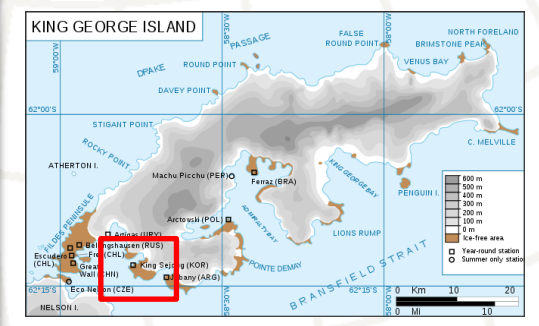
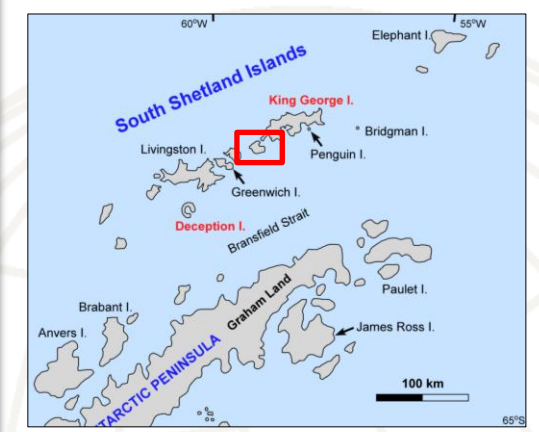
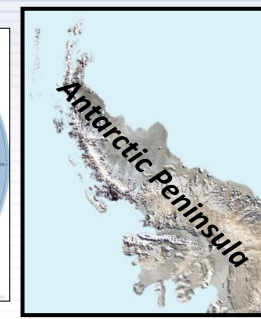
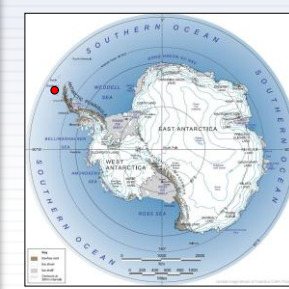
An aerial photograph of a research station on a rocky, sparsely vegetated peninsula. The station consists of several red and white containers, a small white building, and various pieces of equipment. A dirt road leads from the station towards the water. The background shows a large body of water under a clear sky.

Comparative analysis of bacterial taxonomic and functional diversity in terrestrial environments of Barton Peninsula in King George Island

Ok-Sun Kim, Ahnna Cho, Hyounsoo Lim, Hyun Joo Noh,
Jung Soo Oh and Soon Gyu Hong

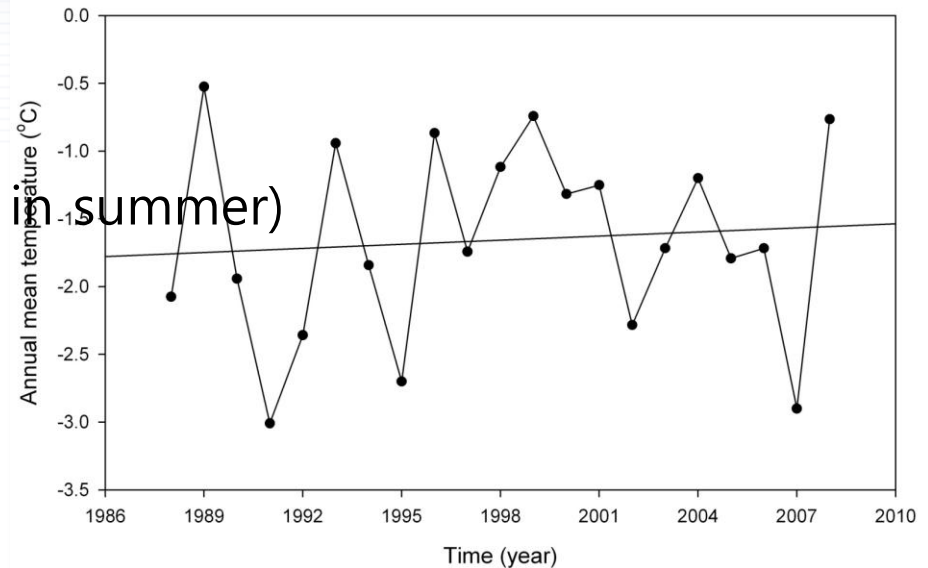
Korea Polar Research Institute

Location of Barton Peninsula in King George Island



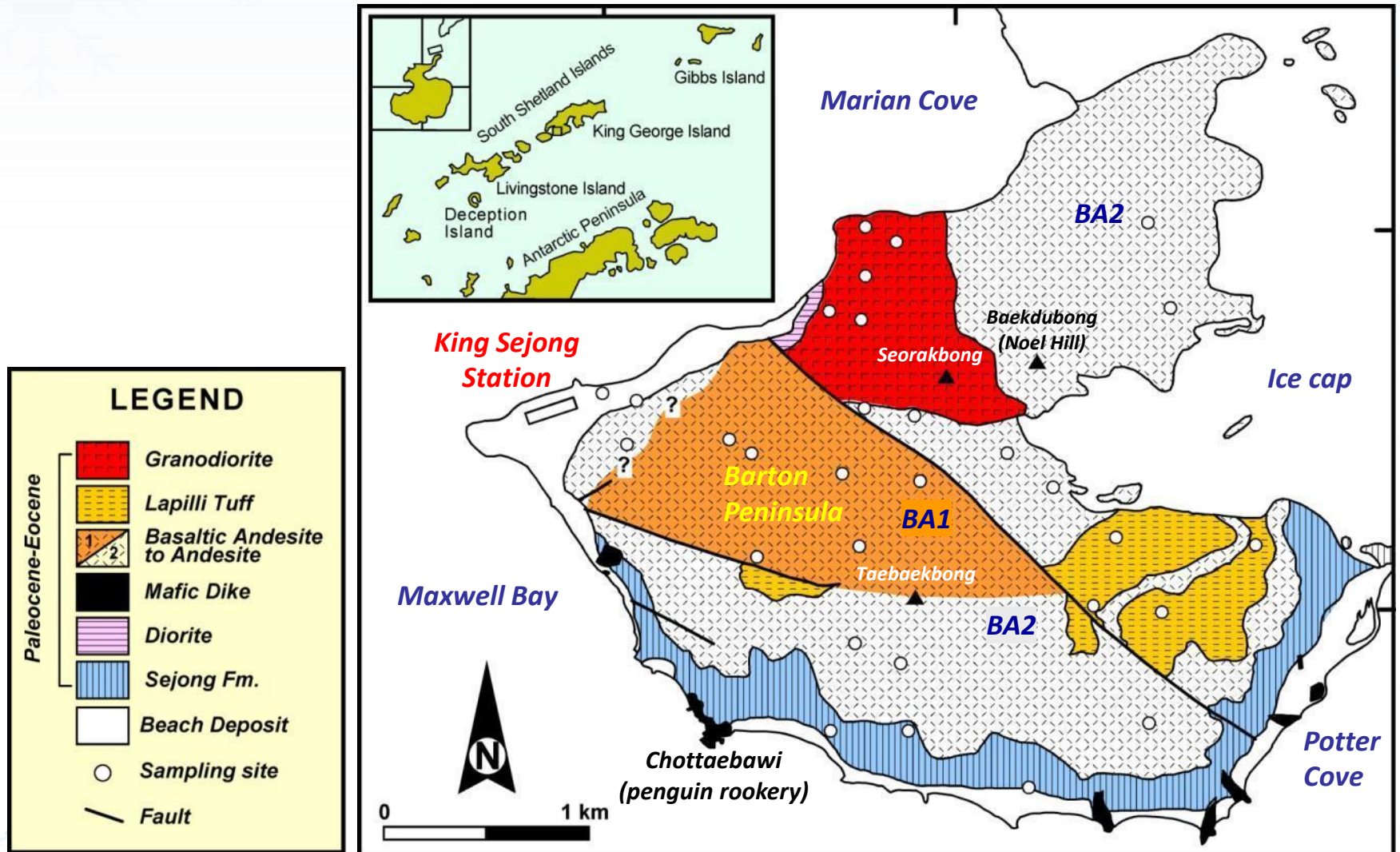
Weather condition

- Cold oceanic climate
- Mostly covered by an ice sheet
- Mean annual temp: -1.8°C ($>0^{\circ}\text{C}$ in summer)
- Relative humidity: 89%
- Precipitation: 437.6 mm
- Wind velocity: 7.9 m/s
- Dominant wind direction: NW/ SW (Lee et al., 1997)



