伊平屋北フィールドにおけるハビタットマッピング
Benthic Habitat Mapping in the Iheya North Hydrothermal Field

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Deep-sea hydrothermal systems can support large and diverse populations of vent-associated organisms. In this paper, we describe a practical method to rapidly assess the distribution and diversity of megabenthos over wide areas based on a two-phase multi-resolution visual mapping technique. The technique is applied to two areas in the Iheya North Field of the Okinawa trough, in regions that were drilled to varying extents during the IODP 331 expedition. A total area of more than 30,000m2 was mapped in a single dive with a remotely operated vehicle (ROV) and more than 80,000 organisms were identified from six different species. The results give insight into the effects that drilling activity has had on the distribution of megabenthos in this area. The method described forms a practical way to quantitatively assess the distribution of megabenthos over statistically meaningful spatial scales in a way that is repeatable and is suitable for comparison between sites or for monitoring sites over time.

キーワード：３D画像マッピング、ハビタットマッピング、熱水フィールド
Keywords: 3d visual reconstruction, Habitat mapping, Hydrothermal vent

海洋表層から海溝底に至る硝化菌の棲み分け構造
Niche separation of nitrifiers from the sea surface to the hadal ocean

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Ammonium (ammonia) and nitrite are important intermediates of oceanic nitrogen cycle, but these are depleted in most of the oceanic waters. In contrast, availability of ammonia most likely influence on niche separation of nitrifiers, and thus the niche separation would be a signature of geochemical interface in oceanic environments. In fact, niche separation of nitrifiers has been observed in Arctic to tropical oceans, and sea surface to hadal ocean (Sintes et al. 2013, Nunoura et al. 2015 and references therein). In this study, we analyzed single amplified genomes (SAGs) to know genomic backgrounds of niche separation of ammonia-oxidizing thaumarchaeotes from sea surface to hadal oceans.

キーワード：硝化、海洋、窒素循環
Keywords: nitrification, ocean, nitrogen cycle

海底下生命圏の探究における技術的ブレークスルー
Technological breakthroughs in search of the deep subseafloor biosphere

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During the first microbiology-dedicated scientific ocean drilling, the Ocean Drilling Program (ODP) Leg 201 off Peru and Eastern Equatorial Pacific in 2002, the number of microbial cells was evaluated by direct counting of acridine orange-stained cells under fluorescent microscopy, and the minimum quantification limit (MQL) of cell number was approximately 10^5 cells/cm^3 of sediment. Althought this technique is still applicable to high-biomass sedimentary habitats such as shallow organic-rich sediments near the seafloor, some innovative technological breakthroughs have been long required in order to explore low-biomass habitats close to the limit of biosphere. A decade later since Leg 201, we developed a computer image-based cell detection and enumeration method for deep sedimentary microbes. It enabled discriminable cell recognition based on the difference of fluorescence color between intracellular DNA and non-biological mineral particles after DNA stain with SYBR Green I, and resulted in objective and statistically mean cell numbers with higher reproducibility. In addition, we standardized a new protocol for effective cell separation from sedimentary mineral grains using a multi-layer density centrifugation. The combined use of this cell separation technique with flow cytometry or cell sorter opened the way to more fast, sensitive, and precise cell counting than before, even for very low-biomass sediment samples. For example, under the strictly controlled ultra-clean lab condition, our current minimum quantification limit approaches to less than 10 cells/cm^3 of sediment, at least 4 orders of magnitude lower than that during Leg 201. The sorted cells in each well are applicable for single cell-genomic study using the genome amplification techniques. Moreover, the separated cells can be concentrated and placed at one place on the membrane filter, and then isotopic ratios (i.e., $^{13}C/^{12}C$, $^{15}N/^{14}N$) and elemental abundances of each single cell can be analyzed on rastered ion imaging with nano-scale secondary ion mass spectrometry (NanoSIMS). To date, based on these technological breakthroughs, we are finally ready for exploring the limits of subseafloor life and the biosphere through scientific ocean drilling.

