

Unique microbial community supported by hot fluids from the aging ocean crust in the eastern flank of Juan de Fuca Ridge.

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There is increasing evidences that the mass flux of seawater through ridge flanks is much greater than that through the ridge crests. However, none of the microorganisms was isolated from basement on ridge flanks, and very little is known about how the microbes live in-situ and about their potential impact in the alteration of chemical composition of the earth-ocean-atmosphere. Although it is still nearly impossible for the current ocean drilling program to recover uncontaminated hard rocks, an exceptional chance to investigate the occurrence of microbes within the crustal fluids has been given by a borehole observatory, CORK (Circulation Obviation Retrofit Kit). The CORK consists of two parts, i) instruments installed in the sealed part of the cased borehole drilled by the Ocean Drilling Program (ODP), and ii) a data logger and fluids sampling port sitting on the seafloor. Recently, a study using the CORK suggested the presence of unique microorganisms in -64 deg. C of crustal fluids emanated from a 295-meter-deep borehole in the eastern flank of Juan de Fuca Ridge (3.5 Ma crust) (Cowen et al., 2003, Science, 299, 120-123). Most of the 16S rRNA gene detected in the fluids related to sulfate-reducing genera (Ammonifex, Desulfonatronovibrio, and Desulfotomaculum), implying that fluids circulating within aging ocean crust potentially support microbial sulfate- and nitrate-reduction. However, physiological characteristics, viability, or trophic status of this unique microbial community remained unknown.

When we recovered the CORK during the Integrated Ocean Drilling Program (IODP) Leg 301, we found black rust-like deposits attached to the CORK body. Since it is known that the CORK began leaking soon after its deployment, the deposits was probably formed by the interactions between seawater and crustal fluids emanated from the borehole. The microbial community in the deposits inferred by clone sequencing of environmental 16S rRNA genes was distinct from those hitherto reported for other microbial habitats including natural deep-sea vents on ridge crests and subduction zones, but similar in part with that reported for the fluids collected from the same CORK. Semi-quantitative cultivation experiments revealed that culturable microbial community consisted mainly of members of the hydrogenotrophic and thermophilic methanogen, and which also included diverse thermophilic fermenters and thermophilic sulfate reducers belonging to the previously uncultivated phylogroups. Prevalence of dissimilatory sulfite reductase (dsrAB) genes, together with the SEM-EDX analysis, confirmed the occurrence of microbial sulfate-reduction in-situ. Stable carbon isotopic analysis indicated the microbial community mainly depended on photosynthesized, buried organic matter. Although the microbial community characterized in this study is most probably different from that in natural basement rock, our study demonstrated that the occurrence of diverse, unique, and active thermophiles supported by fluids emanated from the deep basaltic crust, which is probably driven by dissolved photosynthesized organics in the hydrothermal fluids. This study not only provided new insights into the microbial ecosystem on the buried aging ocean crust on ridge flanks, but also suggested the borehole observatory provided outstanding opportunities in retrieving microbes inhabiting in deep ocean crust.