By Namyi Chae

Geological map of Barton Peninsula



By Hyounsoo Lim

Terrestrial Sector-B: Vegetation Map

Antarctic Environmental Monitoring Program

King Sejong Station, Republic of Korea

2003 © Polar Research Center, KORDI

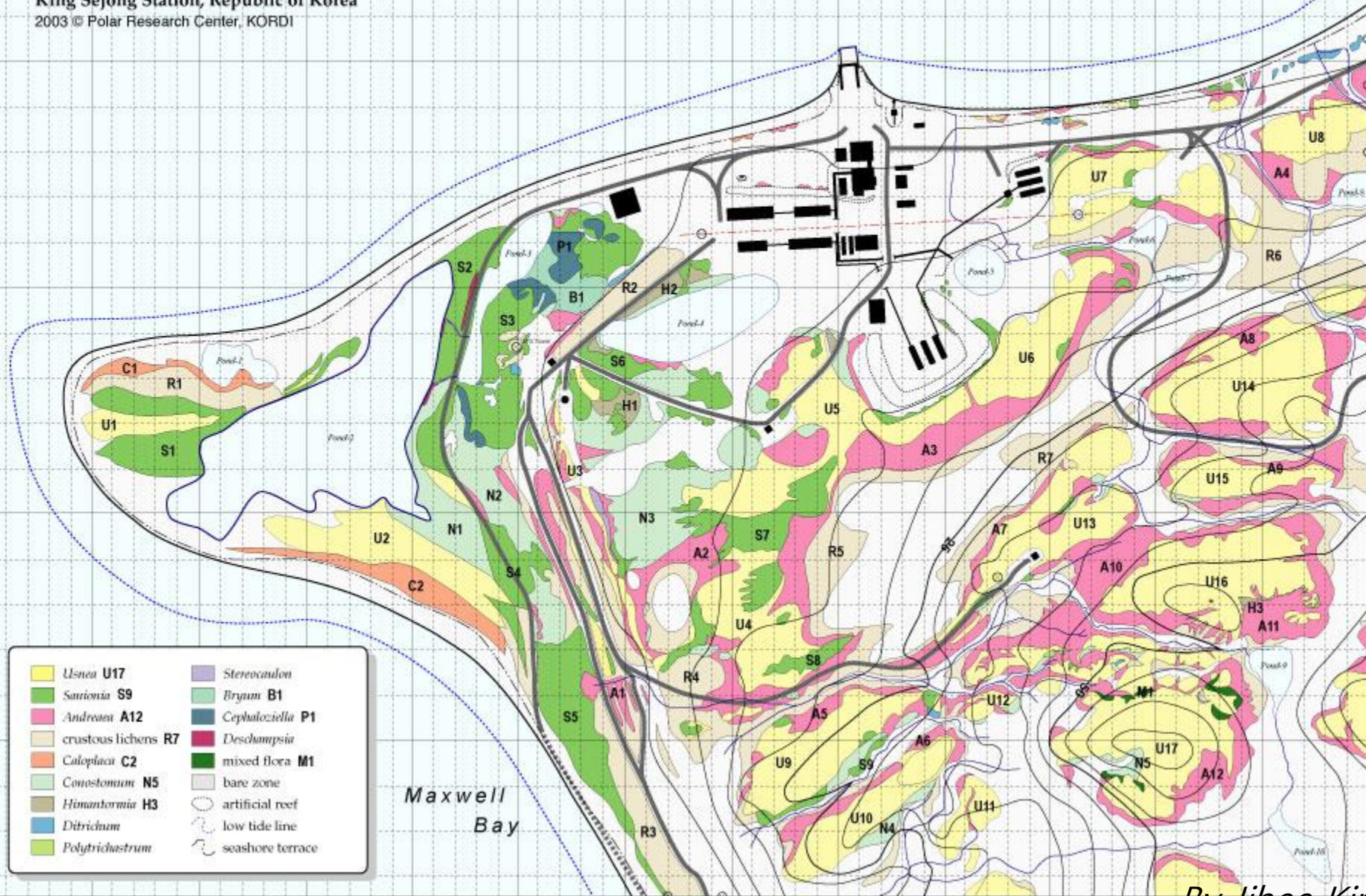
Marian Cove

62° 13'20"S

25°

30°

35°

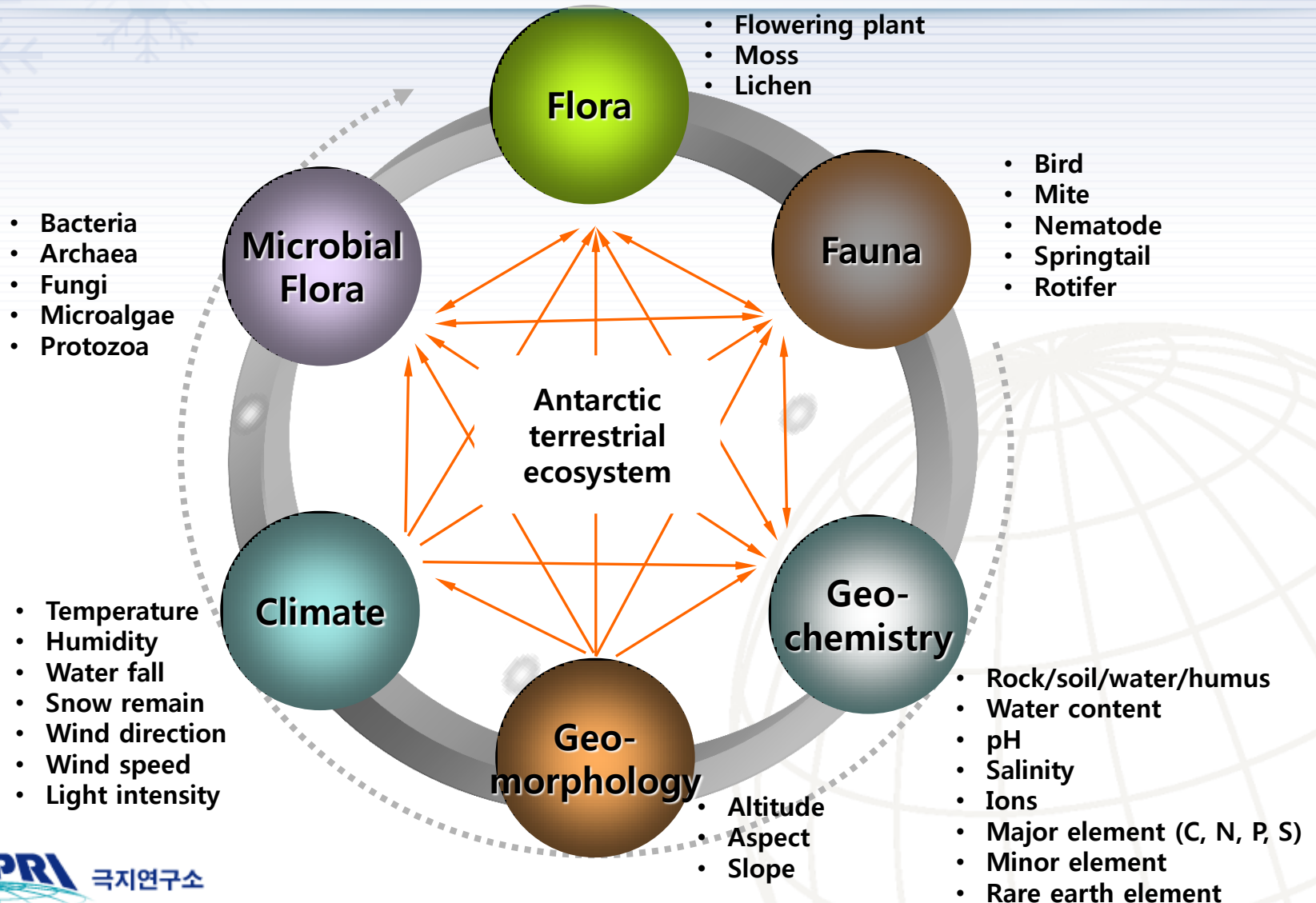


<i>Usnea</i> U17	<i>Stereocaulon</i>
<i>Saurionia</i> S9	<i>Bryum</i> B1
<i>Andreaea</i> A12	<i>Cephalozella</i> P1
crustose lichens R7	<i>Deschampsia</i>
<i>Caloplaca</i> C2	mixed flora M1
<i>Conostomum</i> N5	bare zone
<i>Himantormia</i> H3	artificial reef
<i>Ditrichum</i>	low tide line
<i>Polytrichastrum</i>	seashore terrace

