Abstract

In this report, we compile a study of microbial populations in deep-sea hydrothermal plumes with providing some new data set, and discuss the relationships with geological settings and the type of the hydrothermal system, e.g. ridge or subduction, in the context of the hypothesis “four TAIGAs” (Urabe et al. Chap. 1). Deep-sea hydrothermal plumes represent one of the best habitats for chemolithotrophic microbes to drive primary production in hydrothermal systems. Microbial cell densities in hydrothermal plumes are up to several times more elevated than in the general abyssal seawater. Putative sulfur utilizers, e.g. SUP05 and Alcanivorax in gammaproteobacteria, SAR324 in deltaproteobacteria, and several epsilonproteobacteria, are the dominant microbes that are detected from most of hydrothermal plumes. The microbial community compositions in the plume of an arc-backarc system are different from those of a mid-oceanic ridge hydrothermal system. This is because the cell densities and community composition of the putative sulfur oxidizers may be regulated by reduced sulfur species due to the pH and Eh conditions of the subsurface and surrounding seawater. Aerobic methanotrophs are found in hydrothermal plumes which contain high concentrations of molecular hydrogen and methane. Quantitative microbial cell analysis by catalyzed reporter deposition based fluorescent in situ hybridization (CARD-FISH) show that the SUP05 populations are 60–100 % responsible for increased microbial cell densities in the hydrothermal plumes of arc-backarc fields. The contribution of the SUP05 cell densities in the plume microbial community is closely connected with the chemical energy from hydrothermal fluids in various types of TAIGA.

Keywords

Deep-sea hydrothermal plume • Fluorescence in situ hybridization (FISH) • Quantitative microbial community analysis • SUP05 (Thioglobus)

3.1 Introduction to Hydrothermal Plumes and the TAIGA Concept

Deep-sea hydrothermal plumes have been found in hydrothermal fields located in mid-oceanic ridges, subduction zones, and hotspot submarine volcanoes all over the world. Hot hydrothermal fluids emanated from hydrothermal vents are less dense than general abyssal seawater, therefore the fluids rise into the deep sea, mix with surrounding seawater, and form a deep-sea hydrothermal plume. The first, rising stage of hydrothermal plume evolution is termed the
buoyant plume. The buoyant plume undergoes substantial dilution with surrounding seawater due to accompanying turbulence. The mixing causes progressive dilution, and then the plume becomes less buoyant among stratified abyssal seawater and eventually reaches some finite maximum height above the seafloor to spread out laterally. This later stage is termed the nonbuoyant plume (or the neutrally buoyant plume) (German and Von Damm 2003).

The hydrothermal fluids are hot and contain many chemical species originated from magma and subseafloor rocks. Therefore the hydrothermal plume, which is formed by the spouting hydrothermal fluid, acts as an important and major interface between the oceanic lithosphere and seawater, and is important for exchanging heat flux and for the reaction between hydrothermal fluid-derived reduced chemicals and oxidants from the surface of the earth. A hydrothermal plume contains both reduced chemicals from hydrothermal fluids and oxidants from seawater, thus a hydrothermal plume is one of the most important habitats for chemolithotrophic microbes in deep-sea hydrothermal systems. According to the TAIGA concept (see Urabe et al. Chap. 1), the chemical components of the hydrothermal fluid and plume are regulated by the geological background, and the hydrothermal systems can be categorized into four groups: (1) sulfur TAIGA with reduced sulfur from magma, (2) methane TAIGA with high methane and ammonium from the sediments around the channels of hydrothermal fluid circulation beneath the seafloor, (3) hydrogen TAIGA with molecular hydrogen (H$_2$) from serpentinization or the breaking of rocks due to fault activity, and (4) iron TAIGA with Fe$^{3+}$ leached from fresh basalt by acidic hydrothermal fluids. The chemical compositions of the four types of TAIGA control and restrict the microbial community and their functions. In addition, hydrothermal systems are often categorized according to their tectonic background; mid oceanic ridge (MOR) systems, arc-backarc systems, and hot spot systems.

