The effect of artificial water infiltration on microbial diversity and potential of the Uppsala esker

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Introduction

In Uppsala, drinking water comes from groundwater which is naturally cleaned via passage through the Uppsala esker, a ridge that was formed during the last Ice Age through the movement of glaciers.

Due to the city's growing water demand, several infiltration systems were installed in the late 60s to artificially recharge the groundwater with water from river Fyrisån or lake Tämnaren. For the present study, soil core samples from different depths along the Uppsala esker were subjected to microbial community sequencing. The aim was an overall biological assessment of the esker, showing microbial community patterns in relation to their environment, and to investigate the effects of artificial water infiltration on these communities.

Material & Methods

Core samples from 0–36 m depth were taken in September 2014 at nine different drilling points across the esker, which included sites of artificial water infiltration, upstream (unaffected by infiltration) and downstream (affected by infiltration). The samples that were analysed in this study, consist of the cores that were subdivided into smaller sections. From each of these soil subsamples, various chemical parameters were measured.

The DNA of three replicates was extracted from each sample and subjected to next generation sequencing (Illumina) of the 16SrRNA gene, in order to assess the identity of the microbial community members.

Statistical analyses to relate patterns of bacterial diversity with environmental properties were then performed in the R package VEGAN.

Results & Discussion

Nonmetric multidimensional scaling (NMDS) analysis grouped the unaffected reference sites close together, with infiltrated and downstream (affected) sites being most similar to each other (p-value < 0.0001) (Fig. 1).

PERMANOVA was used to test which factors have the strongest effect on the microbial community pattern. The highest significant impact was the sampling site ($R2 = 0.14$, p-value = 0.0025), followed by infiltration (infiltrated, affected or unaffected) ($R2 = 0.11$, p-value < 0.0001) and the degree of water saturation (dry, unsaturated or saturated) ($R2 = 0.06$, p-value = 0.0015).

The overall community composition was not highly different in terms of species, but in the abundancy of certain community members when comparing the infiltration with a reference site. E.g. *Actinobacteria* were found at a higher relative abundance in the infiltration (35 %) than the reference site (12 %), whereas *Alphaproteobacteria* were more prominent at the reference (21 %) compared to the infiltration site (14 %).

The microbial richness (chao1) of the infiltration sites and downstream (affected) was significantly higher than compared to the upstream (unaffected) sites (Fig. 2), showing a clear effect of artificial water infiltration on microbial community patterns.

This difference in microbial diversity was to be expected, since the microbes closest to the infiltration site have covered a shorter distance (vertically) than those from the natural groundwater, which travelled longer horizontally through the esker and thus were stronger filtered out in this process.

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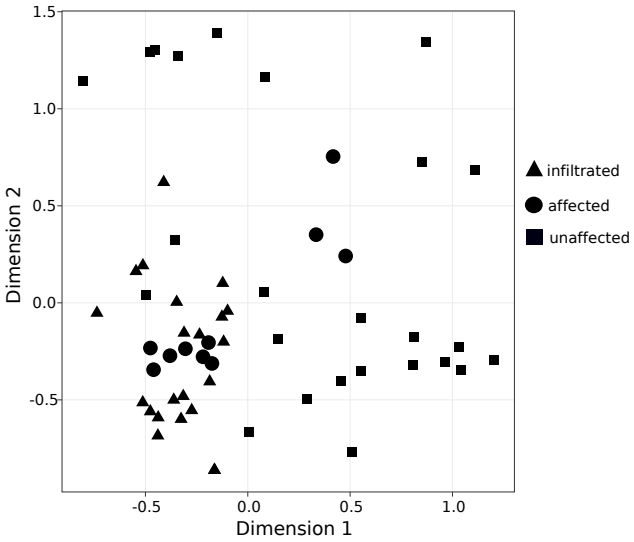

Figure 1 *NMDS grouping of the microbial communities by infiltration impact*

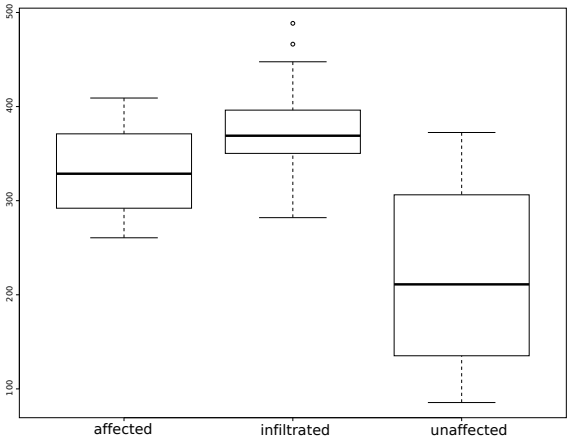

Figure 2 *Microbial richness (chao1) by infiltration impact*