

Comprehensive Survey of Soil Bacterial Community Structure in Barton and Weaver Peninsula of King George Island, Antarctica

Ahna Cho^{1, 3*}, Mincheol Kim¹, Hyoun Soo Lim², Soon Gyu Hong¹, Hyunju Noh¹, Tae-Seok Ahn³, and Ok-Sun Kim¹

¹Division of Polar Life Sciences, Korea Polar Research Institute, Incheon, Republic of Korea | ²Department of Environmental Science, Kangwon National University, Chuncheon, Republic of Korea | ³Department of Geological Sciences, Pusan National University, Busan, Republic of Korea



Introduction

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 microbial flora, flora, fauna and geochemistry, while climate can be affected by geomorphology.

In recent years, expansions of molecular biological methods to study microbial communities have detected unexpectedly high diversity and complexity of bacteria community in this harsh environment. *Actinobacteria*, *Bacteroidetes*, *Gemmatimonadetes* and *Alphaproteobacteria* were dominant in McMurdo Dry Valleys of Antarctic continent (Lee, *et al.*, 2011). 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 258 soil samples from 51 sites were collected during the period from December 2010 to February 2012.

Results

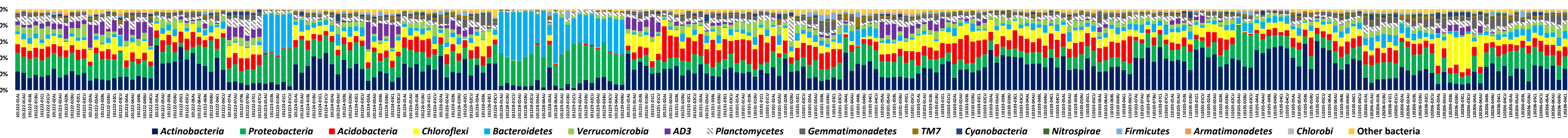


Figure 2. Bacterial phyla distribution of 258 soil samples in King George island. Phylum-level bacterial community structure largely corresponded to the habitat locality.

