,42–45]. Plants select for a also previously reported that bulk and rhizosphere soils harbored maritime Antarctic sites [19]. In more temperate settings, it was vegetation cover was previously reported as having a strong differences in soil characteristics, microbial communities within a each individual site, we found significant differences between the microbial communities found in bulk soil and rhizosphere samples in both the microarray and the qPCR datasets. Similarly, in view of the very large differences between the soils characteristics of the different sampling sites used in this study, we limited our search for a rhizosphere effect to each site separately. Even though the microbial communities were predominantly driven by differences in soil characteristics, microbial communities within a site were significantly influenced by the presence of plants. Within each individual site, we found significant differences between the microbial communities in their rhizosphere [41]. In view of the very large differences between the soils characteristics of the different sampling sites used in this study, we limited our search for a rhizosphere effect to each site separately. Even though the microbial communities were predominantly driven by differences in soil characteristics, microbial communities within a site were significantly influenced by the presence of plants. Within each individual site, we found significant differences between the microbial communities found in bulk soil and rhizosphere samples in both the microarray and the qPCR datasets. Similarly, vegetation cover was previously reported as having a strong influence on the bacterial community composition in a range of maritime Antarctic sites [19]. In more temperate settings, it was also previously reported that bulk and rhizosphere soils harbored different microbial communities [5,42–45]. Plants select for a specific microbial community in their rhizosphere through root exudation [46] and since different plants exude different compounds, the rhizosphere effect is thought to be plant-specific [43]. However, in the present study, we did not find any clear difference between the microbial communities in the rhizosphere of C. quitensis and D. antarctica, in line with a previous report that used pyrosequencing and DGGE [11]. Other previous studies also report similar results, suggesting that the soil characteristics could be a determinant factor shaping the microbial communities instead of the rhizosphere plant species [9,10].

In a previous study from our group that used 16S rRNA gene pyrosequencing on D. antarctica and C. quitensis rhizosphere samples from Admiralty Bay, it was shown that the Firmicutes were the most abundant phylum followed by the Proteobacteria and then the Actinobacteria [11]. In the present study, although the same three groups were still the most abundant, the qPCR approach showed a dominance of Actinobacteria followed by Proteobacteria and Firmicutes. These discrepancies could be due to the fact that we did not use primers targeting the same positions in the 16S rRNA gene for both techniques. Furthermore, the primers used for the Actinobacteria in qPCR are not perfectly specific to this group and unspecific amplifications could artificially increase their abundance in qPCR assays [47]. However, the main goal of this study was to compare bulk soils and rhizospheres from different sampling sites and the results from these comparisons are valid since all samples were subjected to the same bias. Our results nonetheless showed that the Actinobacteria and the Proteobacteria are the main bacterial taxa present in the soils of Admiralty Bay. Similar results were found in several other studies on soil bacterial diversity around the world [11,48,49] and in maritime Antarctica [11,16,27].

Conclusions

Our results showed that the presence of vascular plants (D. antarctica and C. quitensis) and of birds play important roles in shaping the microbial communities of Antarctic soils. For the plant influence, the observed rhizosphere effect varied between the different sampling sites, probably due to differences in soil parameters, indicating that plant colonization will not have the same effect on microbial communities in all soils. Firmicutes and Acidobacteria were more abundant in bulk soils while Actinobacteria was more abundant in rhizosphere samples. For the bird influence, the effect varied with the level and the type of ornithogenic input and, in highly ornithogenic soils, seemed to be also modulated by the species of bird present, due to differences in diet. This indicates that the soils associated with bird colonies will influence microbial communities differently depending not only on the type of birds (flying birds vs. penguins), but also on the diet of the birds. Based on these results, we can hypothesize that not only will climate change directly influence Antarctic soil microbial communities, but it will also indirectly influence them through changes in plant and bird populations.

Further research will be conducted to directly test the guano (chemical and microbiological) of different penguins and even test the chemical attributes of exudates (or rhizosphere) of the two plants to confirm/deny the correlations, which may explain the resulting overlapping bacterial communities.

Acknowledgments

The authors are very grateful to Caio Rachid for his excellent support in soil analysis experiments.

Author Contributions

Conceived and designed the experiments: LCRST EY RSP CWG ASR. Performed the experiments: LCRST EY MP. Analyzed the data: LCRST EY RSP CWG ASR. Contributed reagents/materials/analysis tools: ASR CWG MP. Wrote the paper: LCRST EY RSP CWG ASR.

References

1. Avery LM, Smith RIL, West HM (2003) Response of rhizosphere microbial communities associated with Antarctic hairgrass (Deschampsia antarctica) to UV radiation. Polar Biology 26: 525–529.
2. Fowbert JA, Smith RIL (1994) Rapid Population Increases in Native Vascular Plants in the Argentine Islands, Antarctic Peninsula. Arctic and Alpine Research 26: 290–296.
3. Convey P, Smith RIL (2006) Responses of terrestrial Antarctic ecosystems to climate change. Plant Ecology 182: 1–10.
4. Aslabie J, Jordan S, Aytan J, Klassen JL, Barker GM, et al. (2009) Bacterial diversity associated with ornithogenic soil of the Ross Sea region, Antarctica. Canadian journal of microbiology 55: 21–36.
5. Hatchar EZ, Marol C, Berge O, Rangel-Castro JJ, Proser JI, et al. (2008) Plant host habitat and root exudates shape soil bacterial community structure. The ISME journal 2: 1221–1230.
6. Kislick A, Pijl AS, van Veen JA, Kowalchuk GA (2009) Phylogenetic diversity of Acidobacteria in a former agricultural soil. The ISME journal 3: 378–382.
25. Fierer N, Jackson JA, Vilgalys R, Jackson RB (2005) Assessment of soil microbial community structure in grassland soils. Applied Soil Ecology 36: 147–155.

