

Biological communities at Blake Ridge seeps: Faunal distributions and trophic interactions

Cindy Lee Van Dover (clvand@wm.edu, 757-221-2229)
Biology Department
College of William & Mary
116 Millington Hall
Williamsburg, VA 23187

Abstract

Recent reconnaissance of the Blake Ridge Diapir using the submersible *Alvin* resulted in mapping and sampling of dense invertebrate communities associated with the subsurface methane hydrates. The geographic location of the Blake Ridge methane seeps raises questions about the biogeographical affinities of its fauna. The closest known, deep seep sites are those of the Barbados region to the southeast and of the Florida Escarpment, on the opposite side of the Florida. A primary objective of the field program was to obtain quantitative samples that will allow us to make robust comparisons of species lists among these seep sites to determine the degree of endemism of their faunas and thus to provide a preliminary assessment of their sensitivity to habitat degradation.

Megafaunal elements of the chemosynthetically based community mapped onto dive tracks provide a preliminary overview of faunal distributions and habitat heterogeneity. Invertebrate biomass is dominated by a mussel species (*Bathymodiolus heckerae*) that is shared with the Florida Escarpment seep site, and, to a lesser extent, by a vesicomid clam (*Vesicomya* cf. *venusta*). A large proportion of the Blake clams (~60%) hosted 1-4 commensal nautiliniellid polychaetes in their mantle cavities.

Cake urchins (*Sarsiaster griegi*) and xenophyophores (Protozoa) were also common megafaunal elements, occurring just at the margin of the mussel beds. This is to our knowledge the first record of these two taxa in close association with seeps. *Sarsiaster griegi* until recently was known from just a single specimen in the NE Atlantic, but has now been collected from the Gulf of Mexico and this Blake Ridge site. The xenophyophores appear to be a single morphotype, probably of the genus *Syringamina*, which is known in both the Atlantic and Pacific, from bathyal to abyssal depths (800 to 4850 m; J.M. Bernhard, pers. comm.). A complete species list derived from quantitative sampling of the mussel beds is being developed.

Transmission electron microscopy, biomass distributions among species, and stable isotope analyses suggest that while methanotrophic microorganisms are present in mussel gill tissues as endosymbionts, sulfide-oxidizing microorganisms of mussel and clam gills make important contributions (~40%) to the standing crop of living organic carbon at the site. Microbial sulfate reduction using methane is active within the sediments beneath the clams and mussels. The microbially generated hydrogen sulfide is used by the clams and the mussels as well as by other elements of the chemosynthetic community. There is no evidence for a dominant role of surface-derived organic material in the carbon budget of the Blake Ridge Diapir food web.

Priorities for future research include i) expansion of the site survey to define the limits of the active biological community, ii) sampling of tubeworms and other mega- and macrofauna to complete the species list for the site, iii) characterization of fluxes associated with discrete megafaunal habitats (e.g., mussel beds, clam beds, tubeworm fields), iv) quantitative sampling of mussel beds to assess the scope of variation in community structure over time, v) growth rate determinations, especially for mussels, vi) exploration of nearby potential seep sites. These studies will allow the Blake Ridge seep

community to be placed within the larger context of seep and vent community ecology.
This is essential if unique attributes of the Blake site are to be discerned.