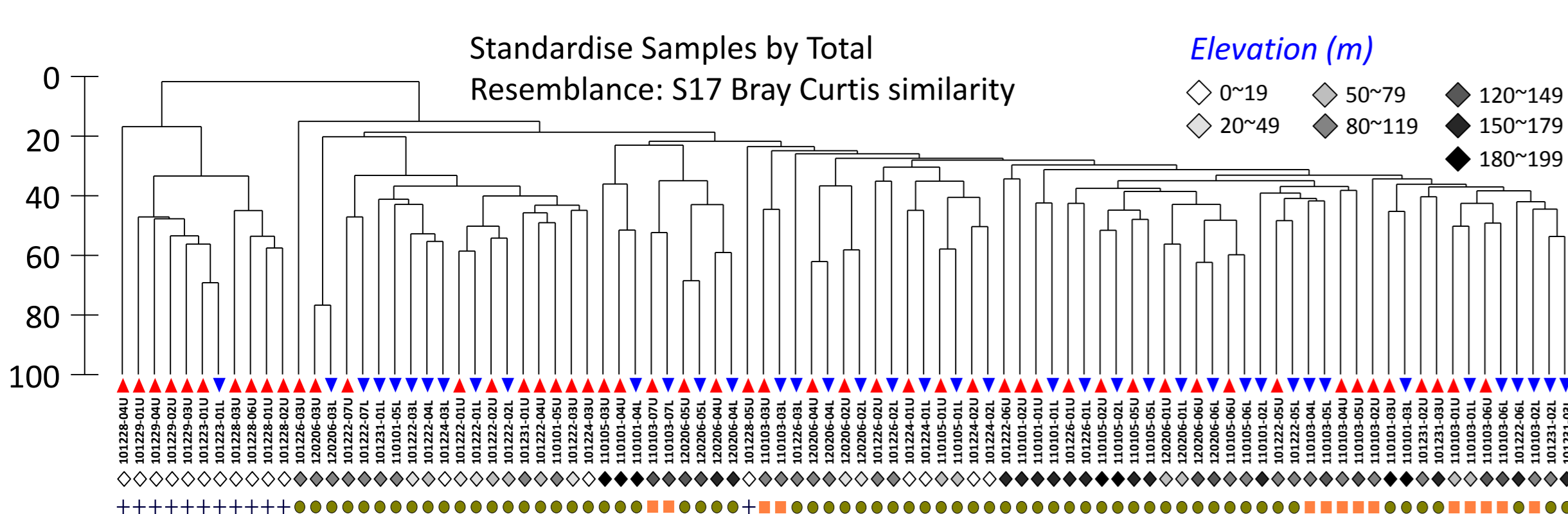


Figure 3. Pattern of OTU-level community clustering between samples. The relative abundance values of OTU were averaged among three samples (point A, B and C) per site. U and \blacktriangle , Upper layer soil (0~3cm); L and \blacktriangledown , Lower layer soil (3~10cm). \bullet , Barton peninsular soil; $+$, Beach sand; \blacksquare , Weaver peninsular soil.

