silicic magmas were erupted explosively through these faults. The fissures were filled by the pyroclastic material and closed the vent after cooling, producing the welded-tuff dikes.

V11C MCC: 106 Monday 0830h

Linking Chemistry and Microbiology in Seafloor Hydrothermal Systems II

(joint with B, OS)

Presiding: **D Butterfield,** University of Washington/NOAA Pacific Marine Laboratory**; J Ishibashi,** Kyushu University**; A Maruyama,** National Institute of Advanced Industrial Science and Technology

V11C-01 0830h

Sub-seafloor Processes and the Composition of Diffuse Hydrothermal Fluids

David A. Butterfield[1] (butterfield@pmel.noaa.gov)

M. D. Lilley[2] (lilley@ocean.washington.edu)

J. A. Huber[2] (huberja@ocean.washington.edu)

J. A. Baross[2] (jbaross@u.washington.edu)

[1]Joint Institute for the Study of the Atmosphere and Oceans, University of Washington, Seattle, WA 98195, United States

[2]School of Oceanography, University of Washington, Seattle, WA 98195, United States

High-temperature water/rock reactions create the primary hydrothermal fluids that are diluted with cool, "crustal seawater" to produce low-temperature, diffuse hydrothermal vent fluids. By knowing the composition of each of the components that combine to produce diffuse fluids, one can compare the composition of calculated mixtures with the composition of sampled fluids, and thereby infer what chemical constituents have been affected by processes other than simple conservative mixing. Although there is always uncertainty in the composition of fluids from the sub-seafloor, some processes are significant enough to alter diffuse fluid compositions from the expected conservative mixtures of hot,primary fluid and "crustal seawater." When hydrothermal vents with a wide range of temperature are sampled, processes occurring in different thermal and chemical environments potentially can be discerned. At Axial Volcano (AV) on the Juan de Fuca ridge, methane clearly is produced in warm sub-seafloor environments at temperatures of $\sim 100^{o}$ or less. Based on culturing and phylogenetic analysis from the same water samples at AV, hyperthermophilic methanogens are present in water samples taken from vents ranging in temperature from 15 to 78^{o} C. Ratios of hydrogen sulfide to pseudo-conservative tracers (dissolved silica or heat) at AV decrease when primary fluids are highly diluted with oxygenated seawater. Phylogenetic signatures of microbes closely related to sulfide-oxidizers are present in these same fluids. Hydrogen sulfide oxidation represents the dominant source of energy for chemosynthesis at AV, as in most hydrothermal systems, but a relatively small proportion of the total hydrogen sulfide available is actually oxidized, except at the very lowest temperatures.

V11C-02 0845h

Changes in Subseafloor Bacterial Diversity Following the 1998 Volcanic Eruption at Axial Volcano, Juan de Fuca Ridge

Julie A Huber[1] (206-543-4911; huberja@ocean.washington.edu)

David A Butterfield[2] (butterfield@pmel.noaa.gov)

John A Baross[1] (jbaross@u.washington.edu)

[1]School of Oceanography and Astrobiology Program, University of Washington Box 357940, Seattle, WA 98195, United States

[2]Joint Institute for the Study of Atmosphere and Ocean, University of Washington, Seattle, WA 98195, United States

The subseafloor associated with hydrothermal systems is a dynamic environment in which habitat characteristics change over time, especially with disturbances such as diking-eruptive events and earthquakes. Little is known about the microbial ecology of the subseafloor at active deep-sea volcanic sites and in particular whether or not there are bacterial and archaeal phylotypes that are unique to this environment or how the microbial communities respond to changes in the geochemistry and temperature of vent fluids. In this study, 16S rRNA gene sequence analysis were used to follow changes in bacterial diversity in subseafloor fluids from a single diffuse flow vent shortly after a volcanic eruption at Axial Volcano, Juan de Fuca Ridge, created the site in 1998 and again in 1999 and 2000. Our results show that bacterial diversity is high in diffuse fluids, and that it changes with the post-eruptive evolution of vent fluid chemistry and temperature. The data also show increases in species richness with time within the ϵ-proteobacteria, the dominant phylotype found to be unique to the subseafloor environment. Other phylotypes unique to the subseafloor included high temperature groups such as *Desulfurobacterium*, gram-positive bacteria, and members of novel candidate divisions WS-6 and ABY-1 that have not previously been detected from deep-sea vents. Phylotype richness was highest in the particle-attached populations ($>3\mu$m) from all three sampling periods, and diversity appeared to increase over that time, particularly among the ϵ-proteobacteria. Over this time period, temperature, hydrogen sulfide concentrations, and chlorinity of vent fluids reflect a cooling of the system according to post-eruptive fluid evolution models. Despite this cooling trend, significant numbers of anaerobic hyperthermophiles, including heterotrophs and methanogens, were cultured from all three years. This suggests that while the system is cooling, there remains a hot biotope where indigenous subseafloor hyperthermophiles are maintained. A preliminary model will be presented that attempts to relate bacterial and archaeal diversity to chemical characteristics of diffuse flow fluids and the degree of mixing of seawater.

