

Seasonal variation in airborne prokaryotic and eukaryotic communities in Ny-Ålesund, Svalbard

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The Arctic region is undergoing rapid environmental changes due to global climate warming. Among the Arctic regions, the surface temperature in the northern Barents Sea, where the Svalbard archipelagos are located, has increased more significantly than in other areas over the last 40 years (Isaksen *et al.* 2022). This warming results in the loss of sea ice in the ocean and glacier ice in terrestrial areas. These changes in surface conditions may impact the emission of bioaerosols from the Earth's surface, which play a crucial role in ecosystem dynamics and cloud formation (Tobo *et al.* 2019). However, there is still limited temporal monitoring in Svalbard and also in entire Arctic. Therefore, in this study, we focus on assessing the temporal changes in bioaerosols during the summer to autumn season in Ny-Ålesund, Svalbard using DNA metabarcoding approaches. Bioaerosol samples were collected using a vacuum pump with a flow rate of 40 LPM onto HEPA-style filters at the outdoor observatory of the Veksthuset building in Ny-Ålesund. Filters were replaced every 24-72 hours from July to November 2022. Those were then preserved in DNA storage medium (DNA/RNA shield) and transported to the laboratory under frozen conditions. Following particle concentration and DNA extraction, we amplified and sequenced three DNA metabarcoding regions (16S, 18S, and ITS) using the MiSeq platform (Illumina). The resulting amplicon dataset was analyzed and visualized using R packages, including DADA2, phyloseq, and MicroViz.

Seasonal changes in the observed number of Amplicon Sequence Variants (ASVs) from each barcoding region exhibit distinct patterns (see Fig. 1 D). These patterns are characterized by high ASV counts during the summer (ITS and 18S) and the autumn (16S). Microbial communities of 16S region at the phylum level remain relatively stable throughout the entire season (Fig. 1A). Otherwise, those within the 18S and ITS regions show significant changes beginning in early September (Fig. 1 B, C). In the presentation, we will provide a more detailed explanation of community changes at the ASV level and discuss the microbial contributions to cloud formation.

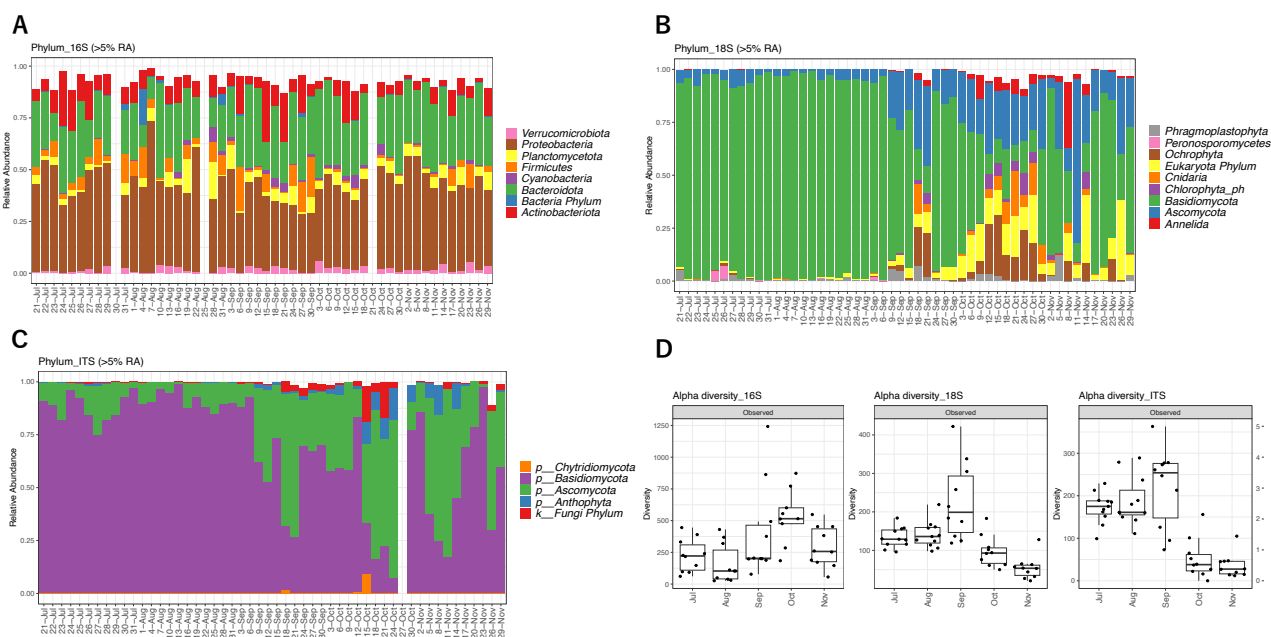


Figure 1. Seasonal changes in microbial communities at the phylum level of 16S(A), 18S (B), ITS (C). Monthly change in the observed number of amplicon sequence variants (ASVs) for those three regions (D).

References

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