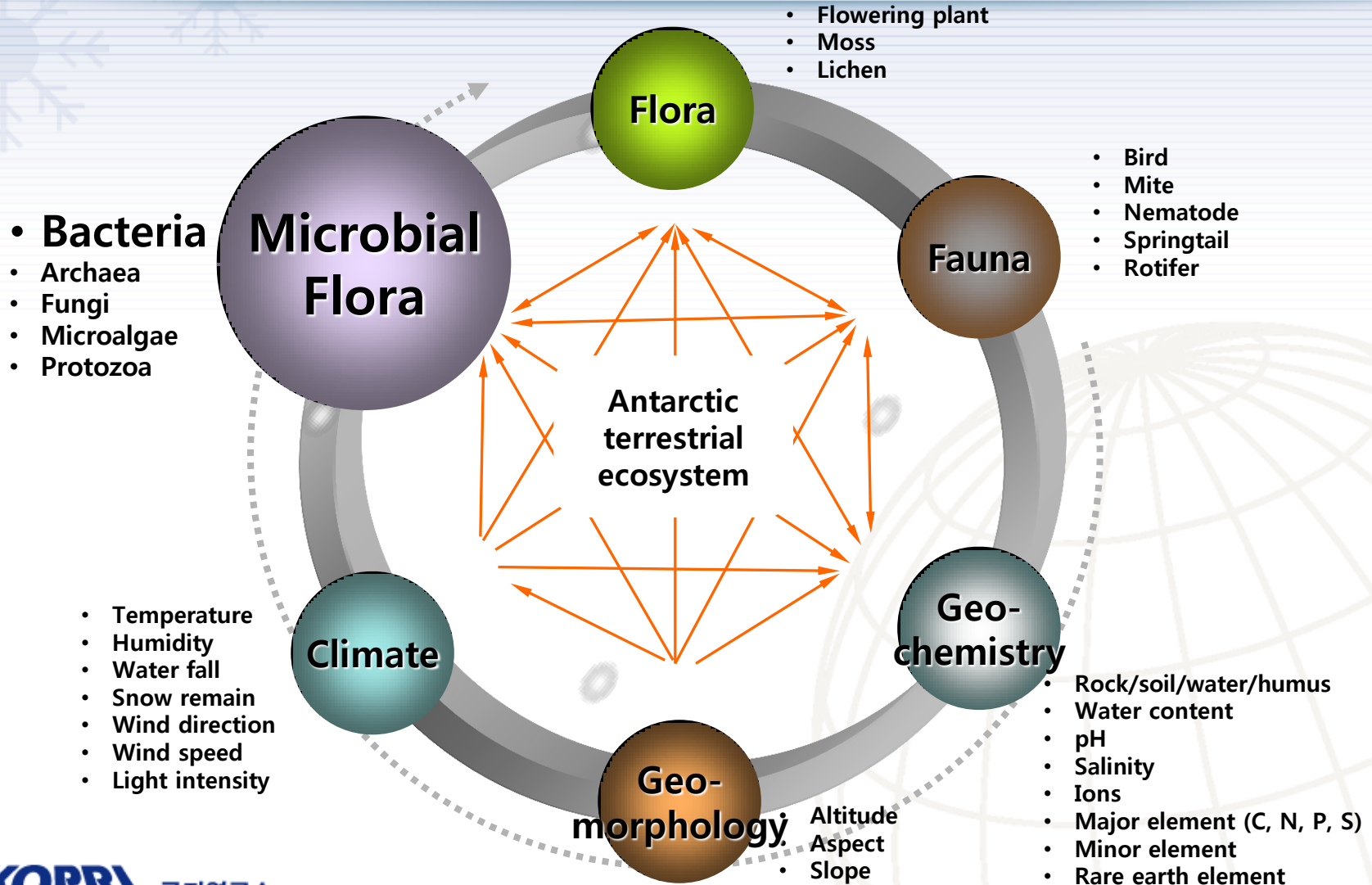
Maxwell Bay

By Jihee Kim

Components of terrestrial ecosystems



Components of terrestrial ecosystems



Microbial community analysis

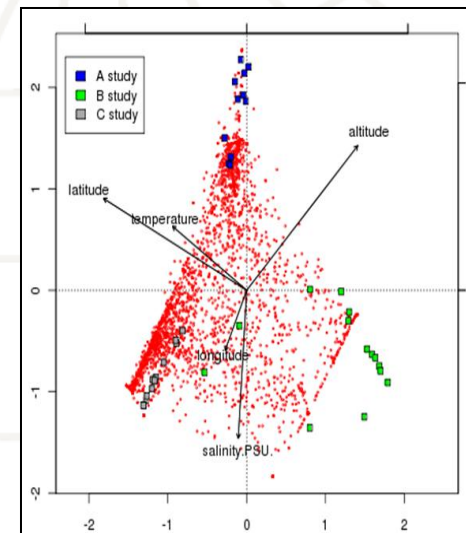
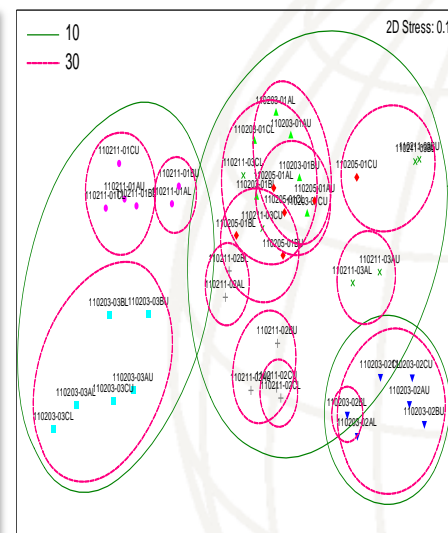
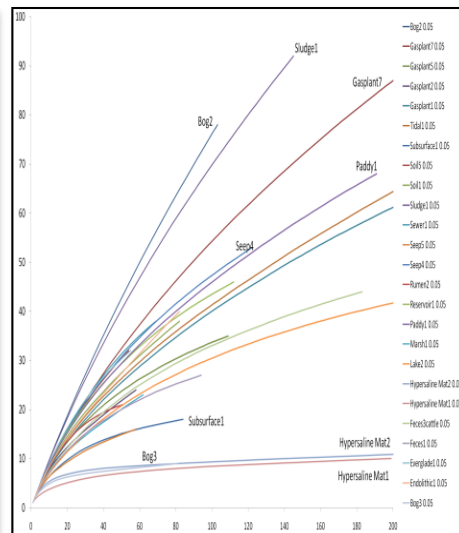
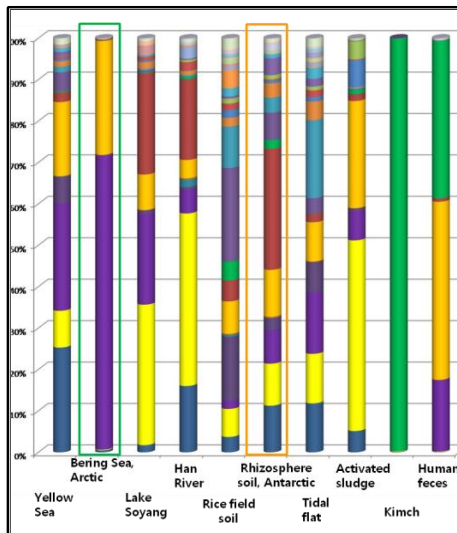
NGS platform
(16S rRNA, *nif*, *amo*, *nir*, *mcr*, *pmo*, *dsr*...)