V11C-03 0900h

Influence of Magmatic Volatiles to Hydrothermal Activity at Suiyo Seamount, Izu-Ogasawara Arc, Western Pacific

Tetsuro Urabe[1] (+81-3-5841-4542; urabe@eps.s.u-tokyo.ac.jp)

Jun-ichiro Ishibashi[2] (ishi@geo.kyushu-u.ac.jp)

Akihiko Maruyama[3] (maruyama-aki@aist.go.jp)

Katsumi Marumo[4] (k.marumo@aist.go.jp)

Nobukazu Seama[5] (seama@kobe-u.ac.jp)

[1]University of Tokyo, Dept. of Earth Planetary Science, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan

[2]Kyushu University, Dept. of Earth Planetary Sciences, 6 Hakozaki, Higashi-ku, Fukuoka 812-8581, Japan

[3]National Institute of Advanced Industrial Science and Technology (AIST) Institute of Biological Resources, 1-1-1 Higashi, Tsukuba 305-8566, Japan

[4]National Institute of Advanced Industrial Science and Technology (AIST), Institute of Marine Resources and Environment, 1-1-1 Higashi, Tsukuba 305-8567, Japan

[5]KURCIS, Kobe University, 2746 Iwaya, Awaji, Hyogo 656-2401, Japan

A high-temperature hydrothermal activity related to dacitic arc magmatism of Suiyo Seamount (28^{o}34'N, 140^{o}38'E), Izu-Ogasawara Arc, western Pacific has been drilled in June 2001 and July 2002 using a tethered, submarine rock-drill system BMS (Benthic Multi-coring System) on-board the *R/V Hakurei-Maru # 2* as a part of **Archaean Park Project***. Impermeable sheath or cap-rock which consists of clay and anhydrite develops beneath the vent field and traps the end-member fluid within the soft sediment layer 1-3 meters thick beneath the seafloor (Urabe et al., 2002). The sheath is likely to be formed by self-sealing process of anhydrite through cementation of sand grains. Most of the anhydrite from upper part of the cap-rock has sulfur isotopic composition similar to seawater value (+20-21 permil). However, those coexisting with pyrite beneath the cap-rock often have δ^{34}S value as low as +17 permil. Besides, carbon isotope fractionation temperature between CH_4 and CO_2 is as high as 700^{o}C (Tsunogai et al., 1994). These lines of evidence strongly suggest that the magmatic volatiles are incorporated into end member fluid as important components. Homogeneous chemistry and stable temperature of the end member fluid for a decade indicate that the hydrothermal circulation system is in quasi-stable condition and the oxygenic nature of the dacite magma has strong influence on the relatively higher redox condition of the fluid compared to that of mid-ocean ridge hydrothermal activity. Such a nature may reduce the extent of hydrogen-based sub-vent biosphere at submarine arc volcanoes such as Suiyo Seamount.

* Funded by MEXT through the Special Coordination Fund.

V11C-04 0915h

Do sulfur isotope compositions of sulfate minerals and occurrence of framboidal pyrite indicate the subvent biosphere at the Suiyo Seamount in Japan?

Takeshi Kakegawa (+81-70-6493-2011; kakegawa@mail.cc.tohoku.ac.jp)

Tohoku University, Graduate School of Science Aramaki Aza Aoba, Sendai 980, Japan

