



Potential sources of hydrocarbons and their microbial degradation in sediments from the deep geothermal Lusi site, Indonesia

Martin Krueger (1), Adriano Mazzini (2), Georg Scheeder (1), and Martin Blumenberg (1)

(1) BGR, Resource Geochemistry, Hannover, Germany (martin.krueger@bgr.de), (2) Centre for Earth Evolution and Dynamics (CEED) University of Oslo, Oslo, Norway

The Lusi eruption represents one of the largest ongoing sedimentary hosted geothermal systems, which started in 2006 following an earthquake on Java Island. Since then it has been continuously producing hot and hydrocarbon rich mud from a central crater with peaks reaching 180.000 m³ per day. Numerous investigations focused on the study of microbial communities which thrive at offshore methane and oil seeps and mud volcanoes, however very little has been done on onshore seeping structures. Lusi represents a unique opportunity to complete a comprehensive study of onshore microbial communities fed by the seepage of CH₄ as well as of liquid hydrocarbons originating from one or more km below the surface. While the source of the methane at Lusi is unambiguous, the origin of the seeping oil is still discussed. Both, source and maturity estimates from biomarkers, are in favor of a type II/III organic matter source. Likely the oils were formed from the studied black shales (deeper Ngimbang Fm.) which contained a Type III component in the Type II predominated organic matter. In all samples large numbers of active microorganisms were present. Rates for aerobic methane oxidation were high, as was the potential of the microbial communities to degrade different hydrocarbons. The data suggests a transition of microbial populations from an anaerobic, hydrocarbon-driven metabolism in fresher samples from center or from small seeps to more generalistic, aerobic microbial communities in older, more consolidated sediments. Ongoing microbial activity in crater sediment samples under high temperatures (80-95C) indicate a deep origin of the involved microorganisms. First results of molecular analyses of the microbial community compositions confirm the above findings. This study represents an initial step to better understand onshore seepage systems and provides an ideal analogue for comparison with the better investigated offshore structures.