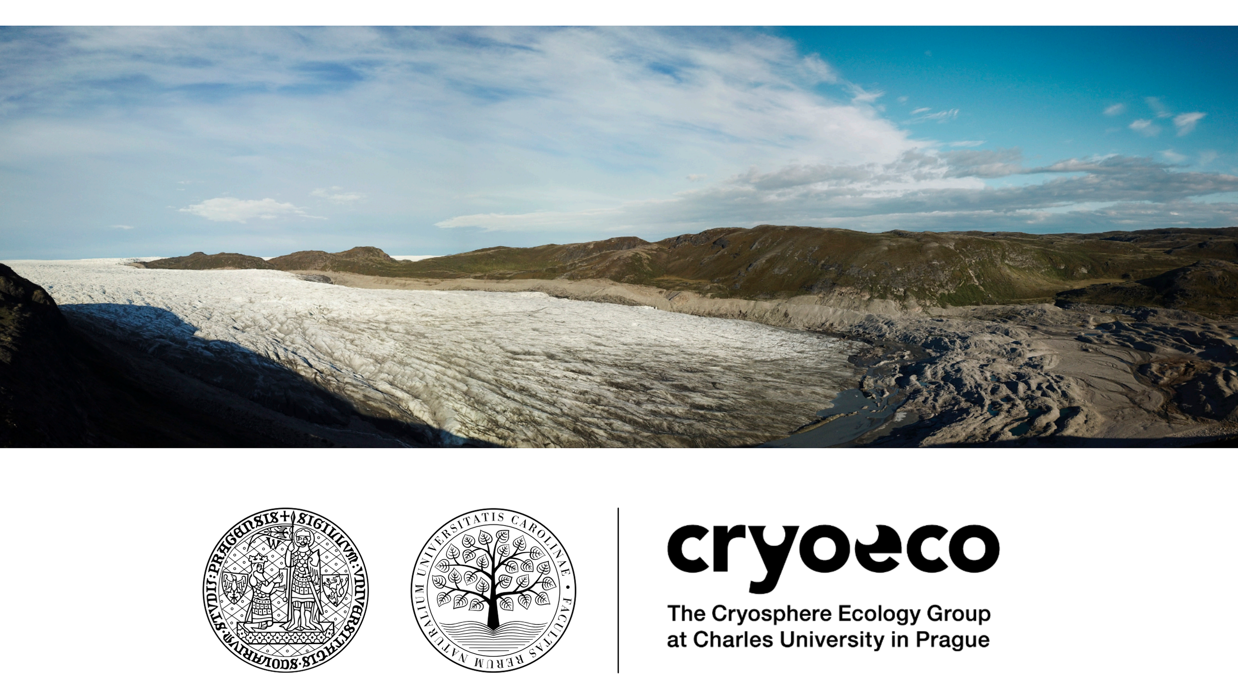
GLACIAL MELTWATER MICROBES:

ARE THERE SEASONAL TRENDS IN EXPORTED ASSEMBLAGES OVER DIFFERENT CATCHMENT SIZES?



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INTRODUCTION

A subglacial drainage system develops annually beneath outlet glaciers of the Greenland Ice Sheet (GrIS), evolving from an inefficient distributed network to an efficient channelized pathway. The extent and interconnectivity of the subglacial drainage system with the glacier surface and bed is hypothesized to differ with catchment size. Glaciers and ice sheets host diverse microbial life within hydrologically connected habitats, and cells are collected from the entire glacial ecosystem by meltwater and exported by proglacial streams. Thus, much can be learned about subglacial hydrological pathways by analysing microbial cells in transport.

Do microbial assemblages exported from GrIS outlet glaciers differ with catchment size?

METHODS

Three outlet glaciers (Isunnguata Sermia, IS; Leverett Glacier, LG; Russell Glacier, RG) of the GrIS with different catchment sizes were sampled for three weeks over the 2018 summer (Figure 1, 2).

16S rRNA gene amplicons sequenced, and principal coordinates analysis (PCoA) and diversity indices (Observed, Chao1, Shannon) were calculated on the rarefied dataset.