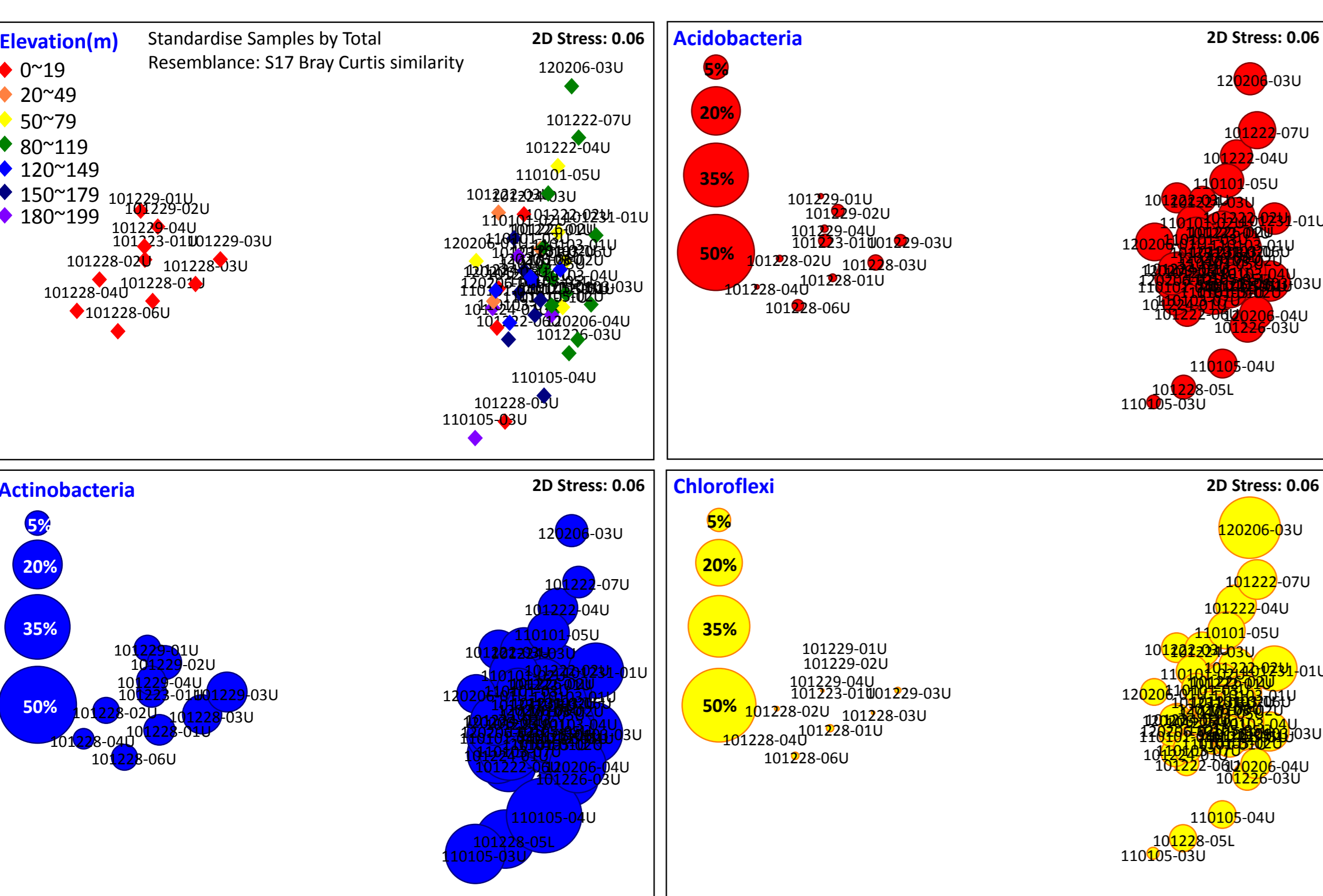


Figure 4. Phylum-level community structure was mainly explained by three bacterial phyla, Acidobacteria, Actinobacteria, Chloroflexi. Non-metric multidimensional scaling (NMDS) plots were generated using Bray-Curtis dissimilarity index based on the relative abundance of bacterial phyla in each upper soil sample. Bubble size represents the relative abundance of the designated bacterial phylum in each sample.

Acknowledgement
This study was supported by the research project Long-Term Ecological Researches on King George Island to Predict Ecosystem Responses to Climate Change (KGI-LTER, PE14020) of Korea Polar Research Institute (KOPRI) Institute

