Extracellular soil DNA (eDNA): a driving force of microbial life in initial stages of soil development?

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Proglacial areas = unique model systems for soil formation processes

1860 (150 yrs)

Deglaciation-Chronosequence

150 years-glacier retreat (= ca. 2 km)

2011 (0 yrs)

150 yrs

SOIL AGE

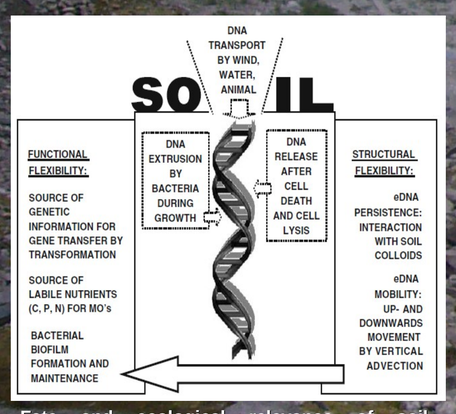
0 yrs

INCREASE

- Soil organic matter (Ctot, Ntot)
- iDNA content (=microbial biomass)
- eDNA content
- Enzyme activities
- Stability of microbial community structures

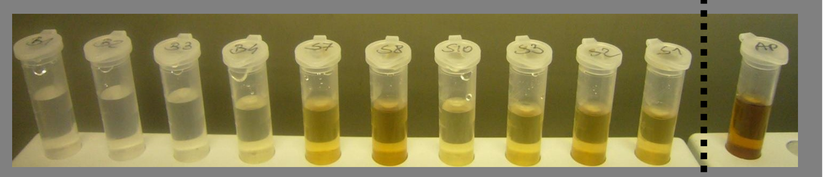
DECREASE

- Microbial phylotype richness (number of dominant community members)
- Bacteria/fungi ratio
- eDNA/iDNA ratio
- pH



Fate and ecological relevance of soil extracellular DNA (eDNA). Pietramellara et al. (2009; Bio Fertil Soils)

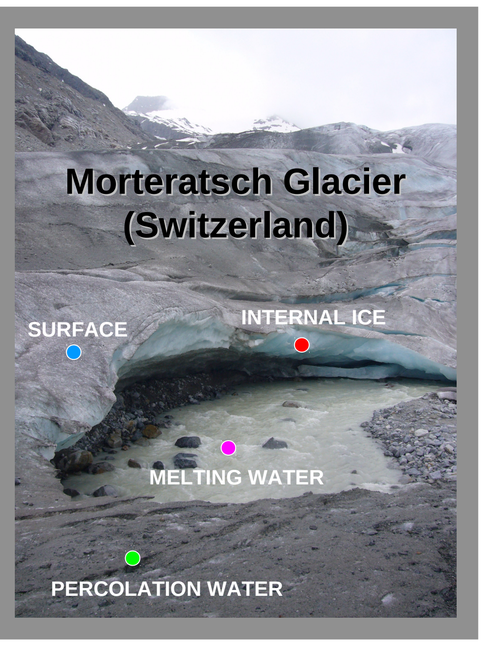
The colour intensity of the extracts containing eDNA, obtained by gentle washings of soil with alkaline buffer (Na_2HPO_4) (Ascher et al. 2009; APSOIL), reflects the increasing amounts of organic matter with increasing soil age.



Agarose gel electrophoresis showed high quality extracellular DNA (molecular weight >2 kb; molecular integrity) along the soil chronosequence with increasing amounts of eDNA with increasing soil formation process.

Next to DNA extraction from soil, we extracted DNA from various glacier-samples (coloured dots). We generally found markedly higher amounts of extracellular DNA (eDNA) than intracellular DNA (iDNA) in the glacier-samples.

Comparative pyrosequencing of eDNA and iDNA from soils and glacier samples is *in progress* to assess the role of "glacier-microflora" in the primary microbial succession in soil.



Biotic and abiotic parameters (Mavris and Egli 2010, Geoderma) were strongly correlated as a function of soil age. DNA based molecular analysis (genetic fingerprinting of microbial communities by SSU rRNA gene fragment PCR-DGGE) and enzyme activities (principal bio-geochemical cycles) along the glacier-forefield provided evidences that the microbial succession (fungi>bacteria>archaea) is a dynamic process. Our molecular data suggested that changes in microbial structures mainly occurred in the early phase of succession (0-120 years after deglaciation) and became stable thereafter (120-150 years, as well as in comparison to a mature forest soil about 1500 years old).

Comparative eDNA and iDNA analyses supported the potential of extracellular DNA as a driving force of microbial life in terms of i) quantitatively relevant portion of the soil metagenome; ii) mobile component of the soil mobilome with evolutionary implications (horizontal gene transfer *via* natural transformation); iii) important component of soil biofilm (physical structure; soil metagenome stability); and iv) source of microbial nutrients.