Identification

Diversity

Community clustering

Correlation



Sampling sites

3 points in each site
A, B & C

2 layers

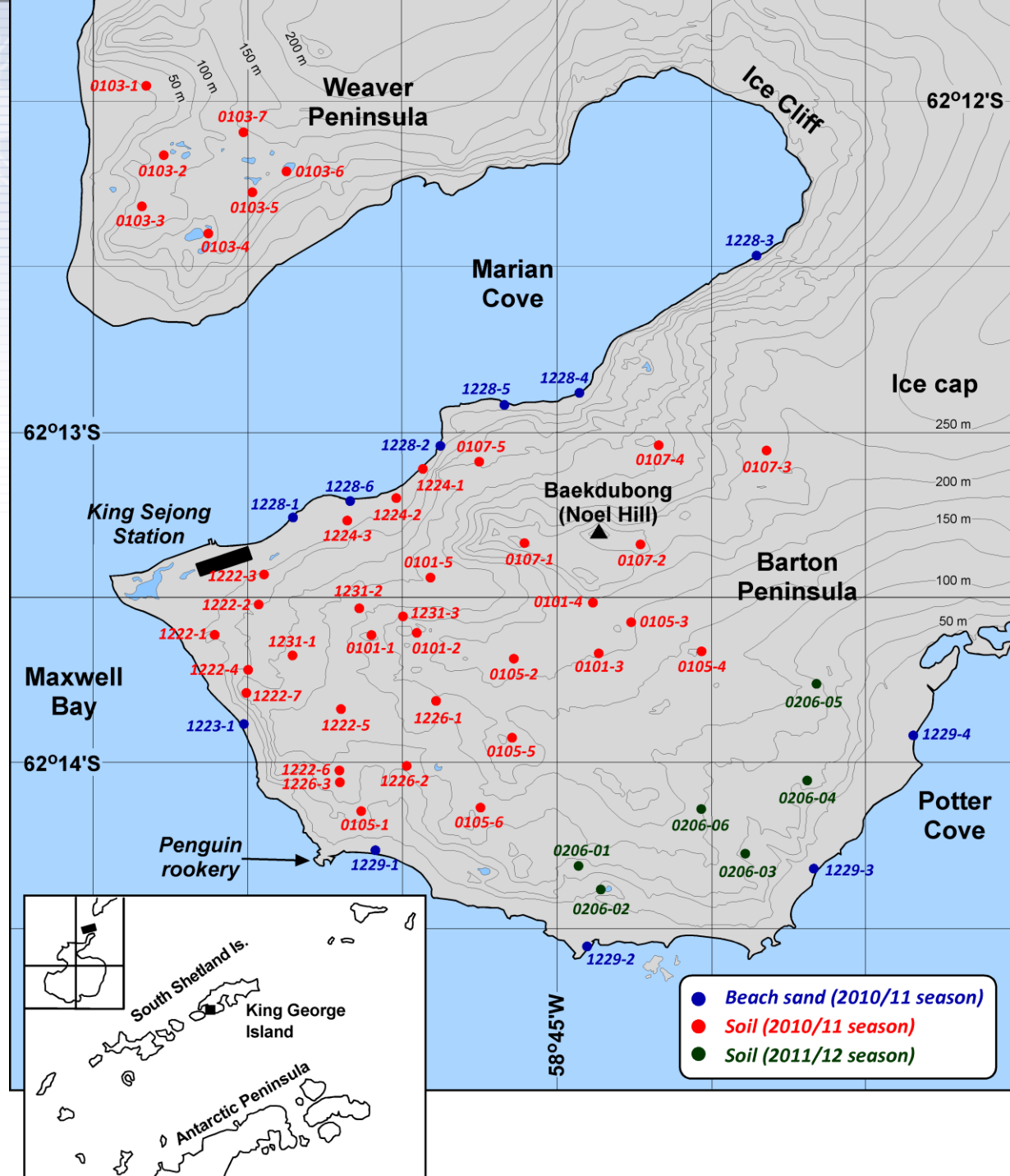
upper (0- 3 cm)

lower (3-10 cm)

57 sites

170 points

385 samples



Sample description

101222-01-A

S 62°13'36.7" / W 58°47'13.1" (35 m)

*Hill area, small soil patches developed
no PPG, light brown soil containing small pebbles
Usnea dominant, moss sparse
near the skua nest*