### 3.2 Microbial Communities in Hydrothermal Plumes

Chemical signals derived from hydrothermal fluids are widely used to detect hydrothermal plumes as anomalies from the general abyssal seawater. These chemical signals include turbidity, oxidation-reduction potential, $^3$He, manganese, iron, methane, and molecular hydrogen. Microbial cell densities in a plume are also elevated up to several dozens times higher than those of the general abyssal seawater (Cowen et al. 1986; Naganuma et al. 1989; Winn et al. 1986). This indicates that the microbial community in the plume interacts strongly with the hydrothermal fluid chemicals in the plume. Indeed, the activities of methane oxidation (DeAngelis et al. 1991, 1993; Tsunogai et al. 2000), ammonium oxidation (Lam et al. 2004, 2008), and iron and manganese oxidation (Cowen et al. 1986) have been detected in the plume. Analysis of microbial community structures (Dick and Tebo 2010; Dick et al. 2013; Sunamura et al. 2004) and metagenome/transcriptome (Anantharamana et al. 2013; Dick et al. 2013; Lesniewski et al. 2012) also has shown sulfur oxidation, ammonium oxidation, aerobic methane oxidation, hydrogen oxidation, and heterotrophic activity in the plumes.

Microbial community structures based on SSU rRNA genes in the plumes have been studied in MOR hydrothermal systems including, for example, Guaymas Basin (Dick and Tebo 2010), Juan de Fuca Ridge (Lam et al. 2008) at the East Pacific Rise (EPR), Mid Cayman Ridge (German et al. 2010) at the Mid Cayman Rise, and Kairei Field (Noguchi et al. Chap. 15) at the Central Indian Oceanic Ridge (CIR). These hydrothermal fields are categorized into methane, sulfur, and hydrogen TAIGA fields. In contrast, there has been little study related to microbial communities in arc/backarc hydrothermal systems in subduction region. Only a hydrothermal plume at the Suiyo Seamount (Sunamura et al. 2004) located on the Izu-Ogasawara Arc has been studied. Figure 3.1 shows the microbial community structures in the plume of arc/backarc hydrothermal system, which we collected and analyzed as a representative of methane and sulfur TAIGA. The key microbial lineages in hydrothermal plumes are selected based on a review paper of microbial studies in hydrothermal plumes and anoxic seawater (Dick et al. 2013).

In these key microbial lineages, the SUP05 phylotype is recognized as the most abundant and universal species in deep-sea hydrothermal plumes of all over the world. The SUP05 phylotype in these plumes was first documented in the Suiyo Seamount hydrothermal plume (Sunamura et al. 2004), and the SUP05 phylotype has been found to be dominant in many anoxic seawater sites (Lavik et al. 2009; Walsh et al. 2009) all over the world. SUP05 is known to be a close relative to symbionts of hydrothermal chemosynthetic mytilids and vesicomyids (Duperron et al. 2005; Fujiwara et al. 2000). These can grow chemolithoautotrophically with sulfur (Marshall and Morris 2012; Walsh et al. 2009) or H$_2$ (Anantharamana et al. 2013; Petersen et al. 2011) as an electron donor, and oxygen or nitrate as an electron acceptor. The representative isolate of SUP05 grow with thiosulfate, which is accumulated as native sulfur vesicles in a cell and, in addition to sulfur compounds, it can grow heterotrophically (Marshall and Morris 2012). This wide variation of energy and carbon metabolism may sustain SUP05 as the primary key species in hydrothermal plume microbial communities. We also found abundant Alcanivorax, SAR324, and several epsilon proteobacterial phylotypes in the plume microbial community. The lineages
of these microbes have sulfur-metabolism genes for dissimilar sulfur oxidation (Lai et al. 2012; Nakagawa et al. 2007; Swan et al. 2011) for Alcanivorax, epsilon proteobacteria, and SAR324, respectively. The abundance of potential sulfur oxidizers in the plume is in the good agreement with the result of thermodynamic calculation, which is that sulfur oxidation was the most effective energy source in the mixing zone of deep-sea hydrothermal fluids and general abyssal seawater based on the chemical composition of EPR hydrothermal fluids (McCollom and Shock 1997). On the other hand, 16S rRNA genes of SUP05 lineage was not detected from hydrothermal plume samples in Wakamiko Creater field. In this field, hydrothermal plume shows low pH (6.3–6.8) due to entrainment of volcanic fumaroles in the crater seawater (Yamanaka et al. 2013). The relatively low SUP05 populations was also notable for NW Rota Seamount hydrothermal plume, where very low pH caused by acid sulfate hydrothermal fluid (Resing et al. 2007). In such low pH condition, dominant reduced sulfur species are not HS⁻ but H₂S and native sulfur species, and thiosulfate is not stable. In addition, the growth zone of SUP05 lineage is restricted to early stage of hydrothermal plume (see next section), therefore it is essential to import substrates quickly into a cell. Lack of availability of substrates could be responsible for absence of SUP05 in hydrothermal plume. To know the difference in the SUP05 populations between the ridge and arc-backarc hydrothermal systems, further studies such as recycling of SUP05 cells within the plume, activities of dissolved sulfur chemicals, and toxicity of hydrothermal fluid chemicals are needed. Close relatives of SUP05 are able to utilize H₂S, HS⁻, native sulfur, and thiosulfate for growth (Marshall and Morris 2012; Walsh et al. 2009). We proposed here that uptake of the substrate into a cell may be regulated by the stability and states of the sulfur species which caused by pH and Eh.

