EVIDENCE THAT ARCHAEA-SRB CONSORTIA ARE RESPONSIBLE FOR ANAEROBIC OXIDATION OF SLOWLY DIFFUSING METHANE

R. D. Pancost (1), S. Kelly (1), G. Kaur (1) and the METROL shipboard scientific parties

(1) Organic Geochemistry Unit, Biogeochemistry Research Centre, School of Chemistry, University of Bristol, CantockŠs Close, Bristol BS8 1TS, UK (r.d.pancost@bristol.ac.uk)

Significant attention has been devoted to the study of the anaerobic oxidation of methane (AOM) due to its critical role in the mediation of methane fluxes from marine sediments. Most recent work Ű especially that employing microbiological and biomarker approaches Ű has focussed on cold seeps, where methane fluxes are high and methane-oxidizing communities are large. However, on a global scale AOM in ocean margin sediments characterized by relatively low diffusive methane fluxes is far more significant. Currently, there is little information on the biology of the organisms that mediate AOM in such settings and it is unclear whether they are the same as those found at cold seeps. As part of METROL, we examined biomarker distributions in marine sediments where methane is completely oxidized below the sediment-water interface (Benguela upwelling system, ODP core 1084; two sites in the Northern Kattegat and four sites in the Skagerrak, Baltic Sea). At all sites, we find archaeal and bacterial biomarkers similar to those observed in cold seep sediments, including archaeol (archaeal methanotrophs) and non-isoprenoidal diethers (sulphate-reducing bacteria). In some Skagerrak sites, sn-2-hydroxyarchaeol, thought to be particularly diagnostic for the archaea involved in AOM at cold seeps, is also present. Archaeol abundances vary from 25 to 400 ng g sediment-1, considerably lower than those commonly found at cold seeps (up to 25 mikro g g sediment-1), indicating that the AOM community was and/or is smaller. Nonetheless, the presence of the same biomarkers suggests that similar organisms mediate AOM in both continental margin and cold seep sediments.