In order to understand terrestrial ecosystem in Barton Peninsula, we have evolved a multidisciplinary project. There are six main components which sustain terrestrial ecosystem. As biotic factors, we considered microflora, flora and fauna, whereas climate, geomorphology and geochemistry can be considered as abiotic factors. Each component also has several sub-factors. For example, geomorphology has such altitude, aspect and slope. Components are related to each other. Climate can affect the composition of microfloral flora, flora, fauna and geochemistry, while climate can be affected by geomorphology.

Over the last few decades, terrestrial environments in Antarctica had been believed as sterilized habitats without any life forms because of the extreme conditions. In recent years, expansions of molecular biological methods to study microbial communities have detected unexpectedly high diversity and complexity of bacterial community in this harsh environment. Actinobacteria, Bacteriodetes, Gammaproteobacteria and Alphaproteobacteria were dominant in McMurdo Dry Valleys of Antarctic continent (Lee, et al., 2013). Then, how about maritime Antarctica? Which bacterial phyla are dominant and how similar are bacterial community structures between soil habitats in this region? We conducted a comprehensive analysis of bacterial communities in soil samples from Barton Peninsula in Antarctica. In total 218 soil samples from 51 sites were collected during the period from December 2010 to February 2012. Among these samples, we here present preliminary results with 83 samples in 15 sites.

**Study Site and Methods**

- **DNA extraction and PCR with barcode primers**
- **Pyrosequencing**: 454 GS FLX Titanium
- **Sequence pre-processing** (Sorting by barcode, Process by quality, Removing non-target sequences)
- **PyroTrimmer** (Oh, et al., 2012)

**DNA extraction** and **PCR** with **barcode primers** were performed. **Pyrosequencing** was carried out using 454 FLX Titanium. Sequences were **processed** for non-target sequences before the actual analysis.

**PyroTrimmer** (Oh, et al., 2012) was used for the process of pyrosequencing data. Non-target sequences were removed from the obtained sequences.

**Clustal** was used for the alignment of obtained sequences. **Representative sequences** of **OTUs** were chosen for the alignment.

**Statistical analysis** was performed using **PyroTrimmer** (Oh, et al., 2012) and **EzTaxon-e Database** (Kim, et al., 2014).

**Taxonomic assignment** was conducted using **EzTaxon-e Database** (Kim, et al., 2014).

**Results**

In total 218 soil samples from 51 sites were collected from the Barton and Weaver Peninsula in King George Island. These samples were processed and analyzed for bacterial community structures.

**DNA extraction** and **PCR** with **barcode primers** were performed. **Pyrosequencing** was carried out using 454 FLX Titanium. Sequences were **processed** for non-target sequences before the actual analysis.

**PyroTrimmer** (Oh, et al., 2012) was used for the process of pyrosequencing data. Non-target sequences were removed from the obtained sequences.

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**Taxonomic assignment** was conducted using **EzTaxon-e Database** (Kim, et al., 2014).

**Conclusions**

- **Actinobacteria**, **Proteobacteria**, **Acidobacteria** and **Chloroflexi** were dominant in the surface soils of King George Island. Different soil bacterial community structure was found in this harsh environment, different from those of other biomes such as tundra and temperate zone.
- **Candidate phylum** AD3 was abundant in several soil samples, which has not been recognized in previous studies. The bacterial community structures in this locality were habitat-specific. Bacteriodetes were more dominant in coastal soil, **Proteobacteria** in upper layer soil and **Actinobacteria** in lower layer soil.
- Highly heterogeneous bacterial communities were observed between both soil depth and habitats in this narrow range of the peninsula (within the range of 2 km).

**References**


**Fig. 1.** Sampling sites in Antarctica. Soil samples were collected from the Barton and Weaver Peninsula in King George Island.

**Fig. 2.** Bacterial phyla distribution of 218 soil samples in King George Island. Phylum-level bacterial community structure largely corresponded to the habitat locality.

**Fig. 3.** Bacterial phyla distribution at two soil depth profiles. U, Upper soil layer (top 0.5–5cm), L, Lower soil layer (1–10cm)

**Fig. 4.** Patterns of OTU-level community clustering between samples. Phyla composition profile was added at the bottom for comparison. The relative abundance values were averaged among three samples per site. U, Upper layer (0–5cm). L, Lower layer soil (1–10cm)

**Fig. 5.** PCA plot based on investigated relative abundance of bacterial phyla. Phylum-level community structure was mainly explained by three bacterial phyla, **Actinobacteria**, **Chloroflexi** and **Bacteriodetes**. Non-metric multidimensional scaling (NMDS) plots were generated using Bray-Curtis dissimilarity index based on the relative abundance of bacterial phyla in each soil sample. Bubbly size represents the relative abundance of the designated bacterial phylum in each sample.