

Invertebrate-microbe symbioses at asphalt volcanoes in the deep Gulf of Mexico

Maxim Rubin-Blum¹, Christian Borowski¹, Chakkiath Paul Antony¹, Lizbeth Sayavedra¹, Thomas Pape², Heiko Sahling², Gerhard Bohrmann², Nicole Dubilier^{1, 2}

¹Max-Planck Institute for Marine Microbiology, Celsiusstrasse 1, 28359 Bremen, Germany; mrubin@mpi-bremen.de

²MARUM - Center for Marine Environmental Sciences, University of Bremen, 28359 Bremen, Germany

Asphalt volcanoes at Campeche Knolls in 3000 m water depth in the southern Gulf of Mexico are characterized by tar flows, oil seepage, and gas venting. Despite these extreme conditions, highly productive communities thrive at Campeche Knolls. These ecosystems are based on symbioses between invertebrates and bacteria that provide their hosts with nutrition by using the carbon and energy sources available at Campeche Knolls. Indigenous chemosynthetic fauna includes *Escarpia laminata* tube worms, which harbor sulfur-oxidizing symbionts, as well as sponges and bathymodiolin mussels, which host both sulfur- and methane-oxidizing symbionts. We investigated these symbioses using a multidisciplinary approach that integrated metagenomics, metatranscriptomics, proteomics, physiological experiments and in situ measurements. Our results revealed that *Bathymodiolus heckerae* mussels and sponges from Campeche Knolls have a novel bacterial symbiont that belongs to the genus *Cycloclasticus*, a ubiquitous clade of marine bacteria commonly found in oil-polluted environments and known to degrade polycyclic aromatic hydrocarbons (PAHs). In contrast to all known *Cycloclasticus*, the symbiotic *Cycloclasticus* lack the genes needed for PAH degradation. Instead, these symbionts use propane and other short-chain alkanes such as ethane and butane as carbon and energy sources. Analyses of short-chain alkanes in the environment of the Campeche Knolls symbioses revealed that these are present at high concentrations (in the μM to mM range). This study expands the limited range of substrates known to power chemosynthetic symbioses and provides yet another example of the remarkable phylogenetic and functional diversity of these associations.