Figure 3.1 clearly shows that the aerobic methanotrophic lineages are found only in hydrothermal systems where abundant methane and H₂ are available (TAIGA of methane and H₂). The results indicate that aerobic methanotrophic

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**Fig. 3.1** Abundance of key microbial community populations in plumes. The 16S rRNA gene sequences were obtained by cloning/Sanger sequencing for the Daiyon-Yonaguni Knoll, Tarama Knoll, and Wakamiko Creater samples, and by 454 pyrosequencing for the Suiyo Seamount, NW Rota Seamount, TOTO Caldera and CIR samples for this study and Noguchi et al. in Chap. 15. The sequences of Mid Cayman and Guaymus Basin were downloaded from DDBJ or VAMPS. The abbreviated names for hydrothermal zones are as follows: Izu-Ogasawara Arc (IOA), Southern Mariana Arc (SMA), Southern Mariana Trough Backarc (MBA), Southern Okinawa Trough (SOT), Northern Okinawa Trough (NOT), Central Indian Ridge (CIR), Mid Cayman Rise (MCR), and East Pacific Rise (EPR).
populations are restricted by high concentrations of methane in hydrothermal fluid as predicted by the TAIGA hypothesis.

Cluster analysis based on the key species populations indicated that the community structures were separated into two groups (Fig. 3.2). The grouping seems to depend on the SUP05 population which is able to use reduced sulfur compounds (Lesniewski et al. 2012; Marshall and Morris 2012) and H2 (Anantharamana et al. 2013; Petersen et al. 2011) as the energy source for chemolithotrophic growth. The first group consists of the plumes of arc-backarc hydrothermal systems with high microbial cell density anomalies. This group contains high SUP05 populations of greater than 50 %. The second group includes the other hydrothermal plumes and could be categorized into three sub-groups. The sub-groups appear to be unrelated to the geological settings of the hydrothermal systems (i.e. ridge or subduction) or to the chemical composition of the original hydrothermal fluids (categories of TAIGA). Analysis of the microbial community structure indicated that the SUP05 lineage was the most important for understanding microbial ecology in the deep-sea hydrothermal plumes.

**3.3 Growth Zone of SUP05**

To understand the sulfur and carbon cycles in a hydrothermal field, it is essential to determine the origin and the growth zone of plume-specific microbial communities. Detection and cultivation of hyperthermophiles in an event plume (Summit and Baross 1998) indicates that subseafloor and high temperature hydrothermal fluids are one of the origin of the plume microbes. The SUP05 phylotypes have been detected in the low temperature diffuse hydrothermal flows at a level of more than 99% (Sunamura et al. 2004), indicating that diffuse flow venting is one of the origins. Quantitative comparison between microbial cell densities and methane concentration among high temperature hydrothermal fluids, low temperature diffuse flows, and hydrothermal plume waters indicated that in situ growth in the plume is most important in the case study of the Suiyo Seamount hydrothermal field (Sunamura et al. 2009) (Fig. 3.3) where SUP05 phylotype dominate microbial communities in the plume (Sunamura et al. 2004). To understand the plume-microbiological impact on deep sea, we need to narrow a more detailed growth zone in the plume.

