Geophysical Research Abstracts
Vol. 20, EGU2018-17026, 2018
EGU General Assembly 2018

Deep versus shallow origin of hydrocarbon degrading microorganisms in sediments from the active Lusi eruption site, Indonesia

Martin Krueger (1) and Adriano Mazzini (2)

(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 (northeast Java Island, Indonesia) is the largest active sediment-hosted hydrothermal system on Earth. Its inception started together with numerous aligned eruptions sites that followed the orientation of a reactivated fault system. Since its birth in May 2006 Lusi has been continuously erupting boiling and hydrocarbon-rich mud from a central crater with peaks reaching up to 180,000 m3/day. Numerous investigations focused on the study of microbial colonies that thrive at offshore methane and oil seeps and mud volcanoes, however very little has been done on onshore active structures. Lusi represents a unique opportunity to complete a comprehensive study of onshore microbial communities fed by the seepage of CH4 and CO_2 rich fluids as well as of liquid hydrocarbons originating from several kilometers below the surface. In the last year several sampling campaigns have been conducted over the entire Lusi structure, including the drone-based sampling of fresh mud collected directly from the main eruption site. In all samples large numbers of especially bacterial microorganisms were present, while numbers of Archaea were generally lower. Several microbial metabolic activities were detected. Rates for aerobic methane oxidation were high, as was the potential of the microbial communities to degrade different hydrocarbons and other carbon substrates. Other metabolic processes, including sulfate, Fe and Mn reduction and carbon dioxide and methane production rates were also observed. Many of these activities were also detectable at elevated temperatures and pressures mimicking deep subsurface conditions, indicating a possible deep origin of the involved microorganisms. Preliminary 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.