Detailed morphological studies and sulfur isotope analyses were performed on sulfides and sulfates in the drilled core samples from the Suiyo Seamount in Japan. Petrographic studies indicate that drilled samples were extremely altered by the submarine hydrothermal process. Notable feature of the examined samples is the high abundance of sulfide (e.g., FeS2, CuFeS2, ZnS and PbS) and sulfate minerals (e.g., CaSO4, BaSO4). The euhedral shape of sulfides is most common morphology in the examined samples. Sulfur isotope compositions of these sulfides are ranging from +1 to +6 per mil, suggesting that sulfides were directly precipitated from isotopically homogeneous H2S in hydrothermal fluids. On the contrary, framboidal form of pyrite was found in subsurface samples (2 m depth) of APSK 03 site (drilled site near eastern edge of caldera wall). Detailed SEM observation indicates that the framboidal pyrite is aggregate (ca. 100 micro-meter in diameter) of small grain of pyrite crystals (5 micro-meter in diameter). Such morphological nature is quite similar to these found in the modern marine sediments. Sulfur isotope compositions of individual framboids were determined using the Nd-YAG laser microprobe system at Tohoku University. Their isotopic compositions are ranging from <ETH>1 per mil to +2 per mil and slightly lighter than these of the contemporary hydrothermal sulfides. Two possibilities are considerable for the origin of framboids: (1) biogenic origin or (2) abiogenic origin. If (1) is the case, sulfate-reducing bacteria in subvent region was responsible for the formation of framboidal pyrite. Average sulfur isotope compositions of sulfate minerals are closed to +20 per mil in entire region. This suggest that the progressive introduction of sea water sulfate into the shallow hydrothermal system. Some sulfate minerals have lighter isotopic compositions (+17 to +19 per mil) than the sea water sulfate value. These lighter values indicate the mixing process between sea water sulfate (+20 per mil) and sulfate formed by oxidation of hydrothermal H2S (1 to 2 per mil). Two possibilities are considerable for oxidation of H2S: (3) biological oxidation and (4) simple mixing between oxic sea water and reduced hydrothermal fluids. Sulfur-oxidizing microorganism in subvent region may be responsible for oxidation of H2S, if (3) is the case.

V11C-05 0930h

Concentration of Biologically Important Chemical Species in Hydrothermal Fluids from Submarine Arc Volcano Suiyo Seamount

Jun-ichiro Ishibashi[1] (81-92-642-2664; ishi@geo.kyushu-u.ac.jp); Yusuke Morimoto[1]; Yuko Umeki[1]; Fumitaka Kozuma[2]; Tomohiro Toki[2]; Urumu Tsunogai[2]; Kenji Nanba[3]; Motoo Utsumi[4]; Toshiro Yamanaka[5]; Hitoshi Chiba[6]; Kei Okamura[7]

[1]Kyushu Univ., Dept. Earth Planet. Sci., Faculty of Science, Hakozaki Higashi-ku, Fukuoka, Fukuoka 812-8581, Japan

[2]Hokkaido Univ., Div. Earth Planet. Sci., School of Science, N10W6 Kita-ku, Sapporo, Hokkaido 060-0810, Japan

[3]Univ. Tokyo, Dept. Aquatic Bioscience, School of Agricultural and Life Sciences, Yayoi Bunkyo-ku, Tokyo 113-8657, Japan

[4]Tsukuba Univ., IAFE, Tennodai Tsukuba, Ibaraki 305-8577, Japan

[5]Kyushu Univ. SCS, Ropponmatsu Chuo-ku, Fukuoka 810-0041, Japan

[6]Okayama Univ., ISEI, Misasa Tohaku-gun, Tottori 682-0193, Japan

[7]Kyoto Univ., ICR, Gokasho Uji, Kyoto 611-0011, Japan

During dive programs conducted by Archaean Park Project (2000-2002), fluid samples were extensively collected from both high-temperature (up to 300^{o}C) and low temperature vents within submarine arc volcano Suiyo Seamount. Concentrations of chemical species are explained by simple mixing between the hydrothermal endmember and ambient seawater, with only some exception. This suggests a single aquifer distributes beneath the caldera floor. Major elements chemistry agrees with the model that the hydrothermal fluid is equilibrated with surrounding alteration minerals by fluid rock interaction at high temperature.

Concentrations of reducing species in the hydrothermal end member were rather low compared with mid-oceanic ridge hydrothermal system. Following two factors may explain this signature. First, concentrations of organic-derived species (CH_4 = 140μM, NH_4 = 10 to 20 μM) reflect little supply of terrigenous organic sediment over Suiyo Seamount. Second, incorporation of magmatic volatiles could control fluid chemistry as higher redox condition. High CO_2 / CH_4 ratio (CO_2 = 40.6 mM), low H_2 concentration (100 to 150μM), low H_2S concentration (around 1.5 mM) are attributed to oxygenic signature of dacite magma beneath the Suiyo hydrothermal field. Carbon isotope systematics ($\delta^{13}C(CO_2$ =-0.5$^o/_{oo}$, $\delta^{13}C(CH_4)$ = -6.0$^o/_{oo}$) and sulfur isotopic ratio of sulfide ($\delta^{34}S(H_2S)$ = +1.5 to +2.0$^o/_{oo}$) supports magmatic volatiles incorporation. The hydrothermal system in the intra-oceanic arc setting would provide less energy sources than that of mid-oceanic ridge for chemosynthetic organisms beneath the seafloor.