**3.4 Changes in the Microbial Community During the “Chemical Evolution” of a Plume**

Biogeochemical studies of chemical composition of substrates (Malahoff et al. 2006; Resing et al. 2009) and the stable isotope analysis of methane carbon (Tsunogai et al. 2000) in plumes have suggested that the chemical features of a plume change with the dilution process and distance from the vent. This is referred to as the “chemical evolution of plume”. Several previous studies could not find any positive and clear correlation between the total cell density and the physicochemical parameters in the plume. Moreover the changes occurring in the microbial community during the chemical evolution of plume are still unclear. Figure 3.4 shows the relationship between cell densities that are higher than the background (cell density anomalies) and bacteria and SUP05 cell densities determined by the (CARD-)FISH method in various hydrothermal plumes. Good linear correlation between the cell density anomalies and the SUP05 cell densities (Fig. 3.4) indicates that very little “microbial community evolution” occurred during the chemical evolution of the non-buoyant plume.
3.5 Contribution of a Specific Microbial Community for Total Plume Microbial Ecosystem

The values of the correlation slope between the microbial cell anomalies and the specific cell densities determined by FISH microscopic counts show the ratios of specific microbial species contributions in the plume microbial communities (Fig. 3.4). Based on these values, bacterial cells are responsible for almost all of the increase in microbial population in the plume and therefore the archaeal contribution is much smaller than that of bacteria. Moreover, SUP05 cells contribute from 60 to 98% of the anomaly biomass in the plume (Fig. 3.4). Microbial population in the plume is regulated by input and removal; the inputs are in situ chemolithotrophic growth, in situ heterotrophic growth, immigration from vent fluids, and the removals are infection by virus, predation, and sedimentation. Because the contributions of specific microbial populations in the plume as estimated above do not consider removal, the contribution values may be overestimated. Our preliminary result in the southern Mariana plume showed the high correlation coefficient between microbial cell densities and manganese concentration. This indicates that the removal of microbial cells is small compared to the increase in microbial cells. We compared the contribution of SUP05 in the total microbial cell anomaly in the plume with the physical and chemical characteristics of the venting hydrothermal fluid which formed the hydrothermal plume. Within the parameters, we found a close correlation between the SUP05 contribution in the total microbial cell anomaly in the plume and the proportion of sulfur oxidation thermodynamic energy in the expected total thermodynamic energy from mixing of each hydrothermal fluid and abyssal seawater (Fig. 3.5). The positive correlation \((r^2 = 0.96)\) suggests that chemical composition of hydrothermal fluids regulates the SUP05 cell density ratios in microbial community, an idea which is proposed in the TAIGA hypothesis. The hydrothermal plume covers and expands from just after hydrothermal fluid spouting out into the seawater to non-buoyant hydrothermal plume. The widespread area and the length of the reaction time in the hydrothermal plume allows most of chemical energy to be used for microbial activity and growth. This idea would explain our conclusion that the composition of hydrothermal fluid chemicals regulates the microbial community structure in the plume. The SUP05 phylotype is known to possess various types of metabolism for growth energy, e.g. sulfur oxidation (Marshall and Morris 2012; Walsh et al. 2009), hydrogen oxidation (Anantharamana et al. 2013; Petersen et al. 2011), and heterotrophy.
To understand the regulation mechanism of the plume microbial community, we will need to determine the status of sulfur chemical species, gas species, and metal species during plume evolution in the future.

### 3.6 Conclusion and Future Perspectives

In this chapter, we compiled our qualitative and quantitative data regarding the plume microbial community of various hydrothermal fields and compare their characteristics in the context of four TAIGA. We conclude that (1) bacteria is the major player in the hydrothermal plume, (2) SUP05 is the most important key species in the plume microbial community, (3) the SUP05 population represents the arc-backarc and ridge plume communities, and it is regulated by the chemical composition of the hydrothermal fluid, (4) the SUP05 major growth area is restricted to the plumes, not below the seafloor, and (5) methanotrophs are a microbial signature of hydrogen and methane TAIGA. To understand the biogeochemical impacts of plume microbes on the deep ocean, in the future we will need to determine the microbial production rate and in situ microbial activities through in situ incubation, transcriptomics, and more dense sampling.