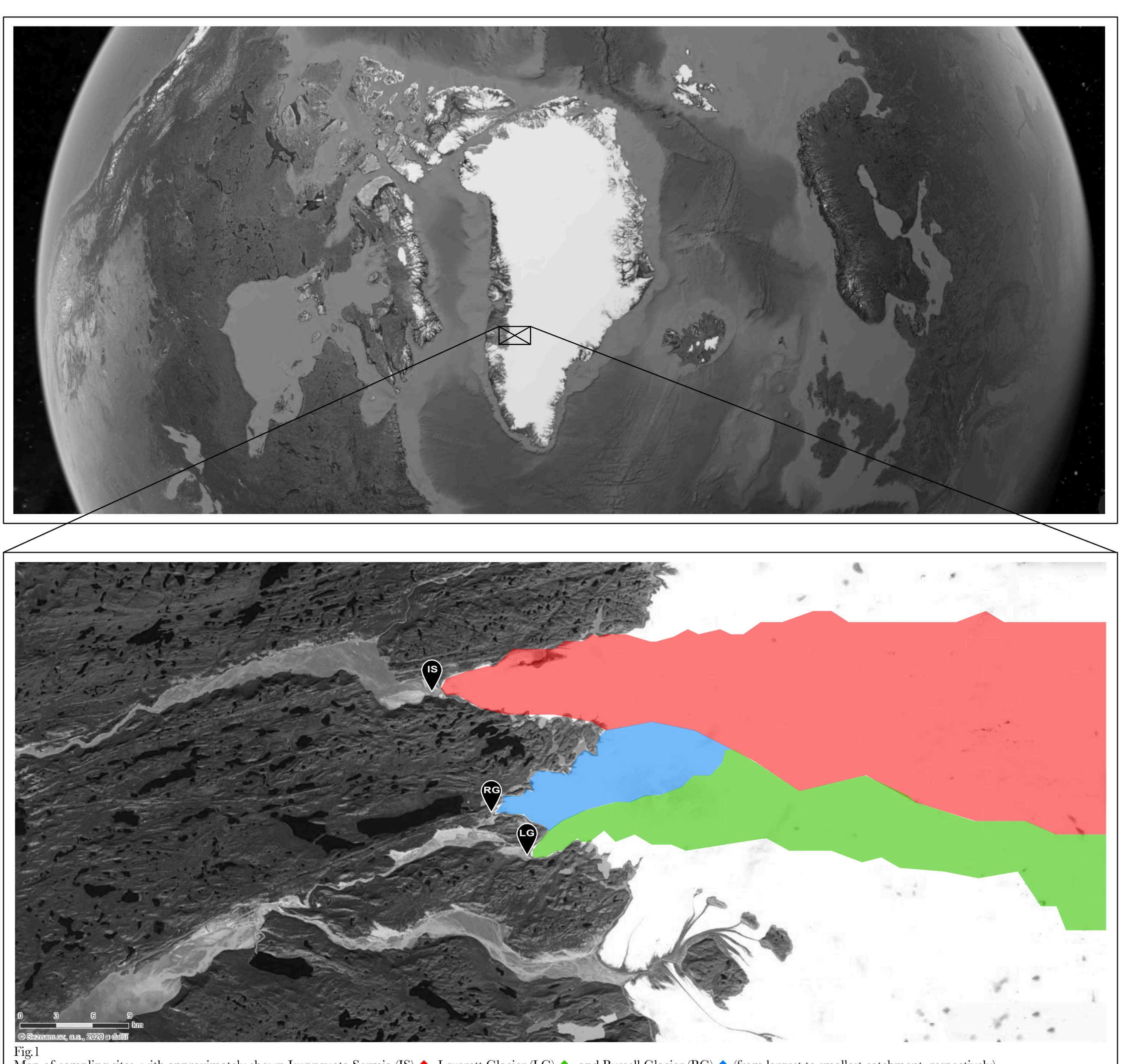


Fig.1
Map of sampling sites, with approximately shown Isunnguata Sermia (IS) ◆, Leverett Glacier (LG) ◆, and Russell Glacier (RG) ◆ (from largest to smallest catchment, respectively)