V11C-06 0945h

Sub-seafloor Archaeal Community at Suiyo Seamount on the Izu-Ogasawara Arc

Kurt Hara[1] (+81-426-76-7141; s947085@educ.ls.toyaku.ac.jp); Takeshi Kakegawa[2] (kakegawa@mail.cc.tohoku.ac.jp); Akihiko Maruyama[3] (maruyama-aki@aist.go.jp); Junichiro Ishibashi[4] (ishi@geo.kyushu-u.ac.jp); Katsumi Marumo[5] (k.marumo@aist.go.jp); Testuro Urabe[6] (urabe@eps.s.u-tokyo.ac.jp); Akihiko Yamagishi[1] (yamagish@ls.toyaku.ac.jp)

[1]Department of Molecular Biology, Tokyo University of Pharmacy and Life Science, 1432-1 Horinouchi, Hachioji, Tokyo 192-0392, Japan

[2]Tohoku University, Graduated School of Science, Aramaki Aza, Aoba, Sendai 980, Japan

[3]Research Institute of Biological Resources, National Institute of Advanced Industrial science and Technology, 1-1-1 Higashi, Tsukuba, Ibaraki 305-8566, Japan

[4]Department of Earth and Planetary Science, Faculity of Science, 6-101 Hakozaki, Higashi-ku, Fukuoka 812-8581, Japan

[5]Research Institute of Biological Resources, National Institute of Advanced Industrial science and Technology, 1-1-3 Higashi, Tsukuba, Ibaraki 305-8566, Japan

[6]Earth and Planetary science, University of Tokyo, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan

Archaeal communities in extreme environment have been analyzed by phylogenetic analysis using 16S rDNA gene and fluorescent whole cell in situ hybridization method. These culture-independent methods revealed archaeal communities with much higher diversities than those found by conventional culture methods. In this work we have extended the culture-independent method to the analysis of microbial diversity in a deep-sea subfloor.

In the Archaean Park Project supported by Special Coordination Fund, several holes were bored and cased in the crater of the Suiyo seamount on the Izu-Ogasawara arc, Japan (about 1,400 m depth) in 2001. Hydrothermal fluids were sampled at various sites of cased hole at Suiyo seamount. Black smoker chimney sample was also collected. The fluids were filtered to collect the microbial cells. Filters and black smoker chimney samples were crushed and DNA was extracted and purified. The DNA was used to amplify archaeal 16S rDNA fragments by PCR using an archaea specific primer set. The PCR fragments were cloned and sequenced. Archaeal PCR clone communities of subseafloor showed different spectrum from that of black smoker chimney. Archaeal PCR clones obtained from sub-seafloor belonged to the order Archaeoglobales and the clones related to the order Methanococcales. These clones reflect the hydrogen dependent chemolithoautotrophic archaea community. However, fluorescent in situ hybridization analysis showed that an archaeal population in hydrothermal fluid from sub-seafloor at the site on Suiyo seamount was low.

V11C-07 1000h

Microbial Diversity in Hydrothermal Surface to Sub-surface Environment of Suiyo Seamount

Yosuke Higashi[1] (+81-298-61-6032; y-higashi@aist.go.jp); Michinari Sunamura[1] (+81-298-61-6032; m.sunamura@aist.go.jp); Keiko Kitamura[1] (+81-298-61-6069; k-kitamura@aist.go.jp); Yasuro Kurusu[2] (+81-298-88-8646; krsy@ipc.ibaraki.ac.jp); Koichi Nakamura[1] (+81-298-61-3768; koichi@gsj.go.jp); Akihiko Maruyama[1] (+81-298-61-6069; maruyama-aki@aist.go.jp)

[1]Advanced Industrial Science and Technology (AIST), 1-1-1 Higashi, Tsukuba 305-8566, Japan

[2]University of Ibaraki, 3-21-1 Chyuou, Ami, Inashiki 300-0332, Japan

After excavation trials to a hydrothermal subsurface biosphere of the Suiyo Seamount, Izu-Bonin Arc, microbial diversity was examined using samples collected from drilled boreholes and natural vents with an catheter-type in situ microbial entrapment/incubator. This instrument consisted of a heat-tolerant cylindrical pipe with entrapment of a titanium-mesh capsule, containing sterilized inorganic porous grains, on the tip. After 3-10 day deployment in venting fluids with the maximum temperatures from 156 to 305degC, Microbial DNA was extracted from the grains and a 16S rDNA region was amplified and sequenced. Through the phylogenetic analysis of total 72 Bacteria and 30 Archaea clones, we found three novel phylogenetic groups in this hydrothermal surface to subsurface biosphere. Some new clades within the epsilon-Proteobacteria, which seemed to be microaerophilic, moderate thermophilic, and/or sulfur oxidizing, were detected. Clones related to moderate thermophilic and photosynthetic microbes were found in grain-attached samples at collapsed borehole and natural vent sites. We also detected a new clade closely related to a hyperthermophilic Archaea, Methanococcus jannashii, which has the capability of growing autotrophically on hydrogen and producing methane. However, the later two phylogroups were estimated as below a detection limit in microscopic cell counting, i.e., fluorescence in situ hybridization and direct counting. Most of microbes in venting fluids were assigned to be Bacteria, but difficult in specifying them using any known probes. The environment must be notable in microbial and genetic resources, while the ecosystem seems to be mainly supported by chemosynthetic products through the microbial sulfur oxidation, as in most deep-sea hydrothermal systems.