### 3.7 Materials and Methods

#### 3.7.1 Samples Used in This Study

The hydrothermal plume samples used in this study were collected at the Okinawa Trough (4 sites: Hatoma Knoll in cruise KT05-26; Daiyon-Yonaguni Knoll in KT09-26; Tarama Knoll in NT08-11; and Wakamiko Creater in KT09-29) (see Ishibashi et al. Chap. 29; Yamanaka et al. Chap. 49), and the Izu-Mariana Arc (4 sites: Suiyo Seamount in cruise KH11-05; Myojin Caldera in NT06-21, TOTO Caldera in KR08-05; NW Rota Seamount in NT10-13) using a Niskin bottle water sampler with CTD-CMS or...
3.7.2 Analytical Methods

Microbial DNA on the filter samples was extracted using an Ultra Clean Soil DNA Extraction Kit (MOBio) according to manufacturer’s instructions. To determine the 16S rRNA gene sequences in the samples, we used cloning/Sanger sequencing method or Roche-454 sequencer with a DNA tag for each sample. For the cloning/Sanger method, the 16S rRNA genes were amplified by PCR method with a 27F-1492R primer set (Reysenbach et al. 2000) using Takara ex taq DNA polymerase (Takara bio) and then the amplified 16S rRNA gene sequences were determined by ABI3100 sequencers after cloning using a TA Cloning Kit (Invitrogen). For the Roche-454 sequencer, the 16S rRNA genes were amplified by a 530F-907R primer set (Nunoura et al. 2012) with adaptor and tags by PCR using LA taq DNA polymerase (Invitrogen). For determination of the SUP05 phylotype, we used a SUP05 mix probe for the SUP05 phylotype, which is a mixture of newly designed SUP05-988 (5′-AAGTTCGCTGTAGTCTAAGA-3′) and SUP05-1245 (5′-GCTTAGCAACCCTTGTCC-3′) probes, in addition to a SUP05-187 probe (Sunamura et al. 2004).

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References

Anantharamana K, Breier JB, Sheika CS, Dick GJ (2013) Evidence for hydrogen oxidation and metabolic plasticity in widespread deep-sea sulfur-oxidizing bacteria. Proc Natl Acad Sci U S A 110:330–335
Cowan JP, Massoth GJ, Baker ET (1986) Bacterial scavenging of Mn and Fe in a mid-field to far-field hydrothermal particle plume. Nature 322:169–171
Daims H, Bruhl A, Amann R, Schliefker K-H, Wagner M (1999) The domain-specific probe EUB338 is insufficient for the detection of all Bacteria: development and evaluation of a more comprehensive probe set. Syst Appl Microbiol 22:434–440
DeAngelis MA, Baross JA, Lilley MD (1991) Enhanced microbial methane oxidation in water from a deep-sea hydrothermal vent field at simulated in situ hydrostatic pressures. Limnol Oceanogr 36(3):565–570
DeAngelis MA, Lilley MD, Olsen EJ, Baross JA (1993) Methane oxidation in deep-sea hydrothermal plumes of the endeavour segment of the Juan de Fuca Ridge. Deep Sea Res I 40(6):1169–1186
Dick GJ, Tebo BM (2010) Microbial diversity and biogeochemistry of the Guaymas Basin deep-sea hydrothermal plume. Environ Microbiol 12(5):1334–1347
Dick GJ, Anantharaman K, Baker BJ, Li M, Reed DC, Sheik CS (2013) The microbiology of deep-sea hydrothermal vent plumes: ecological and biogeographic linkages to seafloor and water column habitats. Front Microbiol 4:124. doi:10.3389/fmicb.2013.00124
Duperron S, Nadalig T, Caprais JC, Sibuet M, Fiala-Medioni A, Amann R, Dubilier N (2005) Dual symbiosis in a Bathymodiolus sp mussel from a methane seep on the gabon continental margin (southeast Atlantic): 16S rRNA phylogeny and distribution of the symbionts in gills. Appl Environ Microbiol 71(4):1694–1700
Edwards KJ, Bach W, McCollom TM (2005) Geomicrobiology in oceanography: microbe–mineral interactions at and below the seafloor. Trend Microb 13:449–456
Fujwara Y, Takai K, Uematsu K, Tsuchida S, Hunt JC, Hashimoto J (2000) Phylogenetic characterization of endosymbionts in three hydrothermal vent mussels: influence on host distributions. Mar Ecol Prog Ser 208:147–155
German CR, Von Damm KL (2003) Hydrothermal processes. In: The Oceans and Marine Geochemistry, 1st Edition, H. Elderfield (ed), Treatise on geochemistry, vol 6, Elsevier (Pergamon), Oxford, UK, 625 pp
German CR, Bowen A, Coleman ML, Honig DL, Huber JA, Jakuba MV, Kinsey JC, Kurz MD, Leroy S, McDermott JM, Lépinay BMD, Nakamura K, Seewald JS, Smith JL, Sylva SP, Dover CLV, Whitcomb LL, Yoerger DR (2010) Diverse styles of submarine venting on the ultraslow spreading Mid-Cayman Rise. Proc Natl Acad Sci U S A 107(32):14020–14025
Hirayama H, Sunamura M, Takai K, Nunoura T, Noguchi T, Oida H, Furushima Y, Yamamoto H, Oomori T, Horikoshi K (2007) Culture-dependent and -independent characterization of microbial
communities associated with a shallow submarine hydrothermal system occurring within a coral reef off Taketomi Island, Japan. Appl Environ Microbiol 73:7642–7656