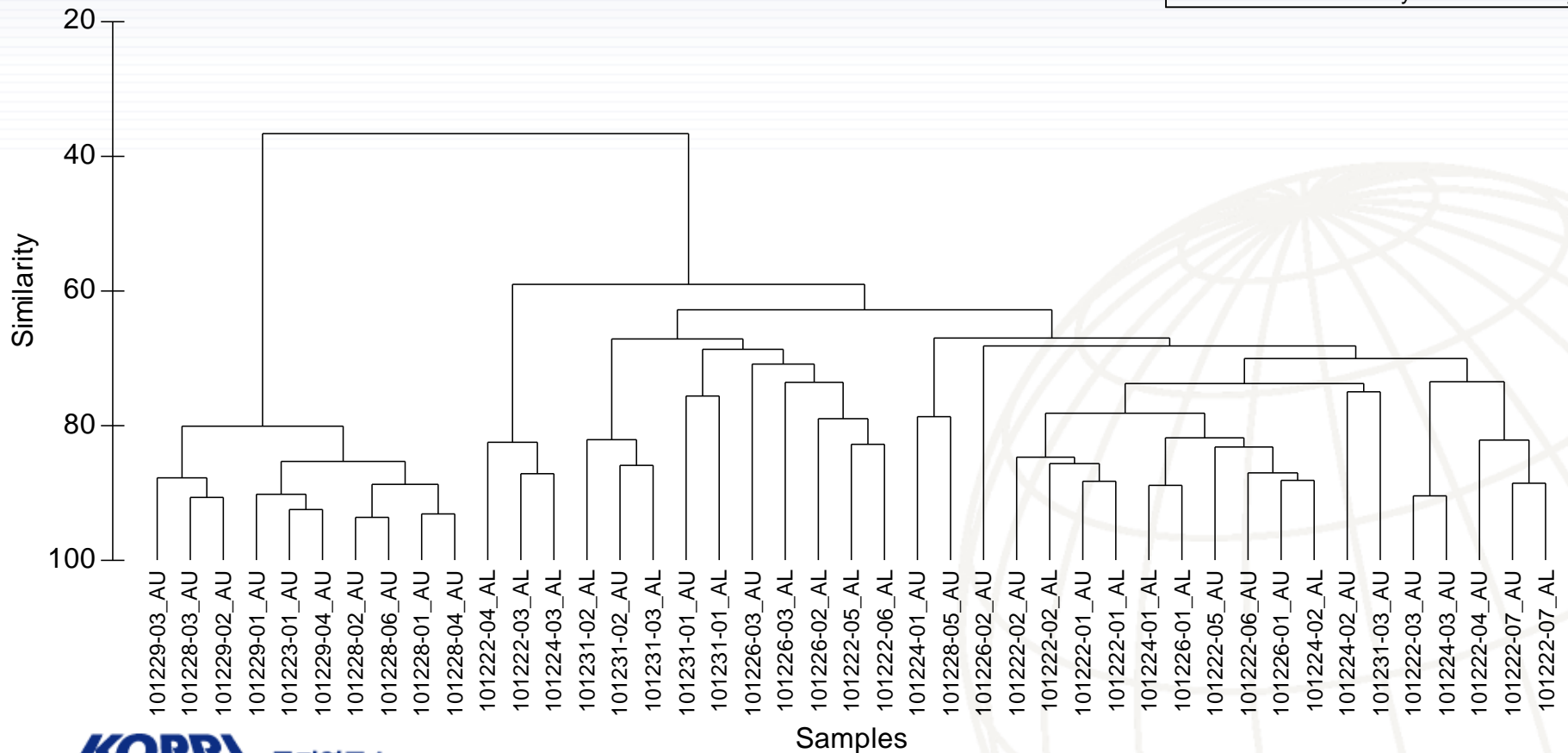


Relationship between samples

Phylum level

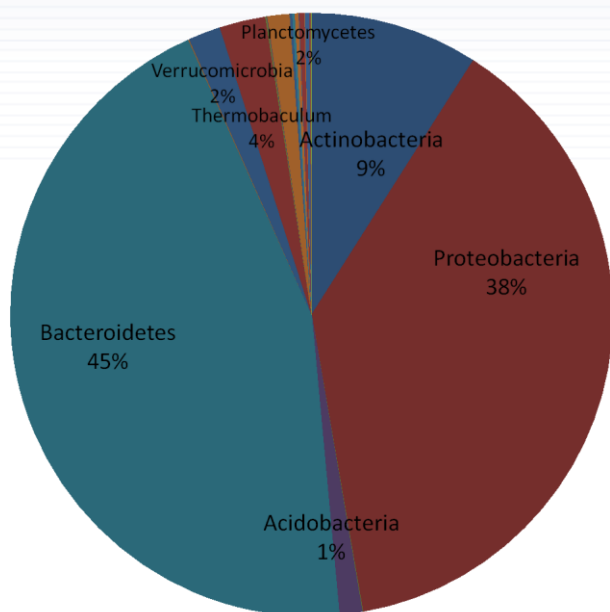
Group average

Standardise Samples by Total
Resemblance: S17 Bray Curtis similarity



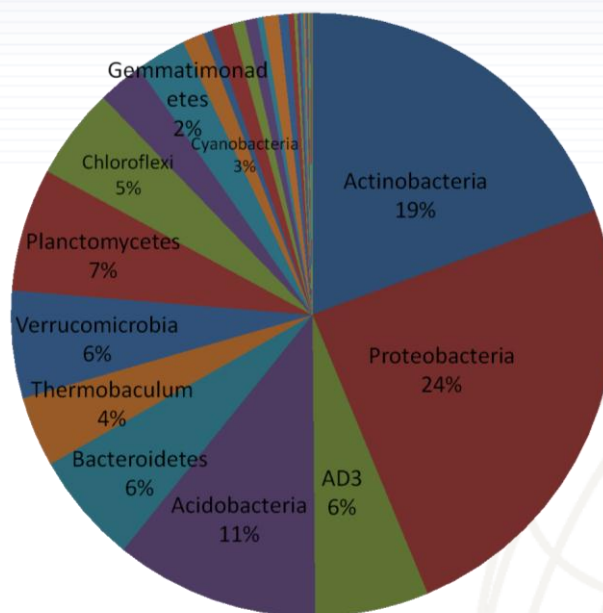
Bacterial community composition

Coastal line



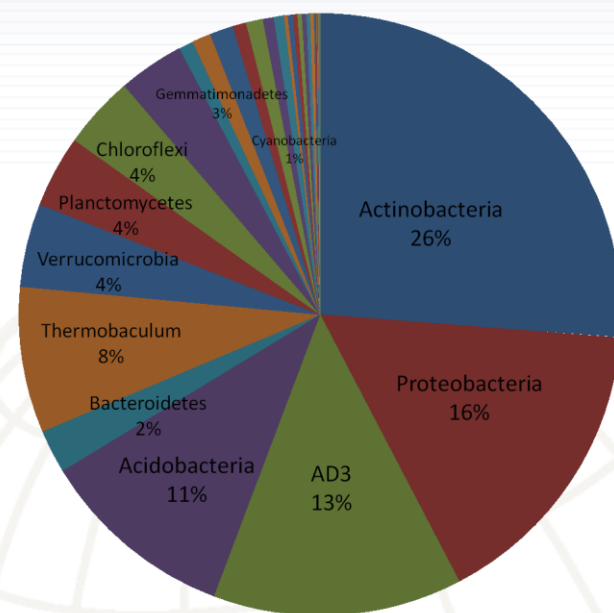
8,576 Reads
1,247 OTUs
23 Phyla

Upper layer

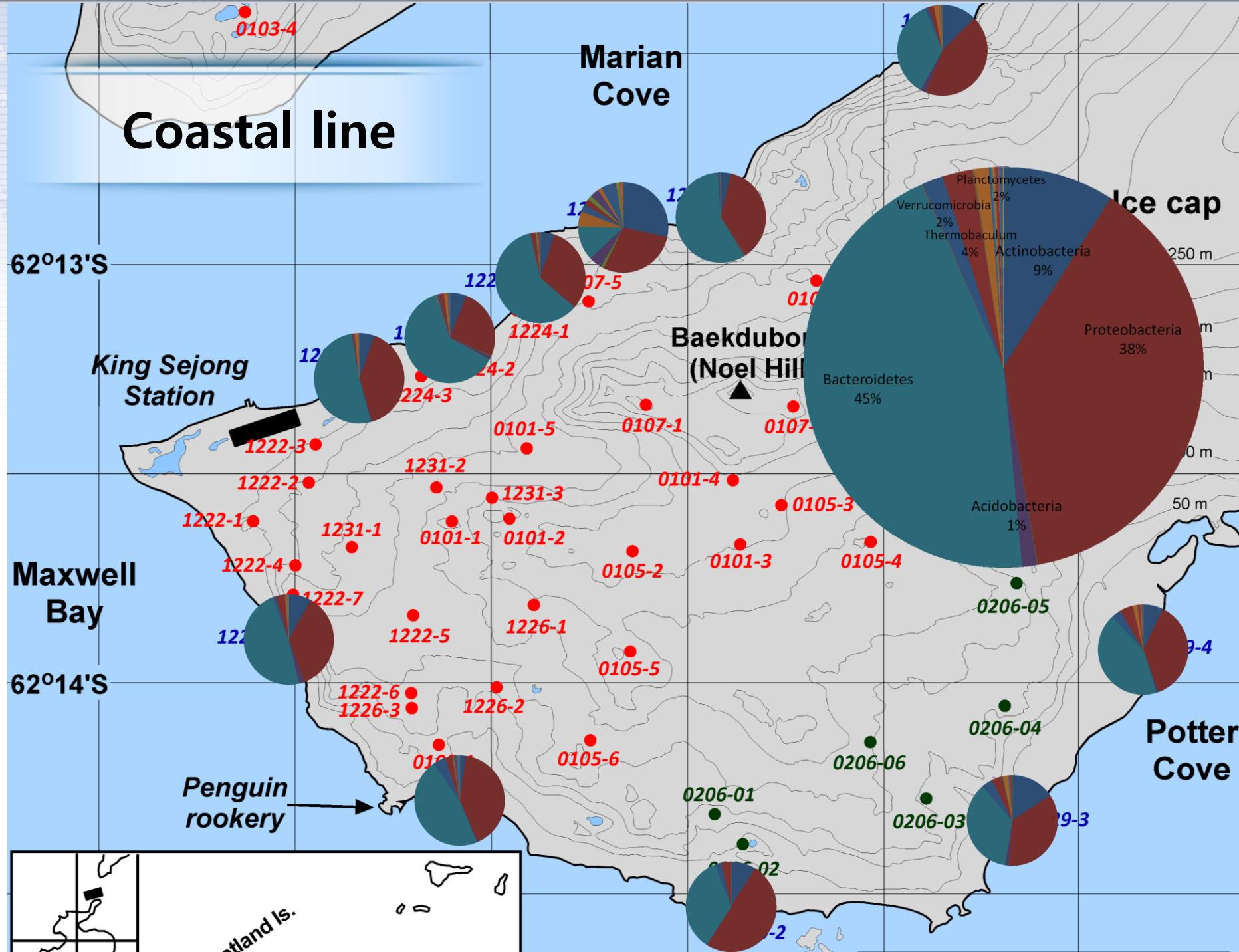


22,236 Reads
4,392 OTUs
37 Phyla

Lower layer



44,111 Reads
5,367 OTUs
41 Phyla



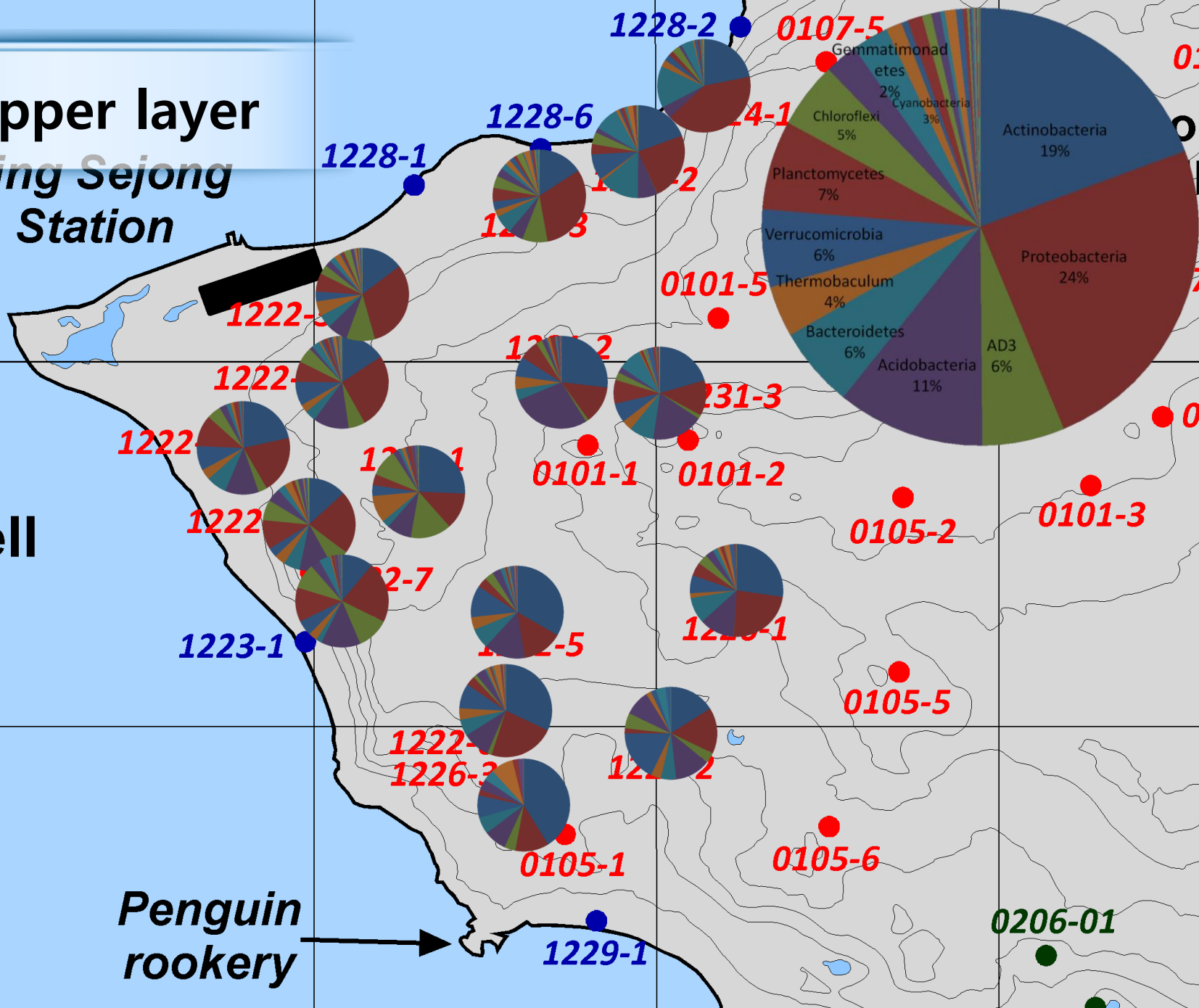
62°13'S

Upper layer
King Sejong
Station

Maxwell
Bay

62°14'S

Penguin
rookery



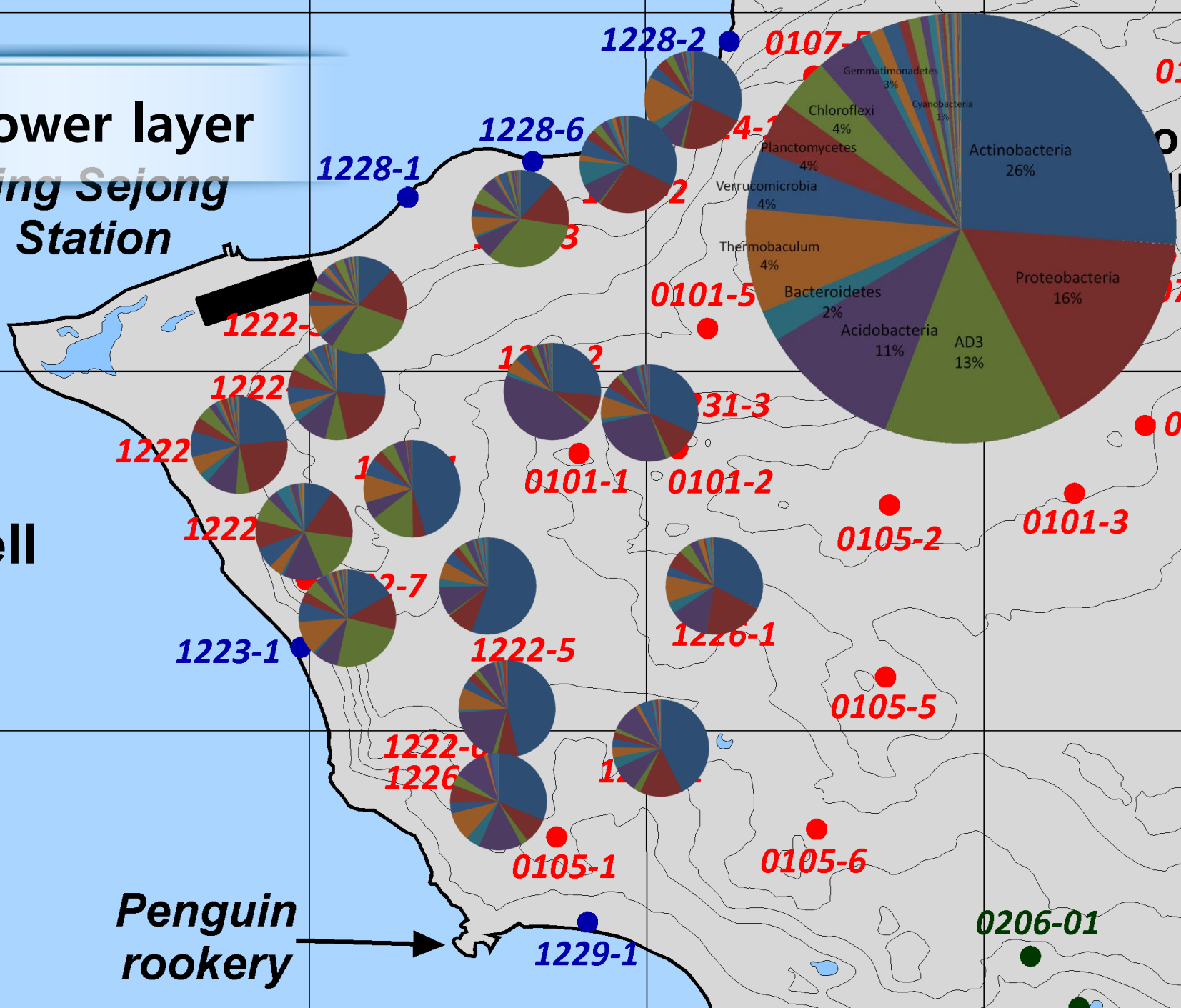
62°13'S

Lower layer
King Sejong
Station

Maxwell
Bay

62°14'S

Penguin
rookery



1228-1

1228-6

1228-2

0107-5

1222-3

1222-1

1222-2

1222-4

1223-1

1222-7

1222-5

1222-6

1226-1

0105-1

1229-1

0101-5

1222-2

0101-1

1226-1

1226-1

0105-5

0105-6

0105-2

0105-5

0101-3

0206-01

0101-2

0101-2

0101-2

1226-1

0105-5

0105-6

1229-1

1228-6

1228-2

0101-5

1222-2

0101-1

1226-1

1226-1

0105-5

0105-6

1229-1

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1226-1

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1229-1

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0105-6

1229-1

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1228-2

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0105-5

0105-6

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1229-1

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0105-5