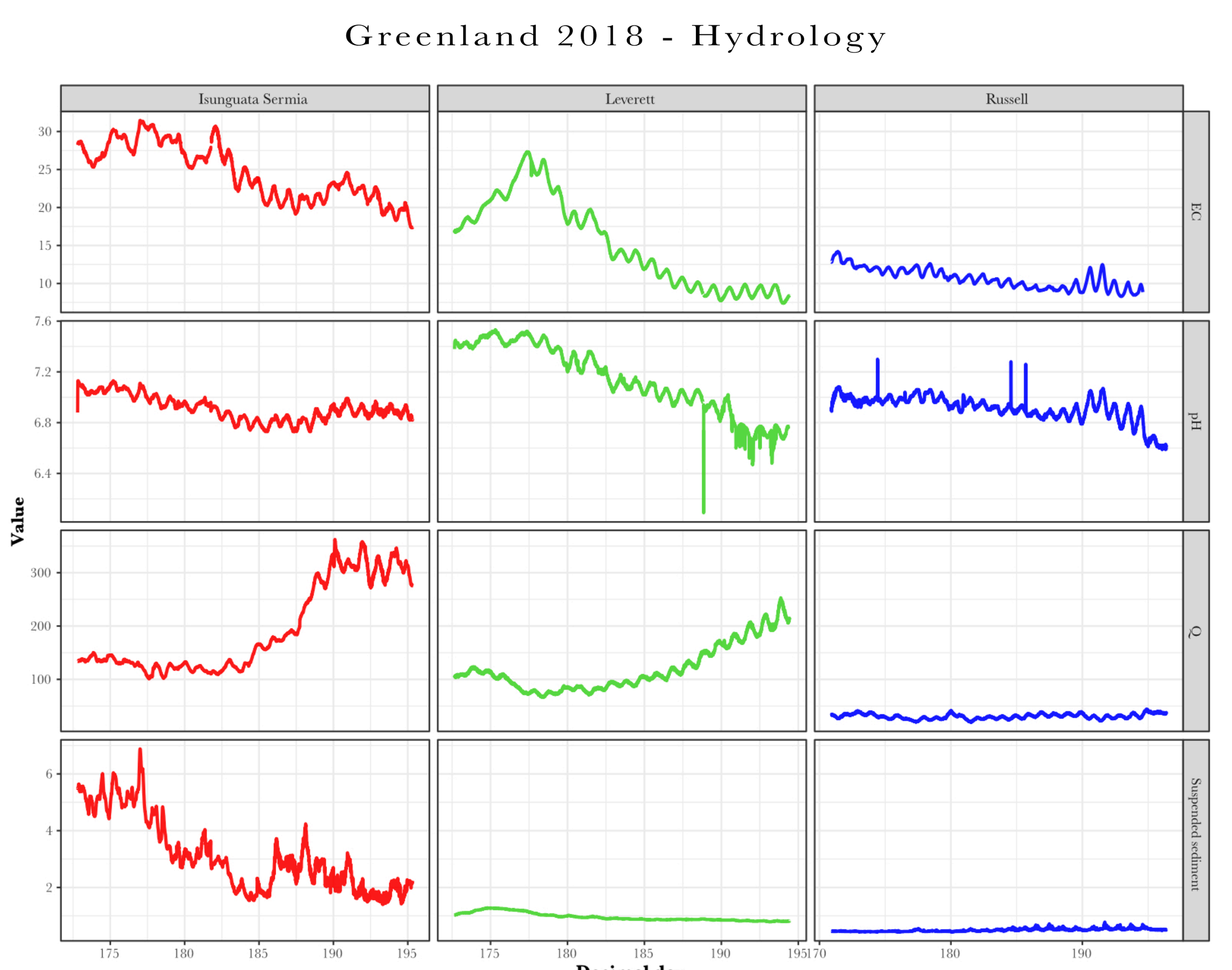
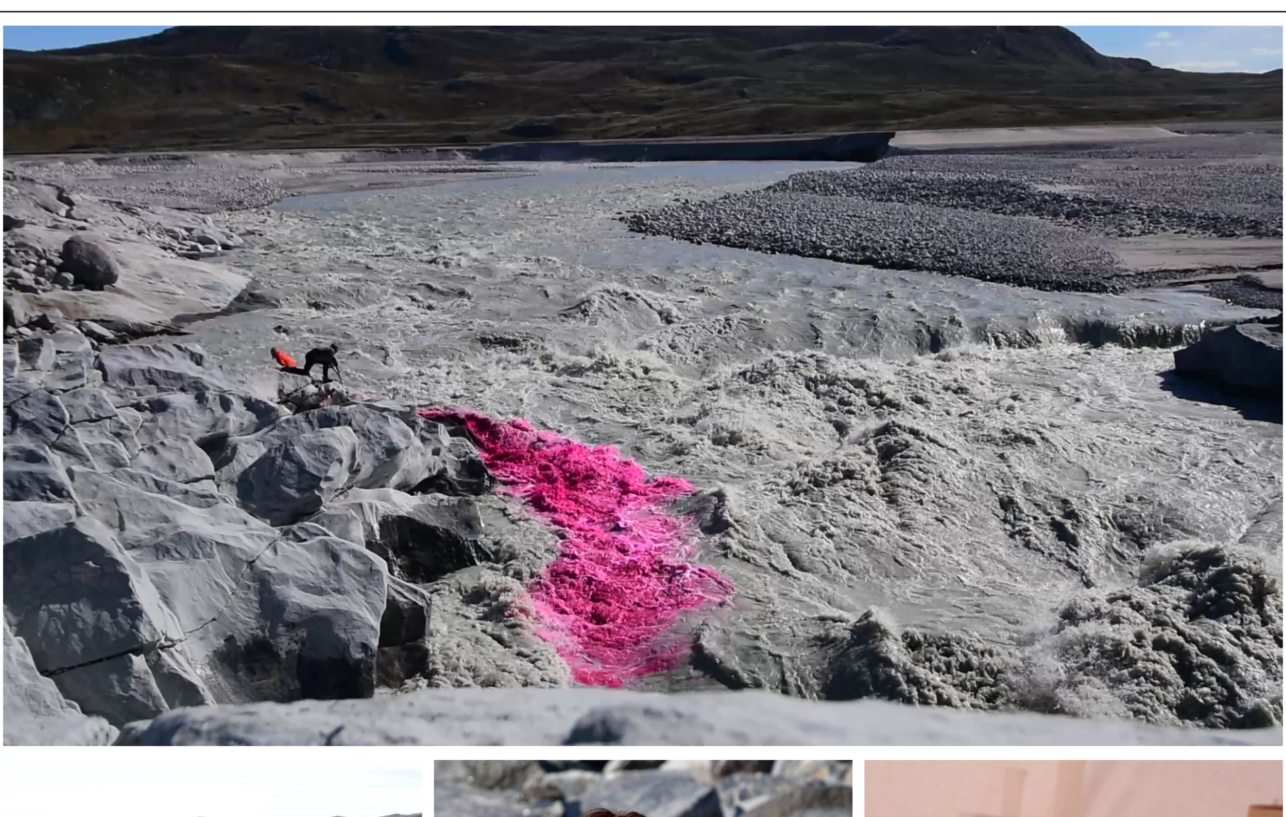
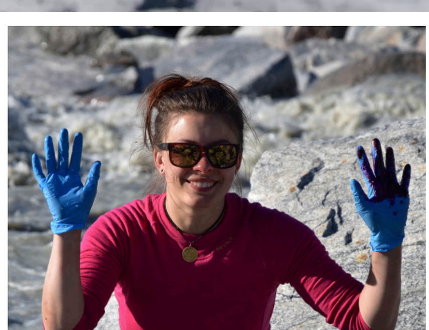