Lai Q, Li W, Shao Z (2012) Complete genome sequence of Alcanivorax dieselolai type strain B5. J Bacteriol 194:6674

Lam P, Cowen JP, Jones RD (2004) Autotrophic ammonia oxidation in a deep-sea hydrothermal plume. FEMS Microbiol Ecol 47 (2):191–206

Lam P, Cowen JP, Popp BN, Jones RD (2008) Microbial ammonia oxidation and enhanced nitrogen cycling in the endovae hydrothermal plume. Geochim Cosmochim Acta 72(9):2268–2286

Lavik G, Stuhrmann T, Bruchert V, Van der Plas A, Mohrholz V, Lam P, Mussmann M, Fuchs BM, Amann R, Lass U, Kuyers MMM (2009) Detoxification of sulphidic African shelf waters by blooming chemolithotrophs. Nature 457(7229):581–586

Lesniewski RA, Jain S, Anantharaman K, Schloss PD, Dick GJ (2012) The metatranscriptome of a deep-sea hydrothermal plume is dominated by water column methanotrophs and lithothrophs. ISME J 6:2257–2268

Malahoff A, Kolotyrkina IY, Midson BP, Massoth GJ (2006) A decade of exploring a submarine intraplate volcano: hydrothermal manganese and iron at Lo’ihi volcano, Hawai`i. Geochem Geophys Geosys 7:Q06002

Marshall KT, Morris RM (2012) Isolation of an aerobic sulfur oxidizer from the SUP05/Arctic96BD-19 clade. ISME J 7:452–455

McCollom TM, Shock EL (1997) Geochemical constraints on chemolithoautotrophic metabolism by microorganisms in seafloor hydrothermal systems. Geochim Cosmochim Acta 61:4375–4391

Naganuma T, Otaki A, Seki H (1989) Abundance and growth-rate of bacterioplankton community in hydrothermal vent plumes of the North Fiji Basin. Deep Sea Res A 36(9):1379–1390

Nakagawa S, Takaki Y, Shimamura S, Reysenbach A-L, Takai K, Tsunogai U, Yoshida N, Ishibashi J-I, Gamo T (2000) Carbon isotopic distribution of methane in deep-sea hydrothermal plume, Myojin Knoll Caldera, Izu-Bonin arc: implications for microbial methane oxidation in the oceans and applications to heat flux estimation. Geochim Cosmochim Acta 64:2439–2452

Nunoura T, Takaki Y, Kazama H, Hirai M, Ashi J, Imachi H, Takai K, Yamanaka T, Maeto K, Akashi H, Ishibashi J, Miyoshi Y, Okamura K, Noguchi T, Yamamoto H, Okamura K (2009) Environmental and ecological impact on deep-sea environment from deep-sea hydrothermal system (in Japanese with English abstract). Chigaku Zasshi 118(6):1160–1173