V11C-08 1035h INVITED

Volatiles Produced and Consumed by Microorganisms in Active Hydrothermal Systems

Marvin D Lilley[1] (206-543-0859; lilley@ocean.washington.edu)

Eric J Olson[1] (206-543-1902; olson@ocean.washington.edu)

David A Butterfield[2] (206-526-6722; butterfield@pmel.noaa.gov)

[1]University of Washington, School of Oceanography, Box 355351, Seattle, WA 98195, United States

[2]University of Washington, Joint Institute for the Study of Atmosphere and Ocean, Seattle, WA 98195, United States

Volatiles are one of the primary links from the mantle to the biological communities at hydrothermal systems. Microorganisms, either free-living or symbionts, are the primary means by which these volatiles are utilized in hydrothermal environments. The volatiles being discharged at active hydrothermal systems of most importance to microbiological communities are CH_4, H_2, H_2S and CO_2. CH_4, H_2 and H_2S can all serve as energy sources to various microorganisms and CO_2 is by far the most abundant carbon source in hydrothermal systems. There are multiple sources of these gases in hydrothermal systems, including magmatic degassing, water/rock reactions and microbial processes. Hydrothermal environments where volatile-microbial interactions may be detected include high temperature black smokers, diffuse (low temperature) fluids and plumes. The only evidence of microbial input to high temperature fluids found to date is on the Endeavour segment of the Juan de Fuca Ridge where very depleted $\delta^{13}C$-CH_4 (-55 per mil vs PDB) is found. It seems inescapable that microbial activity is producing ^{13}C depleted CH_4 somewhere within the Endeavour hydrothermal convection cells. In diffuse flow environments, subsurface microbial activity, primarily CH_4 production and H_2 oxidation, has been noted at 9°N, EPR and the CoAxial segment and Axial Volcano on the Juan de Fuca Ridge. Tubeworm symbionts fix CO_2 and oxidize H_2S in these environments as well. In addition, microbial nitrogen cycle activity in the form of elevated concentrations of N_2O have been seen at Galapagos and Axial Volcano. Both CH_4 and H_2 oxidation have been detected in hydrothermal plumes with typical H_2 lifetimes of order one day and CH_4 lifetimes of order one week.

V11C-09 1050h

Isotopic Evidence of a Sedimentary Carbon Source at the Endeavour Hydrothermal System, a Potential Site of Microbial Methane Oxidation

Giora K Proskurowski[1] (2065437521; giora@u.washington.edu)

Marvin D Lilley[1] (2065420859; lilley@ocean.washington.edu)

Thomas A Brown[2] (9254238507; tabrown@llnl.gov)

[1]University of Washington, School of Oceanography, Seattle, WA 98195, United States

[2]Center for Accelerator Mass Spectrometry, Lawrence Livermore Nationaly Laboratory, Livermore, CA 94551, United States

The hydrothermal systems on the Endeavour Segment of the Juan de Fuca Ridge have long been characterized as bare rock hosted, as there is no sediment cover at Endeavour. However, chemical evidence in the form of anomalously high methane, ammonia and various trace metal concentrations reported in the last 10 years are consistent with a sediment source at Endeavour. Here we present a unique data set of stable and radiocarbon isotopic measurements made on CO_2 from Endeavour hydrothermal vent fluids. When plotted against each other, a linear relationship between $\delta^{13}CO_2$ and CO_2 fraction modern values, suggests mixing of two CO_2 sources. The data supports a mixing model between a -5.4$^o/_{oo}$, radiocarbon dead magmatic endmember, and a 17.8$^o/_{oo}$, 18,500 year old carbon source. The second endmember corresponds extremely well with stable isotopic measurements made on carbonate nodules from sediments at ODP drill sites on Middle Valley, a sedimented hydrothermal site 40km North of the Endeavour Segment. These sediments were emplaced during turbidite flows in the late Pleistocene, nominally 20,000 years ago. The mixing model suggests that about 20% of the CO_2 found in Endeavour hydrothermal vent fluids is from this sedimentary endmember. We propose that the observed sedimentary signal is incorporated as heated hydrothermal fluids migrate upwards beneath the ridge axis through a zone of buried sediments. An alternative explanation is that there is a hydrologic link between Middle Valley and Endeavour, and that the sedimentary signal is imported from observed sediments at Middle Valley.