Fig.2
Discharge and water chemistry for the 2018 summer.





RESULTS & DISCUSSION

The largest catchment, IS, and the smallest catchment, RG, both had comparable meltwater stream alpha diversity, while the intermediate catchment, LG, was significantly lower (Figure 3).

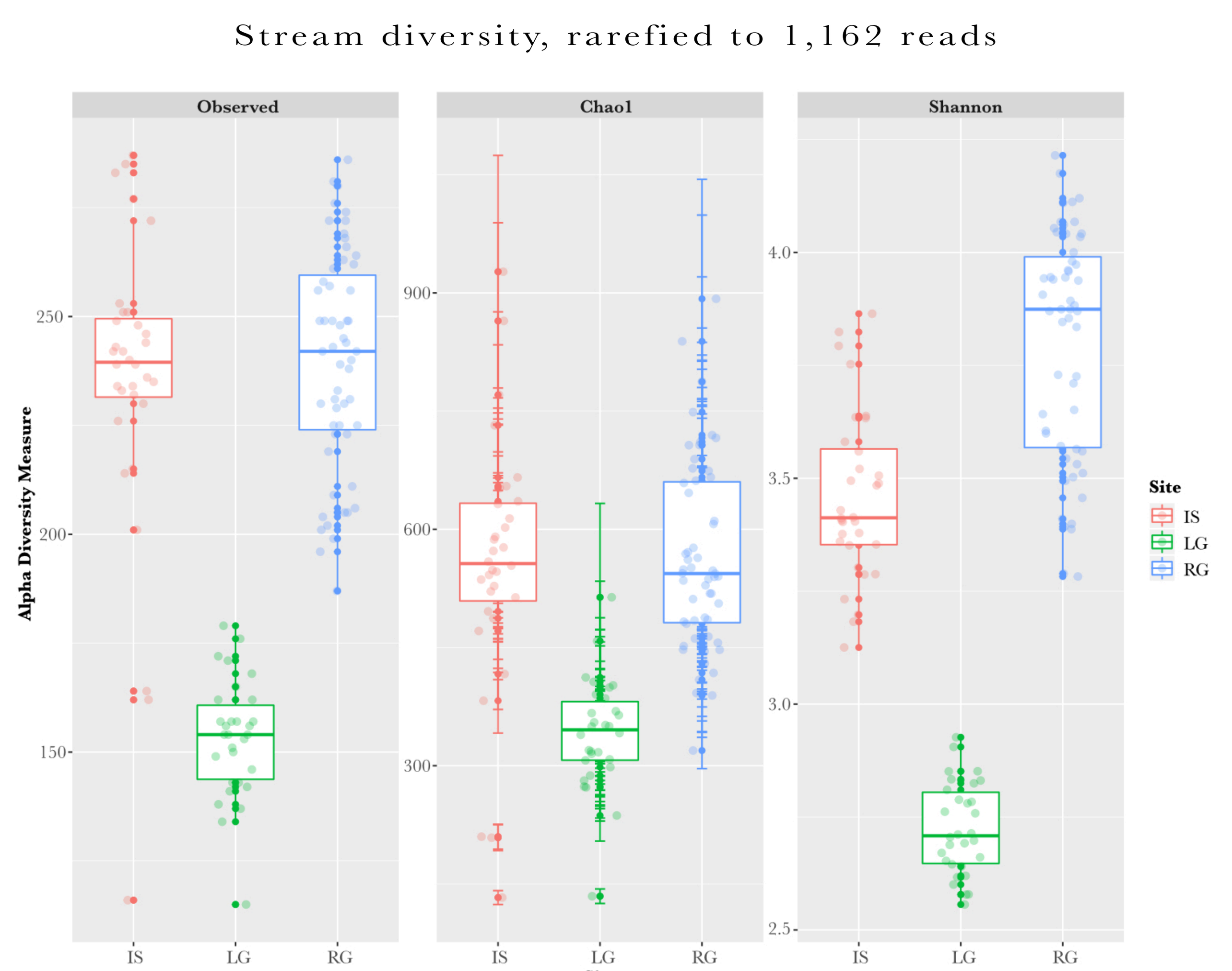


Fig.3
Boxplots comparing the alpha diversity (observed number of OTU's, Chao1 and Shannon diversity index) from the three catchments (IS, LG, RG).