Petersen JM, Zielinski FU, Pape T, Seiftt R, Moraru C, Amann R, Howerd S, Girguis PR, Wankel SD, Barbe V, Pelletier E, Fink D, Borowski C, Bach W, Dubilier N (2011) Hydrogen is an energy source for hydrothermal vent symbioses. Nature 476:176–180

Resing JA, Lebon G, Baker ET, Lupton JE, Embley RW, Massoth GJ, Chadwick WW (2007) Venting of acid-sulfate fluids in a high-sulphidation setting at NW rota-1 submarine volcano. Chigaku Zasshi 118(6):1160–1173

Resing JA, Baker ET, Lupton JE, Walker SL, Butlerfield DA, Massoth GJ, Nakamura K (2009) Chemistry of hydrothermal plumes above submarine volcanoes of the Mariana arc. Geochim Geophys Geosyst 10:Q2009

Resenbach A-L, Longnecker K, Kirschstein J (2000) Novel Bacterial and Archaeal lineages from an in situ growth chamber deployed at a Mid Atlantic Ridge hydrothermal vent. Appl Environ Microbiol 66 (9):3798–3806

Schloss PD, Westcott SL, Ryabin T, Hall JR, Hartmann M, Hollister EB, Lesniewski RA, Oakley BB, Parks DH, Robinson CJ, Sahl JW, Stres B, Thallinger GG, Van Horn DJ, Weber CF (2009) Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities. Appl Environ Microbiol 75(23):7537–7541

Stahl DA, Amann R (1991) Development and application of nucleic acid probes. In: Stackebrandt E, Goodfellow M (eds) Nucleic acid techniques in bacterial systematics. Wiley, Chichester, pp 205–248

Summit M, Baross JA (1998) Thermophilic subseafloor microorganisms from the 1996 north Gorda Ridge eruption. Deep Sea Res Part II Top Stud Oceanogr 45(12):2751–2766

Sunamura M, Higashi Y, Miyako C, Ishibashi J, Maruyama A (2004) Two Bacteria phytopotypes are predominant in the Suiyo Seamount hydrothermal plume. Appl Environ Microbiol 70 (2):1190–1198

Sunamura M, Noguchi T, Yamamoto H, Okamura K (2009) Environmental and ecological impact on deep-sea environment from deep-sea hydrothermal system (in Japanese with English abstract). Chigaku Zasshi 118(6):1160–1173

Swan BK, Martinez-Garcia M, Preston CM, Sczyrba A, Woyte K, Lamy D, Reinthaler T, Poulton NJ, Masland EDP, Gomez ML, Sieracki ME, DeLong EF, Hernll GI, Stepansauskas R (2011) Potential for chemolithoautotrophy among ubiquitous bacteria lineages in the dark ocean. Science 333:1296–1300

Tsunogai U, Yoshiha N, Ishibashi J-I, Gamo T (2000) Carbon isotopic distribution of methane in deep-sea hydrothermal plume, Myojin Knoll Caldera, Izu-Bonin arc: implications for microbial methane oxidation in the oceans and applications to heat flux estimation. Geochim Cosmochim Acta 64:2439–2452

Walsh DA, Zaikova E, Howes CG, Song YC, Wright JJ, Tringe SG, Tortell PD, Hallam SJ (2009) Metagenome of a versatile chemolithoautotroph from expanding oceanic dead zones. Science 326:578–582

Ward JH (1963) Hierarchical grouping to optimize an objective function. J Am Stat Assoc 58:236–244

Winn CD, Karl DM, Massoth GJ (1986) Microorganisms in deep-sea hydrothermal plumes. Nature 320:744–746

Yamanaka T, Maeto K, Akashi H, Ishibashi J, Miyoshi Y, Okamura K, Noguchi T, KUwahara Y, Toki T, Tsunogai U, Ura T, Nakatani T, Maki T, Kubokawa K, Chiba H (2013) Shallow submarine hydrothermal activity with significant contribution of magmatic water producing talc chimneys in the Wakanuima Crater of Kagoshima Bay, southern Kyushu. Jpn J Volcanol Geotherm Res 258:74–84. doi:10.1016/j.jvolgeores.2013.04.007