Study site and Methods

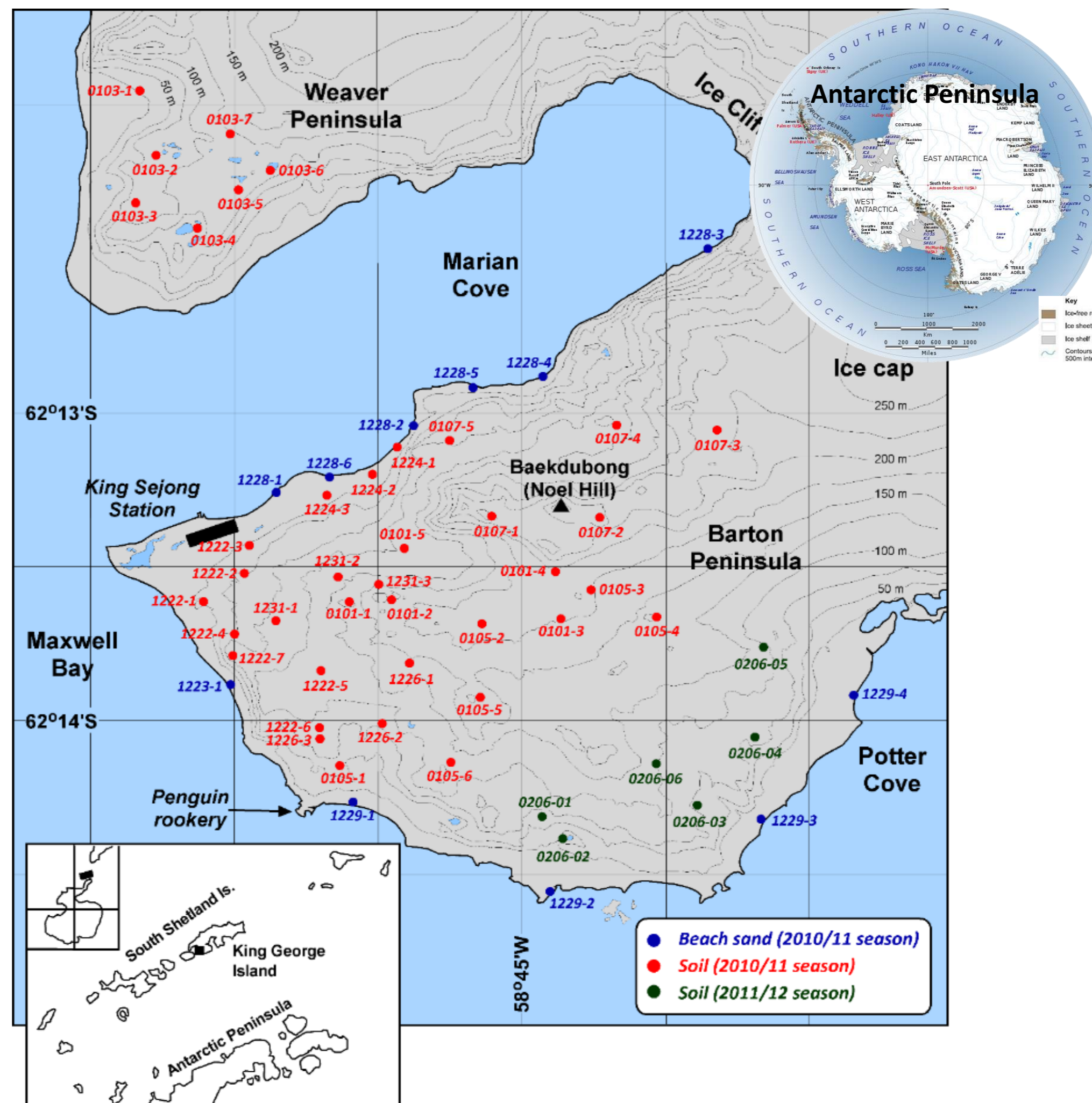


Figure 1. Sampling sites in Antarctica. Soil samples were collected from the Barton and Weaver Peninsula in King George Island.

