Biogeochemical processes and microbial diversity of the Gullfaks and Tommeliten methane seeps (Northern North Sea)

G. Wegener1, M. Shovitri1, K. Knittel1, H. Niemann1,2,* M. Hovland3, and A. Boetius1,2,4
1Max Planck Institute for Marine Microbiology, Bremen, Germany
2Alfred Wegener Institute for Polar and Marine Research, Bremerhaven, Germany
3Statoil, Stavanger, Norway
4Jacobs University Bremen, Bremen, Germany
*now at: Institute for Environmental Geosciences, University of Basel, Switzerland

Correspondence to: G. Wegener (gwegener@mpi-bremen.de)

Received: 21 January 2008 – Published in Biogeosciences Discuss.: 25 February 2008
Revised: 3 June 2008 – Accepted: 11 July 2008 – Published: 18 August 2008

Abstract

Fluid flow related seafloor structures and gas seeps were detected in the North Sea in the 1970s and 1980s by acoustic sub-bottom profiling and oil rig surveys. A variety of features like pockmarks, gas vents and authigenic carbonate cements were found to be associated with sites of oil and gas exploration, indicating a link between these surface structures and the underlying, deep hydrocarbon reservoirs. In this study we performed acoustic surveys and videographic observation at Gullfaks, Holene Trench, Tommeliten, Witch’s Hole and the giant pockmarks of the UK Block 15/25, to investigate the occurrence and distribution of cold seep ecosystems in the Northern North Sea. The most active gas seep sites, i.e. Gullfaks and Tommeliten, were investigated in detail. At both sites, gas bubbles escaped continuously from small holes in the seabed to the water column, reaching the upper mixed surface layer. At Gullfaks a gas emitting, flat area of 0.1 km2 of sandy seabed covered by filamentous sulfur-oxidizing bacteria was detected. At Tommeliten, we found a patchy distribution of small bacterial mats indicating sites of gas seepage. Below the patches the seafloor consisted of sand from which gas emissions were observed. At both sites, the anaerobic oxidation of methane (AOM) coupled to sulfate reduction (SR) was the major source of sulfide. Molecular analyses targeting specific lipid biomarkers and 16S rRNA gene sequences identified an active microbial community dominated by sulfur-oxidizing and sulfate-reducing bacteria (SRB) as well as methanotrophic bacteria and archaea. Stable carbon isotope values of specific, microbial fatty acids and alcohols from both sites were highly depleted in the heavy isotope 13C, indicating that the microbial community incorporates methane or its metabolites. The microbial community composition of both shallow seeps shows high similarities to the deep water seeps associated with gas hydrates such as Hydrate Ridge or the Eel River basin.