Sediments provide labile sources of carbon that may be incorporated into microbial metabolic pathways. Sediments at Middle Valley exhibit strongly depleted $\delta^{13}CO_2$ values (between 27 and 44$^o/_{oo}$) suggesting microbial fractionation, most likely anaerobic methane oxidation. While microbial methane oxidation is likely an active process in sediments at Middle Valley, isotopic evidence at Endeavour suggests that this is not occurring in buried sediments. The high temperatures in the upflow zone of Endeavour may explain why there is no evidence of microbial activity. The fact that Endeavour fluids do not show this significant depletion in $^{13}CO_2$ complicates the hypothesis of a hydrologic link between the two hydrothermal systems.

V11C-10 1105h

Active and Restricted Phylotypes of Bacteria in Suiyo Seamount Hydrothermal Plume

Michinari Sunamura[1] (+81-298-61-6063; m.sunamura@aist.go.jp)

Yosuke Higashi[1] (+81-298-61-6063; y-higashi@aist.go.jp)

Chiwaka Miyako[1] (+81-298-61-6069; c.miyako@aist.go.jp)

Jun-ichiro Ishibashi[2] (+81-92-642-2664; ishi@geo.kyushu-u.ac.jp)

Akihiko Maruyama[1] (+81-298-61-6069; maruyama-aki@aist.go.jp)

[1]Advanced Industrial Science and Technology (AIST), Central 6, 1-1-1 Higashi, Tsukuba 305-8566, Japan

[2]University of Kyusyu, 6-10-1 Hakozaki, Higashi-ku, Fukuoka 812-8581, Japan

Hydrothermal plume contains several orders of magnitude higher concentration of reduced chemicals, such as methane, hydrogen, reduced sulfur compounds and so on, than surrounding seawater. These chemicals are delivered from magmatic activity through hydrothermal venting and provide good energy sources for chemolithoautotrophic microbes. Activity or population of each chemolithoautotrophic group of microbes has been examined using various incubation techniques.

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However, there is little information about the population in the species level, even the phylogenetic type. In this study, microbial community structure in the hydrothermal plume inside a Suiyo Seamount caldera was investigated both qualitatively (16S rDNA phylogenetic analysis) and quantitatively (16S rRNA targeted fluorescent in situ hybridization: FISH). From transmissivity data, hydrothermal plume was detected in the depth layer of 1100m to 1250m. In this plume layer, more than 90% of Bacteria-probable cells belonged to only one phylotype (SUP05) of the gamma-Proteobacteria, which were strongly related with sulfur utilizing symbiontes of mytilids and mussels in hydrothermal areas. A vertical profile of SUP05 cell numbers corresponded well with that of some chemicals, as well as transmissivity. However, cell morphology analysis revealed that there was an obvious boundary at the depth of 1200m, suggesting that plume history may be different between above and below this depth. Another representative Bacteria-probable cells were specified to a group within the epsilon-Proteobacteria (SUP01), showing a close relationship with environmental clones from deep-sea sediments. In addition, the both SUP05 and SUP01 phylotypes of Bacteria were strongly stainable, i.e., very active, in FISH analysis. These microbes may be not negligible in both primary production and sulfur cycling in this deep-sea hydrothermal system.

V11C-11 1120h

Biological nitrogen fixation in the subseafloor associated with mid-ocean-ridge hydrothermal vent systems

Mausmi Mehta[1] (206-543-4911; mausmi@ocean.washington.edu)

David A Butterfield[2] (butterfield@pmel.noaa.gov)

John A Baross[1] (jbaross@u.washington.edu)

[1]University of Washington, School of Oceanography Box 357940, Seattle, WA 98195, United States

[2]University of Washington, Joint Institute for the Study of Atmosphere and Ocean, Seattle, WA 98195, United States