Within the PCoA, samples from the two largest catchments, IS and LG, clustered together, while the smallest catchment samples, RG, clustered separately (Figure 4). At the family level, these differences likely originate from the high proportions of Bacteroidales, Frankiales, and Methylococcales present in the RG stream (Figure 5).

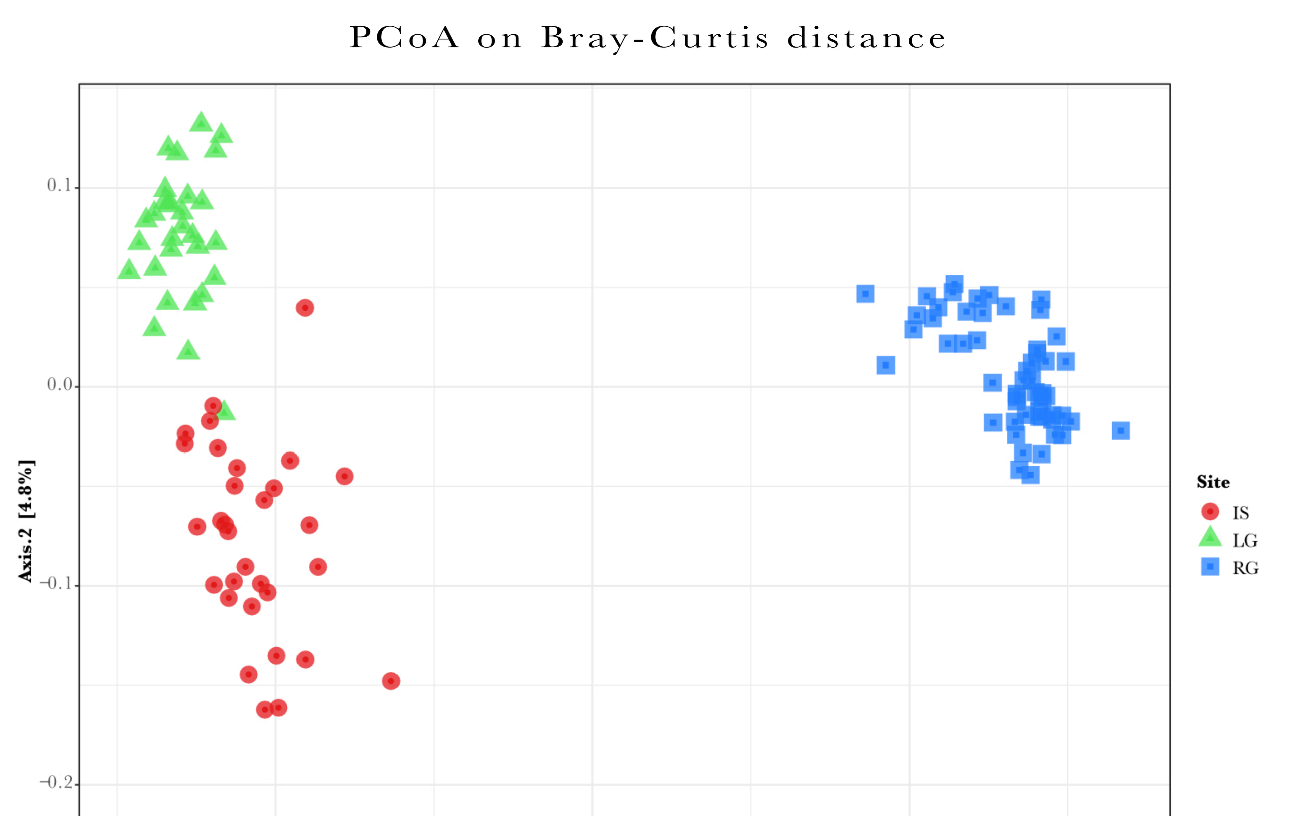


Fig.4
Principal coordinates analysis (PCoA) showing differences between the three sites (Red-IS, Green-LG, Blue-RG) based on Bray-Curtis distance matrices.

