

Comparison of bacterial succession along the chronosequences of two glacier forelands of the High Arctic

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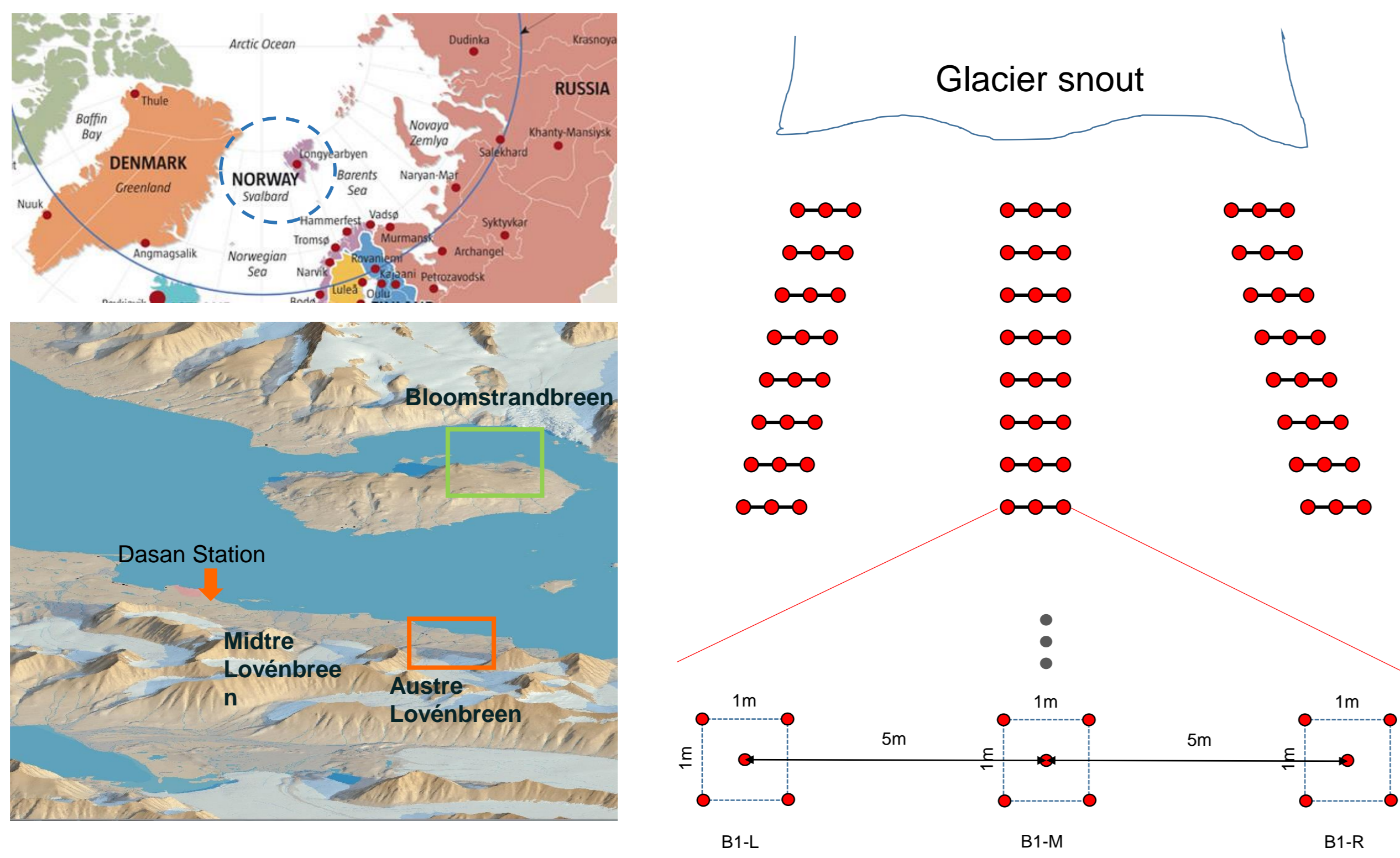
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Abstract

