Microbial activities along a 20 million-year-old pristine oil reservoir

Lisa Voskuhl[‡], Hannah Möhlen[‡], Christian Schlautmann[‡], Sadjad Mohammadian[‡], Ann-Christin Severmann[§], Johannes Koch^I, John Maximilian Köhne[¶], Erling Rykkelid[#], Joachim Rinna[#], Rainer Meckenstock^a

‡ University of Duisburg-Essen, Environmental Microbiology and Biotechnology (EMB), Aquatic Microbiology, Essen, Germany

§ University of Duisburg-Essen, Center for Medical Biotechnology, Developmental Biology, Essen, Germany

| University of Duisburg-Essen, Center for Medical Biotechnology (ZMB), Imaging Center (ICCE), Essen, Germany

¶ Department of Soil System Science, Helmholtz Centre for Environmental Research, Halle, Germany

- # AkerBP, Lysaker, Norway
- ¤ University of Duisburg-Essen, Duisburg, Germany

Corresponding author: Lisa Voskuhl (<u>lisa.voskuhl@uni-due.de</u>), Rainer Meckenstock (<u>rainer.meckenstock@uni-due.de</u>)

Abstract

Studies on oil reservoir microbiology typically take samples from producing reservoirs and sample fluids that have been pumped to the surface. This comes with problems since producing oil reservoirs are affected by production processes leading to changes in environmental conditions and the natural microbiome. Hence, pumped samples do not display an unaltered picture of the spatial distribution and composition of the microorganisms in the reservoir.

We took 13 samples from a freshly drilled sediment core of a pristine, heavily biodegraded oil reservoir in the North Sea. Core samples originated from above, within, and below the reservoir.

16S rRNA gene amplicon sequencing of the microbiome revealed distinct differences between sediments and formation water, indicating that studies on microbiomes from formation water alone are not necessarily representative for the microbial processes in an oil reservoir. Fluorescence microscopy showed that microorganisms live in small microcolonies on the sediment surface. CT-scanning with image analysis visualized the water phase distribution inside the reservoir sediments and clearly indicated water-filled voids that might be habitable for microorganisms, enlarging the surface for potential biodegradation. Employing microcosm experiments and reverse isotope labelling, we were able to determine the first degradation rates measured from cores above, within, and below a reservoir ranging from no activity up to 1 mM $CO_2/(g_{sediment} x year)$, Results indicate significant degradation potential from autochthonous microorganisms in the reservoir above the water-contact-zone.

Evading the general issues of produced oil samples for studying microbiomes results in a more realistic picture of an oil reservoir unaffected by production artefacts.

Keywords

oil leg, 16S rRNA, undisturbed, cores, spatial distribution

Presenting author

Lisa Voskuhl

Conflicts of interest

The authors have declared that no competing interests exist.