24. Solorzano L (1969) Determination of ammonia in natural waters by the phenol-hypochlorite method. Limnology and oceanography 14: 799–801.

23. Yeomans JM, Bremner JC (1988) A rapid and precise method for routine determination of organic carbon in soils. Communications in Soil Science and Plant Nutrition 19: 1467–1476.

22. Embrapa (1997) Manual de Métodos de Análise de Solo. Rio de Janeiro: Centro Nacional de Pesquisa de Solos.–EMBRAPA. 212 p.

21. Forcada J, Trathan PN, Reid K, Murphy EJ, Croxall JP (2006) Contrasting population changes in sympatric penguin species in association with climate warming. Global Change Biology 12: 411–423.

20. Ganzert L, Lipski A, Hubberten HW, Wagner D (2011) The impact of different soil parameters on the community structure of dominant bacteria from nine different soils located on Livingston Island, South Shetland Archipelago, Antarctica. FEMS microbiology ecology 75: 6258–6267.

19. Yergeau E, Schoondermark-Stolk SA, Brodie EL, Dejean S, DeSantis TZ, et al. (2009) Environmental microarray analyses of Antarctic soil microbial communities. The ISME journal 3: 340–351.

18. Yergeau E, Kowalchuk GA (2008) Responses of Antarctic soil microbial community structure to climate warming across a range of Antarctic terrestrial habitats. Environmental microbiology 10: 2223–2235.

17. Yergeau E, Newsham KK, Pearce DA, Kowalchuk GA (2007) Patterns of bacterial diversity across a range of Antarctic terrestrial habitats. Environmental microbiology 9: 2670–2682.

16. Yergeau E, Bokhorst S, Huiskes AH, Boschker HT, Aerts R, et al. (2007) Functional microarray analysis of nitrogen and carbon cycling genes across an Antarctic latitudinal transect. The ISME journal 1: 163–179.

15. Yergeau E, Arbour M, Brousseau R, Juck D, Lawrence JR, et al. (2009) Microarray and real-time PCR analyses of the responses of high-arctic soil bacteria to hydrocarbon pollution and bioremediation treatments. Applied and environmental microbiology 75: 6258–6267.

14. Zdanowski MK, Weglenski P, Golik P, Sasin JM, Borsuk P, et al. (2004) Genesis, properties and classification of Cryosols from Admiralty Bay, maritime Antarctica. The ISME journal 4: 899–1001.

13. Sokal RR, Rohlf FJ (1995) Introduction to Biostatistics. New York: Dover Publications.

12. Lane DJ (1991) 16S/23S rRNA sequencing. In: Stackebrandt E, Goodfellow M, editors. Nucleic acid techniques in bacterial systematics. New York: John Wiley and Sons. 91–150.

11. Riedel-Duine AS, Kowalchuk GA, Gunnewiek PJAK, Smant W, van Veen JA, et al. (2005) Rhizosphere bacterial community composition in natural stands of Carex arenaria (sand sedge) is determined by bulk soil community composition. Soil Biology & Biochemistry 37: 349–357.

10. Singh BK, Munro S, Potts JM, Millard P (2007) Influence of grass species and soil type on rhizosphere microbial community structure in grassland soils. Applied Soil Ecology 36: 147–155.

9. Nunan N, Daniell TJ, Singh BK, Papert A, McNicol JW, et al. (2005) Links between plant and rhizosphere bacterial communities in grassland soils, characterized using molecular techniques. Applied and environmental microbiology 71: 6784–6792.

8. Smalla K, Wieland G, Buchner A, Zock A, Parzy J, et al. (2001) Bulk and environmental microbiology 71: 4742–4751.

7. Marschner P, Crowley D, Yang CH (2004) Development of specific rhizosphere bacterial communities in relation to plant species, nutrition and soil type. Plant and Soil 261: 199–208.

6. Smalla K, Wieland G, Buchner A, Zock A, Parzy J, et al. (2001) Bulk and environmental microbiology 71: 4742–4751.

5. Fierer N, Kane SR, Legler TG, Alvarez PJ (2002) A real-time polymerase chain reaction method for monitoring anaerobic, hydrocarbon-degrading bacteria based on a catalytic gene. Environmental science & technology 36: 3977–3984.

4. Lane DJ (1991) 16S/23S rRNA sequencing. In: Stackebrandt E, Goodfellow M, editors. Nucleic acid techniques in bacterial systematics. New York: John Wiley and Sons. 91–150.

3. Riedel-Duine AS, Kowalchuk GA, Gunnewiek PJAK, Smant W, van Veen JA, et al. (2005) Rhizosphere bacterial community composition in natural stands of Carex arenaria (sand sedge) is determined by bulk soil community composition. Soil Biology & Biochemistry 37: 349–357.

2. Kowalchuk GA, Buma DS, de Boer W, Klinkhamer PGJ, van Veen JA (2002) Effects of above-ground plant species composition and diversity on the diversity of soil-borne microorganisms. Antonie Van Leeuwenhoek International Journal of General and Molecular Microbiology 81: 509–520.

1. Riedel-Duine AS, Kowalchuk GA, Gunnewiek PJAK, Smant W, van Veen JA, et al. (2005) Rhizosphere bacterial community composition in natural stands of Carex arenaria (sand sedge) is determined by bulk soil community composition. Soil Biology & Biochemistry 37: 349–357.