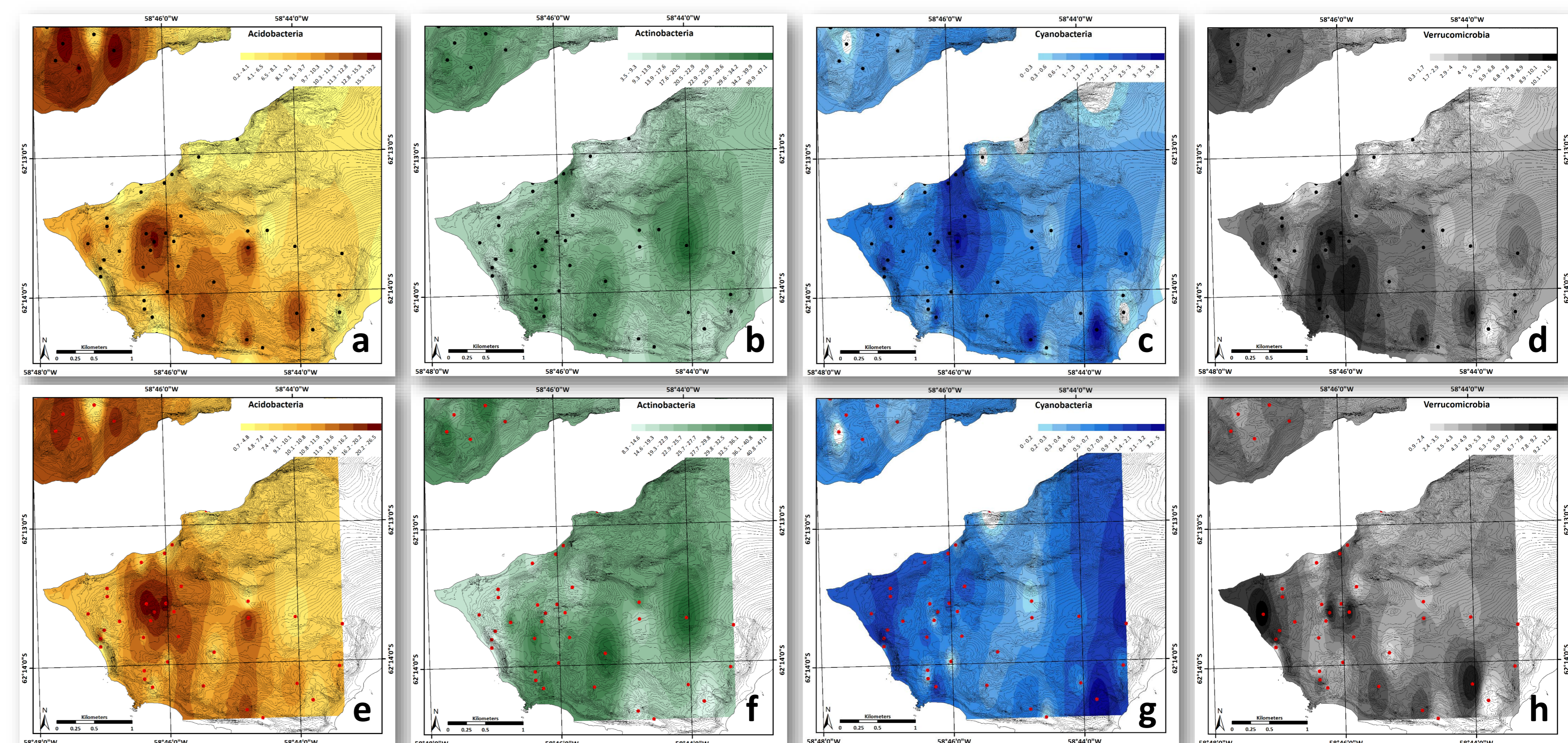
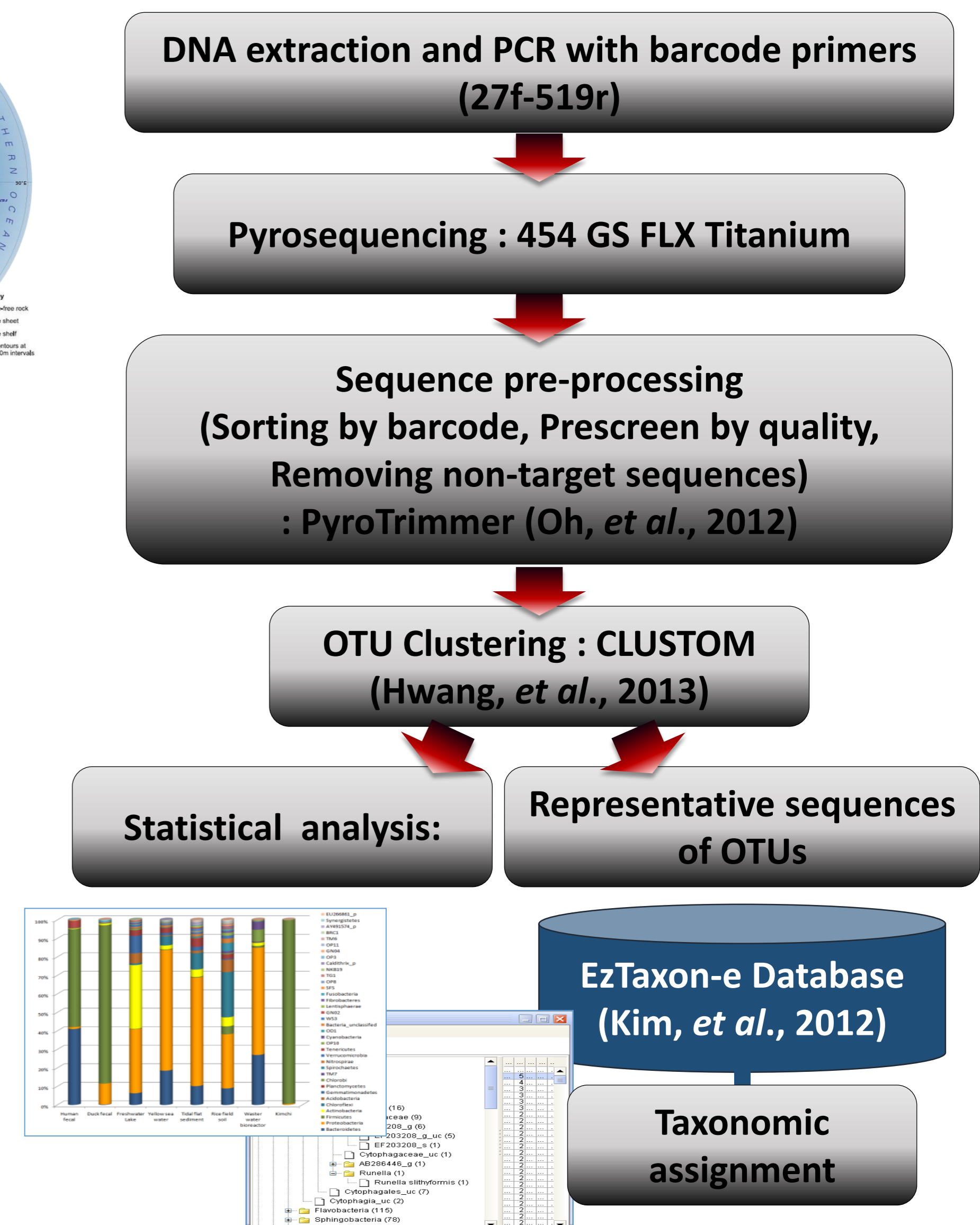


