Geophysical Research Abstracts Vol. 16, EGU2014-3929, 2014 EGU General Assembly 2014 © Author(s) 2014. CC Attribution 3.0 License.



## The influence of vent fluid chemistry on trophic structure at two deep-sea hydrothermal vent fields on the Mid-Cayman Rise

Sarah Bennett (1,2), Cindy Van Dover (3), and Max Coleman (2)

(1) NERC Isotope Geosciences Laboratory, British Geological Survey, Nottingham, UK (sarahb@bgs.ac.uk), (2) NASA Jet Propulsion Laboratory, California Institute of Technology, Pasadena, California, USA, (3) Duke University, Durham, North Carolina, USA

The two known deep-sea hydrothermal vent fields along the Mid-Cayman Rise are separated by a distance of only 21 km, yet their chemistry and faunal diversity are distinct. The deeper of the two vent fields, Piccard (with active venting from Beebe Vents, Beebe Woods and Beebe Sea), at 4980 m is basalt hosted. The shallower vent field, Von Damm, at 2300 m appears to have an ultramafic influence. The Von Damm vent field can be separated into two sites: The Spire and The Tubeworm Field. The dominant vent fluids at the Tubeworm Field are distinct from those at the Spire, as a result of fluid modification in the sub-surface. Von Damm and Piccard vent fields support abundant invertebrates, sharing the same biomass-dominant shrimp species, *Rimicaris hybisae*. Although there are some other shared species (squat lobsters (*Munidopsis* sp.)) and gastropods (*Provanna* sp. and *Iheyaspira* sp.)) between the vent fields, they are much more abundant at one site than the other.

In this study we have examined the bulk carbon, nitrogen and sulfur isotope composition of microbes and fauna at each vent field. With these data we have deduced the trophic structure of the communities and the influence of vent fluid chemistry. From stable isotope data and end-member vent fluid chemistry, we infer that the basis of the trophic structure at Piccard is dominated by sulfur, iron, and hydrogen-oxidizing microbial communities. In comparison, the basis of the Von Damm trophic structure is dominated by microbial communities of sulfur and hydrogen oxidizers, sulfate reducers and methanotrophs. This microbial diversity at the base of the trophic structure is a result of chemical variations in vent fluids and processes in the sub-surface that alter the vent fluid chemistry. These differences influence higher trophic levels and can be used to explain some of the variability as well as similarity in fauna at the vent sites.

Part of this work was performed at the Jet Propulsion Laboratory, California Institute of Technology, under contract with National Aeronautics and Space Administration (NASA).