Glacier foreland chronosequences offer a model setting for understating ecological succession. Bacterial succession is relatively poorly understood in glacier foreland soils of the High Arctic. We investigated the successional changes in bacterial community composition and diversity along the chronosequences of two glacier forelands (Austre Lovénbreen: AL and Bloomstrandbreen: BS). The bacterial communities were analyzed using MiSeq sequencing of 16S rRNA gene. The ANOSIM analysis revealed that bacterial community compositions were significantly shifted along the chronosequences of both AL and BS glacier forelands. There were directional trajectories in the relative abundance of some of the dominant bacterial phyla throughout succession. Bacteroidetes are more abundant at early successional stages and decreased towards later phases in both regions. Planctomycetes showed a contrasting changing pattern along the chronosequence with increasing relative abundance in AL and vice versa in BL. Bacterial diversity decreased significantly along BS chronosequence, whereas it remained unchanged in AL. Overall, our results indicate that bacterial community compositions were changed in a predictable way along chronosequences of both glacier forelands. However, bacterial diversity and phyla relative abundance showed different patterns along both glacier forelands. This discrepancy between two glacier forelands could be further explained by comparing local environmental conditions and vegetation dynamics in the future.

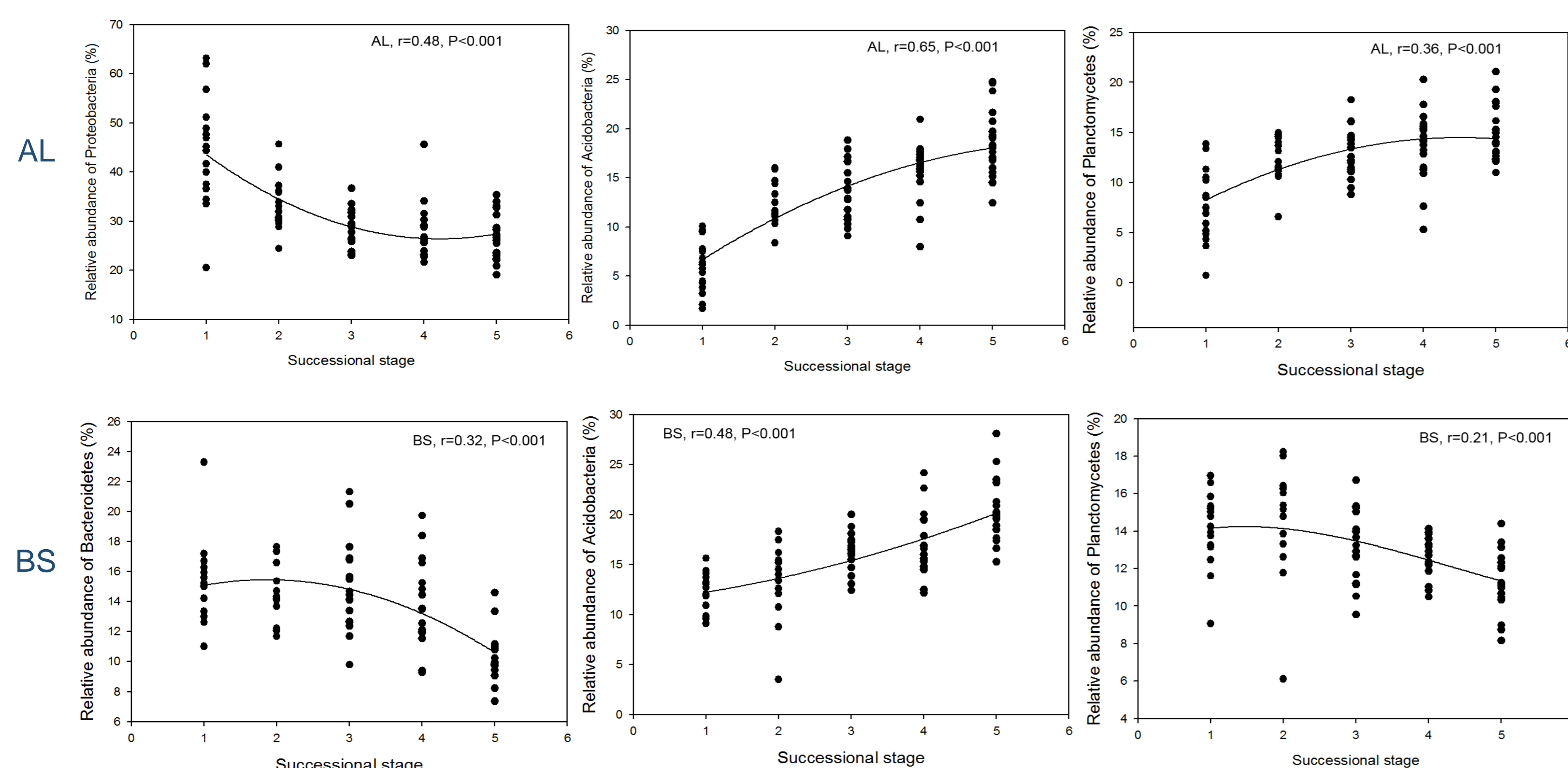
Study site

- ❖ Location : the forelands of Austre Lovénbreen (AL) and Bloomstrandbreen (BS) glacier at the east of NyÅlesund, Svalbard (79°N).



