Contrasting Successional Trajectory of Microbial Community Convergence between Two Glacier Forelands of the High Arctic

> Hye Ryeon Gyeong, Mincheol Kim, Binu Mani Tripathi, Ji Young Jung, Yoo Kyung Lee Korea Polar Research Institute (KOPRI)













## 1. Background







#### Loss of glacier is accelerated





#### Deglaciation is subsequent until present





Myrtille et al. (2005) Kwon et al. (2015)



Sample	otus	Diversity index		
		Chao	ACE	Shannon
ML3	315	692.06	1107.41	4.58
ML4	529	1357.1	2488.53	5.42
ML6	634	1630.96	3364.71	6.03
ML7	638	1743.82	3145.94	6.05
Total	2116			
			17	

Kwon et al. (2015)











- How does above-ground vegetation relate to belowground microbial communities in terms of diversity and community structure along the succession time?
- Do microbial communities converge towards later successional stage?
- How do patterns of species richness and composition shift as glacier retreating in both glacier foreland?
- What are the major drivers of the changes in microbial community structure?



#### Study site





#### Soil sampling



- Three sets of transects on each glacier foreland
- 5 points on each 1m x 1m quadrat were combined to make a composite sample





- Soil sampling 2016. 07
- Vegetation survey Myrtille Moreau, France CNRS
- Soil physiological analysis
  - Soil texture, TC, TN, pH, electric conductivity (EC), water contents, available P and chemical composition of soils
- DNA extraction and sequencing
  - Mi-seq 2 x 300 bp, amplicon sequencing for bacteria, fungi, eukaryote and archaea.



#### Vegetation Survey

- Coverage (%) Lichen, Vascular plant, Bryophyte, Biotic crust
- Determination of vegetation abundance and frequency



2. Each sample was demarcated into four  $1-m^2$  quandrants and further demarcated into 100  $1-cm^2$  cells



3. Veg from s sample within drant

3. Vegetation acquired from six randomly sampled 10-cm<sup>2</sup> cells within each 1-m<sup>2</sup> quadrant



Moreau et al. (2005)

NMDS and community variance of vegetation of both glacier forelands

4. Results

Successional stage





# NMDS of microbial community of Austre Lovenbreen













# NMDS of microbial community of Bloomstrand













Community variance of microbial community along the successional stage, Austre Lovenbreen





Community variance of microbial community along the successional stage, Bloomstrand breen





#### OTU richness of microbial community, Austre Lovenbreen







#### OTU richness of microbial community, Bloomstrand breen









- The plant community structure of both glacial foreland shifted following the successional stage.
- The microbial communities show successional trajectories with the time since deglaciation in Austre Lovenbreen and Bloomstrand breen.
- The bacterial and fungal community converged through stage 1 and 2 in Austre Lovenbreen. This may reflect the vegetation establishment, exist or not, of the site.
- The OTU richness of microbial community, except for archaea, increased along the successional stage in both glacier foreland.
- These results reveal the successional trajectories of bacteria and fungi in both glacier foreland and We are still analyzing soil characteristics to find the major drivers that caused the shifts of microbial community.





Yoo Kyung Lee



Mincheol Kim



Ji Young Jung



Binu Mani Tripathi



Hye Ryeon Gyeong