Thermophilic and hyperthermophilic microorganisms that have been isolated from diffuse hydrothermal vent fluid are assumed to reside within hot, anaerobic zones in the subseafloor. These microorganisms can be metabolically versatile or highly specialized, and utilize a variety of carbon and energy sources that are available in hydrothermal vent fluid. However, the nitrogen sources that support subseafloor microbial communities remain unknown. Chemical analyses indicate that nitrate and nitrite are depleted in diffuse hydrothermal vent fluids relative to deep seawater and are absent in reduced fluids above 30°C. Ammonium concentrations in low temperature vent fluid are similar to the low concentrations in deep seawater, with the exception of sedimented hydrothermal vent systems such as Guaymas Basin and the aberrant, unsedimented Endeavour Segment on the Juan de Fuca Ridge. The largest reservoir of nitrogen in the ocean is dissolved dinitrogen gas, which is abundant in deep seawater and slightly elevated in hydrothermal fluids. Biological nitrogen fixation was first suggested as a potential source of nitrogen to hydrothermal vent ecosystems based on the nitrogen isotope ratios of low trophic level vent fauna, which are much lower than the nitrogen isotope ratios of deep sea organic nitrogen, ammonium and nitrate, but resemble those of deep-ocean dinitrogen gas and marine biota associated with nitrogen fixation. We have detected the genetic potential for nitrogen fixation by amplifying and sequencing one of the genes responsible for nitrogen fixation, *nifH*, from diffuse hydrothermal vent fluid. The *nifH* genes present in hydrothermal vent fluid originate from a diverse *nifH* assemblage in the subseafloor as well as a phylogenetically distinct *nifH* cluster in deep seawater. While there was no major difference in the *nifH* populations between nitrogen-rich and nitrogen-poor diffuse hydrothermal vents, we will attempt to detect the expression of *nifH in situ* and in nitrogen-fixing isolates cultured from vent fluids.

V11C-12 1135h INVITED

Colonization by pioneer populations of ϵ-*Proteobacteria* and community succession at mid-ocean ridge hydrothermal vents as determined by T-RFLP analysis

Craig L Moyer[1] (360-650-7935; cmoyer@hydro.biol.wwu.edu)

Jeffrey J Engebretson[1] (engebrj@cc.wwu.edu)

[1]Western Washington University, Biology Department MS 9160, Bellingham, WA 98225, United States

Terminal-restriction fragment length polymorphism (T-RFLP) patterns were used to track populations of bacteria occurring within multiple bacterial growth chambers (BGCs) deployed at eight diffuse-flow (Tmax=78°C) hydrothermal vent orifices located within the caldera of Axial Volcano, Juan de Fuca Ridge. For comparison, two distal diffuse vents located at the Magic Mountain area on the Explorer Ridge were also examined. Over a five-year sampling period in conjunction with the NeMO (New Millennium Observatory) program, 52 BGCs were recovered after either a short-term (days) or long-term (annual) deployment. Upon recovery, genomic DNA was extracted and amplified using bacterial-specific PCR primers to generate 5' fluorescently-labeled amplicons of small subunit rRNA genes (i.e., SSU rDNAs). These PCR amplicons were digested with multiple tetrameric restriction endonucleases and the respective community diversity and succession patterns were characterized. The average number of populations (a measure of species richness) within the community that developed in short-term deployed BGCs was significantly lower than those detected in long-term deployed BGCs. All short-term BGC communities were dominated by primary colonizers or pioneer populations indicative of ϵ-*Proteobacteria*, of which, specific phylogenetic groups were recognized at vent sites throughout the five-year sampling period. The long-term BGCs showed evidence of successional events by an increased occurrence of numerous other populations accompanying the pioneer populations of ϵ-*Proteobacteria*. The discovery that all primary colonizing populations were most similar to known lineages of ϵ-*Proteobacteria* detected from hydrothermal vents located worldwide provides further evidence that a few cosmopolitan populations are capable of acting as the primary microbial successors of newly-formed hydrothermal vent systems.

V11C-13 1150h

Evaluation of microbial community in hydrothermal field by direct DNA sequencing

yutaka kawarabayasi[1] (81-298-61-6165; kawarabayasi.yutaka@nifty.com)

Akihiko Maruyama[1] (81-298-61-6069; maruyama-aki@aist.go.jp)

[1]National Institute of Advanced Industrial Science and Technology, Higashi 1-1 AIST tsukuba central6, Tsukuba 3058566, Japan