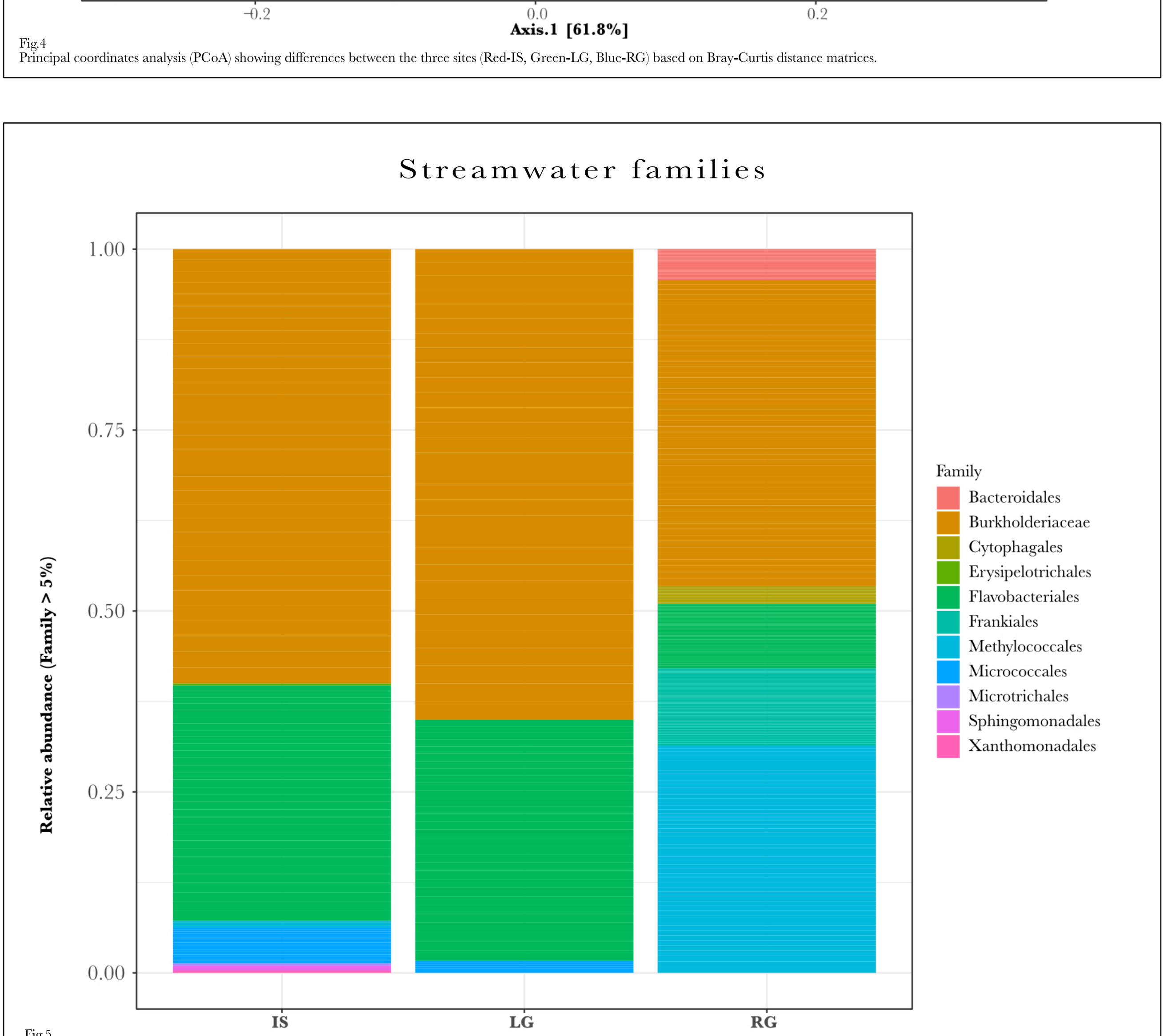


Fig.5
Relative abundance of major bacterial families by catchment.

CONCLUSIONS

These initial results show that catchment size is likely influential for determining exported assemblage structure over the GrIS, while other factors may be at play affecting diversity. Further analysis will focus on seasonal and diurnal patterns of exported material.

ACKNOWLEDGEMENTS

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Map source: Google Earth & Mapy.cz.