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1226-1

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0105-5

0105-6

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0105-5

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1226-1

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1226-1

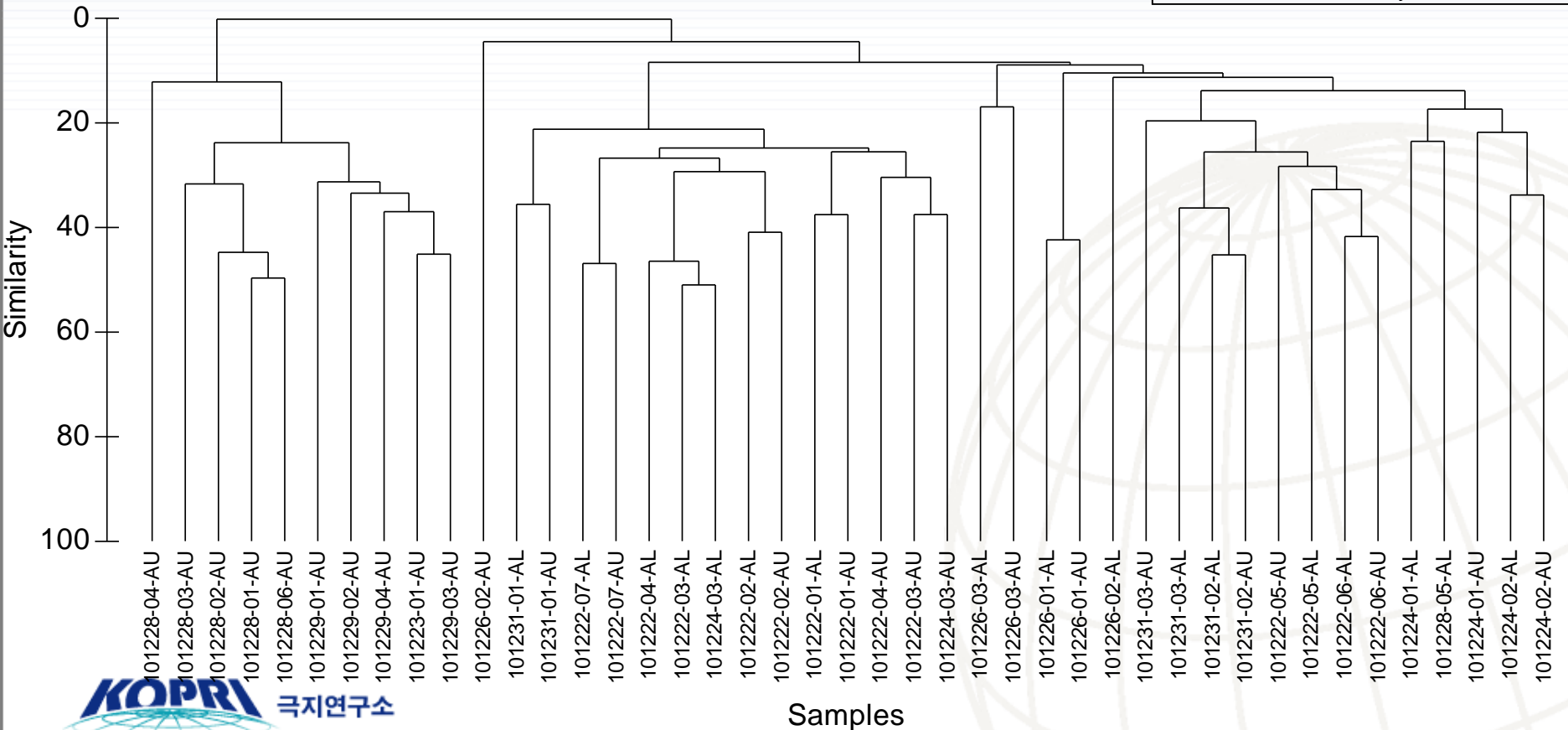
010

Relationship between samples

OTUs level

OTUs
Group average

Standardise Samples by Total
Resemblance: S17 Bray Curtis similarity



Abundant OTUs in soils of coastal line

	1223-01	1228-01	1228-02	1228-03	1228-04	1228-06	1229-01	1229-02	1229-03	1229-04	Phylum	Class	Order	Family	Genus	Species
OTU_8816	12.8	8.9	3.0	4.2	0.8	3.8	5.0	29.6	13.0	5.1	Proteobacteria	Gammaproteobacteria	Chromatiales	Granulosiccaceae	Granulosiccoccus	Granulosiccoccus_coccoides
OTU_7967	2.5	4.2	4.9	1.9	10.6	6.5	0.2	0.9	1.0	0.4	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Cellulophaga_g1	Cellulophaga_g1_uc
OTU_7706		7.0	8.1	1.4	6.0	10.7		0.2		0.2	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Flavobacterium_gillisiae
OTU_5527	2.1	3.4	3.0	1.1		2.2	7.9	4.6	2.3	7.3	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Aestuariibacter	Aestuariibacter_uc
OTU_7167	0.4	0.8	0.9	5.4		0.9			1.4	0.8	Actinobacteria	Acidimicrobiia	Acidimicrobiales	Acidimicrobiales_uc		
OTU_7360	1.2	3.4	1.2	1.9		2.9	0.6	0.2	2.0	4.1	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flaviramulus	Flaviramulus_uc
OTU_6998	3.1	0.8	5.3	1.4		0.7	3.6	0.5	1.4	2.3	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacteriaceae_uc	