Many extremophiles have been discovered from terrestrial and marine hydrothermal fields. Some thermophiles can grow beyond 90°C in culture, while direct microscopic analysis occasionally indicates that microbes may survive in much hotter hydrothermal fluids. However, it is very difficult to isolate and cultivate such microbes from the environments, i.e., over 99% of total microbes remains undiscovered. Based on experiences of entire microbial genome analysis (Y.K.) and microbial community analysis (A.M.), we started to find out unique microbes/genes in hydrothermal fields through direct sequencing of environmental DNA fragments. At first, shotgun plasmid libraries were directly constructed with the DNA molecules prepared from mixed microbes collected by an in situ filtration system from low-temperature fluids at RM24 in the Southern East Pacific Rise (S-EPR). A gene amplification (PCR) technique was not used for preventing mutation in the process. The nucleotide sequences of 285 clones indicated that no sequence had identical data in public databases. Among 27 clones determined entire sequences, no ORF was identified on 14 clones like intron in Eukaryote. On four clones, tetra-nucleotide-long multiple tandem repetitive sequences were identified. This type of sequence was identified in some familiar disease in human. The result indicates that living/dead materials with eukaryotic features may exist in this low temperature field. Secondly, shotgun plasmid libraries were constructed from the environmental DNA prepared from Beppu hot springs. In randomly-selected 143 clones used for sequencing, no known sequence was identified. Unlike the clones in S-EPR library, clear ORFs were identified on all nine clones determined the entire sequence. It was found that one clone, $H4_052$, contained the complete Aspartyl-tRNA synthetase. Phylogenetic analysis using amino acid sequences of this gene indicated that this gene was separated from other Euryarchaea before the differentiation of species. Thus, some novel archaeal species are expected to be in this field. The present direct cloning and sequencing technique is now opening a window to the new world in hydrothermal microbial community analysis.

V12A MCC: Hall C Monday 1330h

Lessons Learned From Santa Maria/Santiaguito, Guatemala: Implications of Long-Lived Silicic Eruptions II Posters *(joint with S)*

Presiding: **W Rose,** Michigan Technological University**; L P Flynn,** University of Hawaii

V12A-1399 1330h POSTER

The extrusion of lava dome and block lava flow units at Santiaguito, 1922-2002

Andrew J. Harris[1] (808-956-3157; harris@higp.hawaii.edu)

Luke P. Flynn[1]

William I. Rose[2]

Oto Matias[3]

Julio Cornejo[3]

[1]HIGP/SOEST, University of Hawaii, Honolulu, HI 96822, United States

[2]Dept of Geological Engineering, Michigan Technological University, Houghton, MI 49931, United States

[3]INSIVUMEH, 7a Av. 14-57, Guatemala City Zona 13, Guatemala

Persistent extrusion at Santiaguito during 1922-2002 has been cyclic. Each cycle begins with a 3-6-year-long high (0.5-2.1 m^3 s^{-1}) extrusion rate phase followed by a 3-11-year-long low (0.2 m^3 s^{-1}) phase. The 8th cycle began in 1996 and was still in its high extrusion rate phase in January 2002. With time, the duration of the low extrusion rate phase has increased, peak extrusion and time-averaged eruption rates for each cycle have decreased, and the difference between extrusion rates during high and low extrusion rate phases of each cycle has decreased. These trends may be explained by continued depressurization and exhaustion of an aging source or by transition to a period of extrusion fed by an increasingly stable magma supply.

The current high extrusion rate phase has been characterized by the emplacement of a 3.75 km long block lava flow field. This flow length is consistent with a trend that has been developing since 1970 whereby successive block lava flows have extended greater and greater distances. This trend is coincident with a 2 wt % decrease in SiO_2 content of erupted products. The associated decrease in lava viscosity may (i) explain the increase in flow length and (ii) be further evidence of chamber exhaustion. However, during 2002 we measured an extrusion rate of 1.4 m^3 s^{-1}, a rate not witnessed at Santiaguito since 1963. It is possible that time averaged estimates made to date have missed such high effusion rate spurts. We note, however, the highest extrusion rate obtained from frequent satellite-based measurements during the previous high extrusion rate phase of 1986-89 was 0.95 m^3 s^{-1}. Thus such high extrusion rate spurts must either be of short (<1 year) duration or Santiaguito is currently reversing an 80-year-long trend of declining extrusion.

V12A-1400 1330h POSTER

The Development of Preferred Pathways in Lava Flow Interiors: Insights from Analog Experiments

Steven W Anderson[1] (steveanderson@bhsu.edu)

Shawn McColley[1] (shawnmccolley@savoy.bhsu.edu)

Jonathan H Fink[2] (jonathanfink@asu.edu)

[1]Department of Science, Black Hills State University, Spearfish, SD 57799-9102

[2]Department of Geological Sciences, Arizona State University, Tempe, AZ 85287

We examined the development of preferred pathways in lava flow interiors using a unique experimental procedure. Various colors of an analog fluid, polyethylene glycol (PEG), were sequentially extruded from a point source into a tank containing a cold sucrose solution to better image the internal structure of the flows. The setup was videotaped from the top, side and bottom to provide time-lapse views of the developing flow. The top- and side-mounted cameras showed the development of the surface morphology, and the bottom-mounted camera captured the interaction of the different PEG colors in the flow interior. We conducted