Results

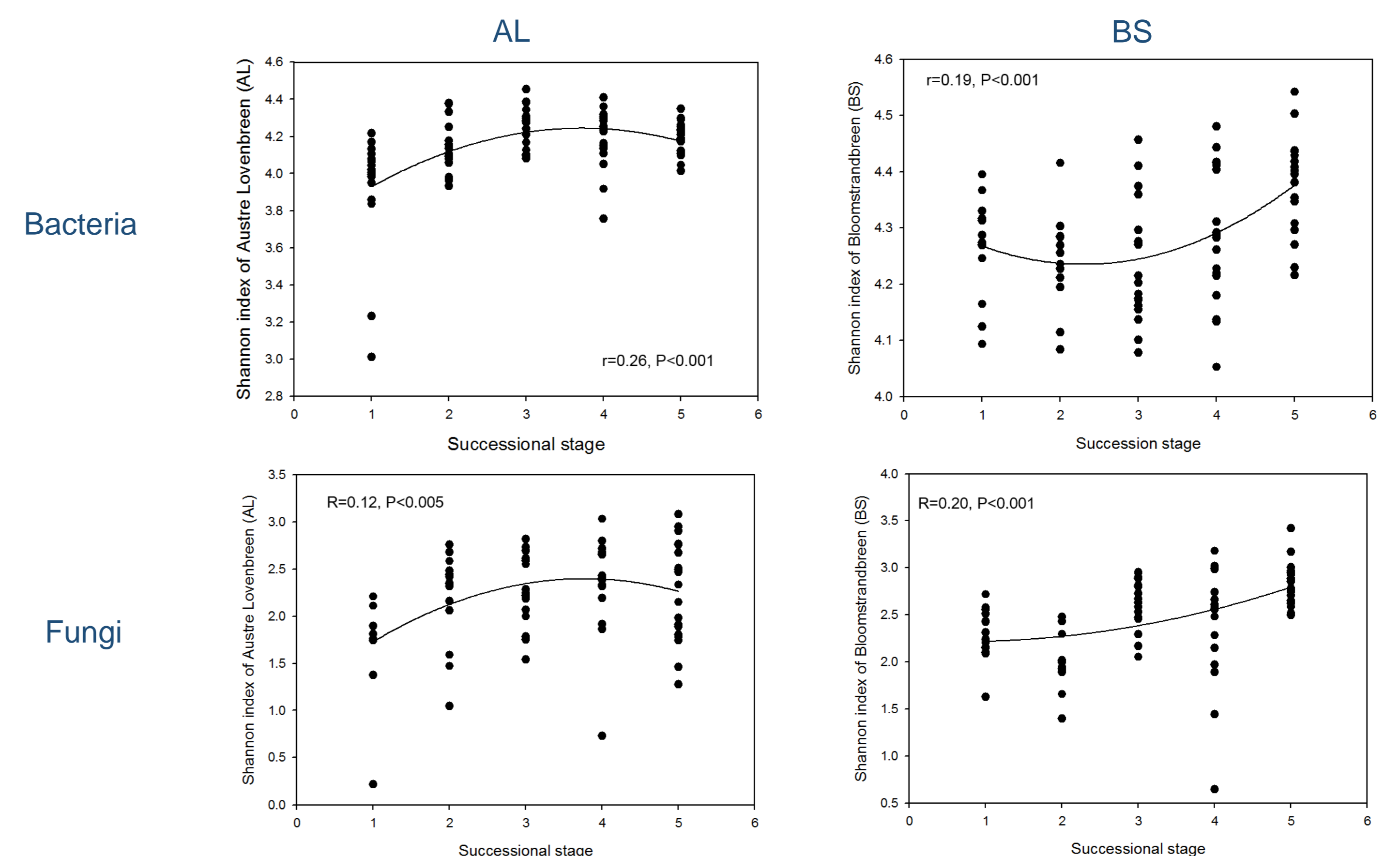
- ❖ Changes in bacterial phyla abundance are in both glacier forelands along the chronosequence



Acknowledgements

- ❖ This study was supported by the Korea Polar Research Institute (PE17280, KOPRI).

