



ARCTIC HEALTH

*An information portal to issues affecting the health and well-being
of our planet's northernmost inhabitants*

Characterization of the bacterial communities on recent Icelandic volcanic deposits of different ages.

<https://arctichealth.org/en/permalink/ahliterature299615>

Author: Bo Byloos
Pieter Monsieurs
Mohamed Mysara
Natalie Leys
Nico Boon
Rob Van Houdt

Author Affiliation: Microbiology Unit, Interdisciplinary Biosciences, Belgian Nuclear Research Centre, SCK•CEN, Boeretang 200, B-2400, Mol, Belgium.

Source: BMC Microbiol. 2018 09 24; 18(1):122

Date: 09-24-2018

Language: English

Publication Type: Journal Article
Research Support, Non-U.S. Gov't

Keywords: Bacteria - classification - genetics - growth & development - isolation & purification
Biodiversity
Carbon - analysis - metabolism
DNA, Bacterial - genetics
Iceland
Nitrogen - analysis - metabolism
Phylogeny
RNA, Ribosomal, 16S - genetics
Soil Microbiology
Volcanic Eruptions - analysis

Abstract: Basalt is the most common igneous rock on the Earth's surface covering. Basalt-associated microorganisms drive the cycling and sequestration of different elements such as nitrogen, carbon and other nutrients, which facilitate subsequent pioneer and plant development, impacting long-term regulation of the Earth's temperature and biosphere. The initial processes of colonization and subsequent rock weathering by microbial communities are still poorly understood and relatively few data are available on the diversity and richness of the communities inhabiting successive and chronological lava flows. In this study, the bacterial communities present on lava deposits from different eruptions of the 1975-84 Krafla Fires (32-, 35- and 39-year old, respectively) at the Krafla, Iceland, were determined.

Three sites were sampled for each deposit (32-, 35- and 39-year old), two proximal sites (at 10 m distance) and one more distant site (at 100 m from the two other sites). The determined chemical composition and metal concentrations were similar for the three basalt deposits. No significant differences were observed in the total number of cells in each flow. 16S rRNA gene amplicon sequencing showed that the most abundant classified phylum across the 3 flows was Proteobacteria, although predominance of Acidobacteria, Actinobacteria and Firmicutes was observed for some sampling sites. In addition, a considerable fraction of the operational taxonomic units remained unclassified. Alpha diversity (Shannon, inverse Simpson and Chao), HOMOVA and AMOVA only showed a significant difference for Shannon between the 32- and 39-year old flow (p

PubMed ID: 30249184 [View in PubMed](#) 