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Microbial Ecology

**MICROBIAL SUCCESSION DYNAMICS IN THE FOREFIELD OF BREIÐAMERKURJOKULL
GLACIER (ICELAND)**

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Backgrounds

One key consequence of glacier recession, as effect of climatic change, is the creation of new habitats for colonization. In glacier forefields, primary succession occurs simultaneously in soils and rocks recently discovered offering a type of natural experiment in which temporal colonization dynamics can be analyzed.

Objectives

A chronosequence established at Breiðamerkurjökull Glacier forefield, was used as a framework to analyze primary microbial succession processes in subarctic regions. This outlet glacier stretches to southeast from Vatnajökull Glacier and has been dramatically retreating during the 20th century.

Methods

Soil samples from different succession stages were collected. Microbial community structure was analyzed by high-throughput amplicon sequencing. Potential microbial activity (microbial respiration, N mineralization) as well as different soil attributes were also measured in these samples.

Conclusions

Microorganisms play a fundamental role in the initial colonization of exposed soils after glacier ice retreat. They are the only colonizers at soils close to the glacier front and are functionally relevant in later successional stages. High-throughput amplicon sequencing of fungal and bacterial communities revealed that the structure of microbial communities from soils close to the glacier front considerably differed to that found in later successional stages. After a first abrupt change in community composition at the beginning of the succession, changes occur smoothly but showed a clear trend along the chronosequence. We found a significant decrease in soil pH, and a significant increase in the size of both, the soil organic matter and the organic and mineral N pools, in parallel with the succession process. Rates of microbial respiration and N mineralization also significantly increased with time of exposure after glacier retreat. Hence, our results demonstrate that primary succession along this chronosequence is accompanied by both a replacement of microbial taxa and changes in soil functionality.

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ABSTRACT BOOK



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