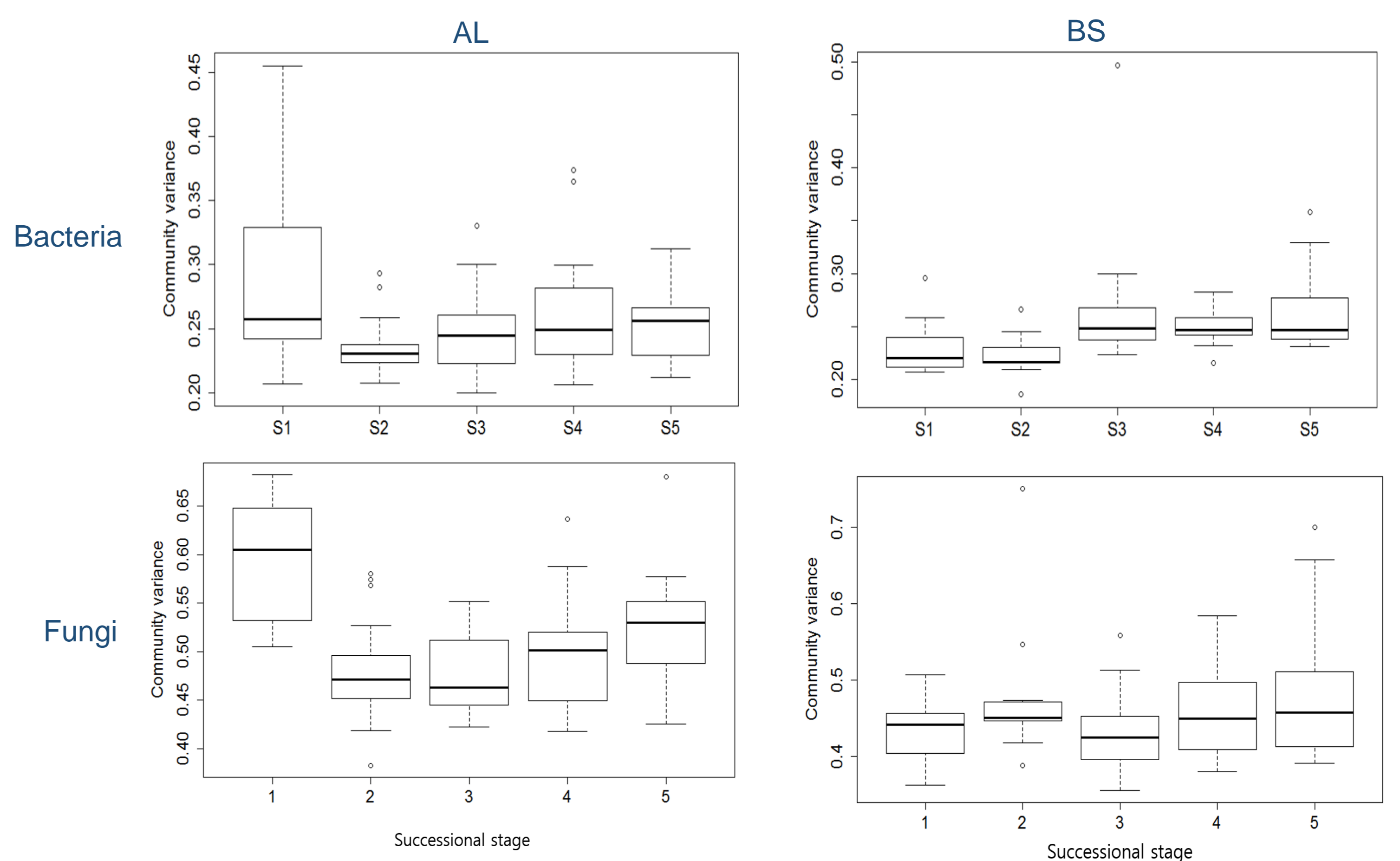
- ❖ Changes in bacterial community diversity along the chorosequence



- ❖ Shifts in bacterial and fungal structure over successional time



- ❖ Variance of bacterial and fungal community structure are changed over successional time



Conclusions

- ❖ Bacterial diversity index increased and phyla abundance changed over successional time, but some bacterial abundance showed contrary changing patterns.
- ❖ Microbial community structure shifted from initial to later stages of succession in both glacier foreland.
- ❖ Microbial community variance of Austre Lovénbreen decreased along the chronosequence in contrast Bloomstrandbreen.