Geophysical Research Abstracts,
Vol. 10, EGU2008-A-06809, 2008
SRef-ID: 1607-7962/gra/EGU2008-A-06809
EGU General Assembly 2008

Methane fluxes into the benthic food web at cold seeps – a case study from the Costa Rica subduction zone (Mound 12, 1020 m water depth).

H. Niemann (1,2), P. Linke (3), K. Knittel (1), A. Boetius (1), W. Brückmann (3), U Schacht(3,4), D. Hilton (5), G. Rehder (3,6), K. Brown (5), the AT11-28 and M66-2 shipboard scientific parties

(1) Max Planck Institute for Marine Microbiology, Celsiusstr. 1, 28359 Bremen, Germany

(2) present address: Institute for Environmental Geoscience, University of Basel, Bernoullistrasse 30, 4056, Basel, Switzerland

(3) Leibniz Institute of Marine Sciences, Wischhofstraße 1-3, 24148 Kiel, Germany

(4) present address: Cooperative Research Centre for Greenhouse Gas Technologies, Australian School of Petroleum, The University of Adelaide, Adelaide, Australia

(5) Scripps Institution of Oceanography, University of California, San Diego, 9500 Gilman Dr., 0244, La Jolla, CA 92093-0244, USA

(6) present address: Institute for Baltic Sea Research Warnemünde, Seestraße 15, 18119, Warnemünde, Germany

Cold seep ecosystems support enormous biomasses of free-living and symbiotic, chemotrophic organisms, which metabolise hydrocarbons or sulphide. However, These systems are also characterised by high amounts of non-symbiotic seep megafauna and even invaders from the surrounding deep sea such as fish, echinoderms and crustaceans. So far it is unclear to which extent these higher trophic levels utilise the abundant chemosynthetic biomass as a food source. To answer this question, we conducted two cruises with R/V Atlantis (AT11-28) and R/V Meteor (M66-2) to Mound 12, a cold seep at the Costa Rica subduction zone. Here, high fluxes of sulphide produced by the anaerobic oxidation of methane (AOM; $\sim$5 mol m^2 yr^{-1}) with sul-

phate fuels thiotrophic bacteria which from dense mats at the sediment surface. During several dives with DSV Alvin, ROV Quest as well as on the video footage of a benthic lander system, numerous specimens of a lithodid crab were observed to feed on these mats. To evaluate the dietary carbon source of the crabs, the stomach contents of one specimen were screened for 16S rDNA sequences. Furthermore, lipid biomarker as well as compound specific and bulk stable carbon isotope compositions were analysed from the stomach (including its contents) and muscle tissue. The stomach content analyses revealed a dominance of clone sequences of ε-proteobacteria closely related to seep related, free-living sulphur oxidisers and substantial amounts of bacterial fatty acids such i-C15:0 and C17:1ω6c with stable carbon isotope compositions as low as -53$^{o}/_{oo}$. These results indicate a dietary input of microbial, chemosynthetic carbon, probably methane derived, from the bacterial mats. Furthermore ^{13}C-depleted bacterial fatty acids were also found in the muscle tissue, which had a bulk stable carbon isotope composition of -46$^{o}/_{oo}$. The presence of these biomarkers in the muscle tissue, with its highly ^{13}C-depleted isotope composition, suggests that chemosynthetic biomass is a major carbon source over the entire life cycle of the lithodid crabs at Mound 12.