OTU_7975				3.4	0.3	2.9			0.3	0.1	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Flavobacterium_uc
OTU_4347				4.4							Proteobacteria	Betaproteobacteria	Thiobacillus_o	Thiobacillus_f	Thiobacillus	Thiobacillus_uc
OTU_5951	1.1	1.4	0.2	1.7		0.7		0.2	2.7	1.1	Actinobacteria	Acidimicrobiia	Acidimicrobiales	Ilumatobacter_f	Ilumatobacter_f_uc	
OTU_7479	0.2	2.0	0.2	0.7	7.0	2.0	0.2		0.8	0.1	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Rhodoferax	Rhodoferax_uc
OTU_6653	2.5	1.7	3.3	0.2	1.3	1.2	4.4	0.9	0.1	0.2	Proteobacteria	Gammaproteobacteria	Thiotrichales	Thiotrichaceae	Cocleimonas	Cocleimonas_uc
OTU_6945		2.8	2.1	0.1	8.6	1.8					Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Maribacter	Maribacter_arcticus
OTU_7179	0.9		0.7	1.2		0.6	0.6	1.4	0.5	2.4	Proteobacteria	Gammaproteobacteria	Chromatiales	Granulosiccaceae	Granulosiccoccus_uc	
OTU_8288		1.4	1.6	0.5	2.7	3.9			0.1	0.1	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Flavobacterium_frigoris
OTU_8665	0.1	1.1	1.9	0.9	4.6	1.0	0.4				Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Flavobacterium_uc
OTU_8369	2.1	1.1	0.2			1.0	2.1	2.1	2.5	0.5	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacteriaceae_uc	
OTU_8353	3.0	2.0	0.9	0.0		0.3	0.2	0.2	1.0	2.5	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacteriaceae_uc	
OTU_4028	1.1	0.3	0.5	0.1	0.3	0.7	0.8		0.8	3.8	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Maritimimonas	Maritimimonas_uc
OTU_6349	0.4	1.1	2.1	1.4		1.0				0.1	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Ulvibacter	Ulvibacter_litoralis