Figure 5. Spatial mapping of bacterial communities across Barton peninsula using the relative abundance of bacterial phyla in each site. The relative abundance values of phyla were averaged among three samples (point A, B and C) per site. (a-d) Map of upper layer soil (0~3cm); (e-h) map of lower layer soil (3~10cm); (a, e) map of Acidobacteria (maximum value 26.5%); (b, f) map of Actinobacteria (maximum value 47.1%); (c, g) map of Cyanobacteria (maximum value 5.0%); (d, h) map of Verrucomicrobia (maximum value 11.2%).

Conclusions

- Actinobacteria, Proteobacteria, Acidobacteria and Chloroflexi were dominant in the surface soils of King George Island. Distinct soil bacterial community structure was found in this harsh environment, different from those of other biomes such as tropics and temperate zone.
- The bacterial community structures in this locality were habitat-specific. Bacteroidetes 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

- Hwang K, Oh J, Kim T-K, Kim BK, Yu DS, Hou BK, Caetano-Anolles G, Hong SG & Kim KM (2013) CLUSTOM: A Novel Method for Clustering 16S rRNA Next Generation Sequences by Overlap Minimization. PLOS Computational Biology.
- Kim O-S, Cho Y-J, Lee K, et al. (2012) Introducing EzTaxon-e: a prokaryotic 16S rRNA gene sequence database with phylotypes that represent uncultured species. International Journal of Systematic and Evolutionary Microbiology 62: 716-721.
- Lee CK, Barbier BA, Bottos EM, McDonald IR & Cary SC (2011) The Inter-Valley Soil Comparative Survey: the ecology of Dry Valley edaphic microbial communities. ISME J 6: 1046-1057.
- Oh J, Kim BK, Cho WS, Hong SG & Kim KM (2012) PyroTrimmer: a software with GUI for pre-processing 454 amplicon sequences. Journal of microbiology 50: 766-769.