Abundant OTUs in upper layer

	1222-01	1222-02	122-03	122-04	122-05	122-06	122-07	122-04-01	122-04-02	122-04-03	122-06-01	122-06-02	122-06-03	123-01-01	123-01-02	123-01-03	Phylum	Class	Order	Family	Genus	Species
OTU_8249	0.2	1.0	2.8	0.6		0.9	0.8			3.3			3.9	4.2	0.5	1.1	AD3	AD3_c	AD3_o	EF018548_f	EF019899_g	EF019899_s
OTU_8255	1.2	2.2	2.0	1.5	0.3	0.1	2.2	0.1	0.8	1.9				0.6	0.3	0.7	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Afipia_g1	Afipia_g1_uc
OTU_6916	0.7	0.5	0.3	2.0	1.0	0.1	0.1	3.2	2.0	1.2	3.9	1.8		0.9	0.8		Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	EU979111_g	EU979111_g_uc
OTU_6689	0.6	1.0	1.2	1.0			1.1			2.0				5.1	0.1		AD3	AD3_c	AD3_o	AD3_f	AD3_f_uc	
OTU_8456				0.1		2.4	0.1				0.7			1.1	9.4	3.2	Acidobacteria	Solibacteres	FJ479064_o	FJ479064_f	EF494375_g	EU223939_s
OTU_8900	1.7	1.1	0.4	2.1			1.4			1.1				3.2			Actinobacteria	Thermoleophilia	Solirubrobacterales	Conexibacteraceae	Conexibacter	Conexibacter_uc
OTU_8784	0.3	0.4	0.0		1.3	0.4		0.3		0.1	0.2		2.0	0.2	8.7	1.4	Acidobacteria	Solibacteres	FJ479064_o	FJ479064_f	EU132075_g	EU132075_g_uc
OTU_8054	0.2	2.1	1.7	1.0		0.1	0.9			0.6				0.3	0.2		Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Pseudolabrys	Pseudolabrys_uc
OTU_5679		0.0			0.1			7.2	2.0			1.8					Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Psychrobacter	Psychrobacter glaucincola
OTU_7240	1.0	0.7	1.3	1.3	0.2		0.4			3.3				0.5	0.3	0.2	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rudaea	4P000036_s
OTU_7446	0.9	0.1	0.0		1.8	3.3	0.2		0.6				5.9	1.1	2.4	0.2	Actinobacteria	Rubrobacteria	Gaiellales	Gaiellaceae	EF516148_g	EU861844_s
OTU_6296	0.6	0.8	1.4	0.4			0.2			0.4				2.7	0.9	0.5	Thermobaculum	Thermobaculum_c	AY221067_o	EF516242_f	EF516242_g	EF018866_s
OTU_7572	0.1	0.7	0.3	1.0		0.7	2.1			0.4				0.1		0.2	AD3	AD3_c	AD3_o	EF018548_f	EF018548_g	EF018976_s
OTU_8291					7.5	1.8									1.4	1.4	Actinobacteria	Thermoleophilia	Solirubrobacterales	DQ413118_f	DQ413118_g	EF516859_s
OTU_7493		0.2	0.4	0.7			2.2			0.2				0.1			AD3	AD3_c	EU861914_o	EF516692_f	EF516692_g	EF516692_g_uc
OTU_7883	0.7	0.6	0.4	0.4			1.9			0.1				0.2			AD3	AD3_c	EU861914_o	EU861914_f	EF018387_g	EF018387_s
OTU_8602		0.0	0.1			2.7		3.2	0.4	0.1			5.9		0.2		Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Polaromonas	Polaromonas glacialis
OTU_8794		0.1	0.3			0.1		3.7	1.4	0.3							Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Curvibacter	Curvibacter_uc
OTU_8662	1.0	0.4	1.3	1.4			0.4			0.1				0.6			Actinobacteria	Thermoleophilia	Solirubrobacterales	Solirubrobacteraceae	Solirubrobacter	Solirubrobacter_uc
OTU_8623	0.6	0.1	0.8	0.8	0.1	0.1	0.3	0.2	1.8	0.4	0.1	1.8		0.4	0.5		Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	Sphingomonas_uc

Abundant OTUs in lower layer

	1222-01	1222-02	1222-03	1222-04	1222-05	1222-06	1222-07	1224-01	1224-02	1224-03	1226-01	1226-02	1226-03	1228-05	1231-01	1231-02	1231-03	Phylum	Class	Order	Family	Genus	Species
OTU_8249	1.3	1.3	10.0	8.2		0.9	1.4		0.4	19.1		1.9		0.6	6.8	1.0	1.3	AD3	AD3_c	AD3_o	EF018548_f	EF019899_g	EF019899_s
OTU_6296	1.8	1.6	2.8	4.4		0.4	0.9	0.1		2.7		0.2	1.2		3.0	0.4	2.1	Thermobaculum	Thermobaculum_c	AY221067_o	EF516242_f	EF516242_g	EF018866_s
OTU_5505	0.0		0.0	3.5						0.0					13.8			Actinobacteria	Rubrobacteria	Gaiellales	Gaiellaceae	EF516148_g	EF516148_g_uc
OTU_7502	0.0		7.4	2.0						1.2								AD3	AD3_c	AD3_o	EF018548_f	EF019899_g	EF019899_s
OTU_8456	0.0	0.1		0.0	0.5	3.8	1.2	0.3	0.2	0.1	0.2	0.2		0.6	22.5	7.5		Acidobacteria	Solibacteres	FJ479064_o	FJ479064_f	EF494375_g	EU223939_s
OTU_7446	1.2	0.1		0.2	5.8	3.9		0.4	8.8	0.2			7.2	1.3	3.4	3.4	1.5	Actinobacteria	Rubrobacteria	Gaiellales	Gaiellaceae	EF516148_g	EU861844_s
OTU_8054	2.1	3.0	2.6	1.9		0.1	0.7	0.0		3.4		0.3			0.5		0.2	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiacae	Pseudolabrys	Pseudolabrys_uc
OTU_6689	1.2	0.7	2.0	2.8			0.7		0.0	3.4					3.0	0.1	0.1	AD3	AD3_c	AD3_o	AD3_f	AD3_f_uc	
OTU_8310	0.1	10.6	0.2	0.4	1.7	2.2		0.5	0.3	0.1	0.3	0.1		1.3	0.2	0.2	2.3	Actinobacteria	Rubrobacteria	Gaiellales	Gaiellaceae	FJ479094_g	FJ479094_s
OTU_8118	0.4	0.6	2.3	1.4			1.2			3.0					0.5	0.0	0.2	Gemmatimonadetes	Gemmatimonadetes_c	Gemmatimonadales	EU421850_f	EU421850_g	EU421850_g_uc
OTU_8865	0.1				1.7	3.9		0.2	0.4	0.2			3.6		5.2	2.8	2.2	Actinobacteria	Rubrobacteria	Gaiellales	Gaiellaceae	EU881252_g	EU881252_g_uc
OTU_8830	0.4	0.7			4.2	2.2		0.5	0.0	0.1	0.0				4.3	2.7	4.6	Actinobacteria	Rubrobacteria	Gaiellales	Gaiellaceae	EU881141_g	EU881141_g_uc
OTU_8255	0.7	2.6	1.2	0.9		0.1	1.9	0.3	0.6	1.8	0.1	0.3		0.7	0.3	0.3	0.6	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiacae	Afipia_g1	Afipia_g1_uc
OTU_7493	0.0	0.6	1.4	2.5			2.5			3.6					0.0			AD3	AD3_c	EU861914_o	EF516692_f	EF516692_g	EF516692_g_uc
OTU_7572	0.4	0.7	0.9	2.3	0.5	0.7	3.9	1.0	0.0	2.4			2.4	0.6	0.0	0.0		AD3	AD3_c	AD3_o	EF018548_f	EF018548_g	EF018976_s
OTU_6913	0.4	0.8	1.0	0.2	0.1	1.3		0.2	0.6	0.5		1.5			2.1	0.2	1.0	Actinobacteria	Rubrobacteria	Gaiellales	Gaiellaceae	EF516148_g	EF516148_g_uc
OTU_8291					17.6	5.7			0.1	0.0	0.0				0.0	2.6	0.2	Actinobacteria	Thermoleophila	Solirubrobacterales	DQ413118_f	DQ413118_g	EF516859_s
OTU_8590	1.3	0.5	1.5	0.9	0.6		1.3			1.7					0.1	0.2		Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	DQ823227_g	DQ823227_g_uc
OTU_8903		1.3		1.6			0.4						0.1		4.2			AD3	AD3_c	AD3_c_uc			
OTU_8784	0.3	0.2	0.0	0.7	0.7	2.4		0.6	0.1	0.1	0.3	0.3		0.4	0.6	4.6	5.0	Acidobacteria	Solibacteres	FJ479064_o	FJ479064_f	EU132075_g	EU132075_g_uc

Future works

- Different bacterial communities have been significantly observed between coastal soils and inland soils.
In addition, inland soil bacteria between upper and lower layer showed similar composition but different proportion.
- What are the core microorganisms that drive terrestrial ecosystems of Barton Peninsula?
- How do bacterial community composition correlate with other biotic/abiotic environmental components?
- Where can be the representative site to establish long-term monitoring of bacterial community impacted by climate change?

A group of penguins, likely King penguins, are gathered on a rocky, pebbly shore. The penguins have black heads and backs with white chests and bellies. One penguin in the foreground is standing and looking towards the camera. A semi-transparent, light green speech bubble is overlaid on the image, containing the text "Thank you for your attention!!!". The background shows more penguins, some sitting and some standing, on the same rocky terrain.

**Thank you
for your attention!!!**