キーワード：海底下生命圏、生命検出
Keywords: Subseafloor biosphere, Life Detection

メタン生成・酸化のバイオマーカー: 補酵素F430

Coenzyme F430 as a biomarker for methanogenesis and anoxic methane oxidation

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Coenzyme factor (F430) is a prosthetic group of a key enzyme for methanogenesis, methyl coenzyme M reductase (MCR) [e.g. Ellefson et al., 1982]. Coenzyme F430 should be a practical biomarker to investigate distribution of methanogens and methanogenic potential in natural environments for the following reasons: 1) it should be common in all methanogens, 2) it has a potential to reflect only modern methanogenic activity due to its unstable nature, 3) it is clear proxy because other source organisms are highly restricted (only anaerobic methane oxidizing archaea [Krüger et al., 2003; Mayr et al., 2008]).
Recently we developed quantitative analysis of coenzyme F430 by triple quadrupole mass spectrometry coupled with liquid chromatography, which allow to detect coenzyme F430 in environmental samples including marine sediment with fmol level concentration [Kaneko et al., 2014].
The major concerns in application of the coenzyme F430 analysis as a biomarker tool are stability of coenzyme F430 and discrimination of source archaea (methanogens vs. ANMEs). Previous studies reported that free (not bound to MCR) coenzyme F430 changed to epimers in hour scale at 200C and hour to day scale at room temperature [e.g. Diekert et al., 1981]. However, it is still ambiguous how the epimerization is observed in environmental conditions. In general marine setting, methanogenesis occurs after sulfate reduction and the habitats of methanogens and ANME are clearly controlled by sulfate concentrations. On the other hands, these archaeal sources should be discriminable by compound specific isotope analysis of coenzyme F430 because isotope effects involved with their metabolic pathways are quite deferent [Hinrichs et al., 1999].
In this talk, we will show distribution of coenzyme F430 in environmental samples including paddy soils, ANME microbial mats and marine sediments, and carbon isotopic composition of coenzyme F430 from ANME archaea to address stability of coenzyme F430 and discrimination of source archaea.
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キーワード：補酵素F430、機能特異バイオマーカー、メタン生成
Keywords: Coenzyme F430, function specific biomarker, methanogenesis

電気化学による炭酸固定
Electrochemical Carbon fixation

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The emergence and evolution of proto-metabolic networks have recently attracted much interest as an essential initial step for the origin of life (Braakman and Smith, 2013). Alkaline hydrothermal systems have been proposed as a plausible site to drive proto-metabolism (Russell et al., 2010), where reduction and fixation of CO2 could have proceeded with the aid of ample and continuous supplies of reductive chemicals such as H2, H2S, and FeS, together with active mineral catalysts (Huber and Wachtershauser, 1997). Recently, a direct electrochemical measurement of a deep-sea hydrothermal vent in the Okinawa Trough demonstrated that the geochemical redox potential between hydrothermal fluid and seawater generates electrical current through the vent structure, and electrons are concentrated at the vent-seawater interface (Yamamoto et al., unpublished). Electrochemistry is an effective means for CO2 reduction and fixation. It has been experimentally shown that electrocatalytic reduction of CO2 on metal sulfide deposits produces CO and CH4 with excellent efficiencies under naturally plausible electrochemical conditions (from -0.4 to -1.3V; Yamamoto et al., 2014). There is a good probability that the geo-electrochemical systems occurring at alkaline hydrothermal vents served as a source of energy and reducing power to drive proto-metabolic reactions. Following there geological and experimental findings, we have been conducting electrochemical experiments in ELSI. Here, we will introduce our research progress and its implication for the origin and early evolution of life.

キーワード：生命の起源、アルカリ熱水噴出孔、代謝
Keywords: Origin of Life, Alkaline hydrothermal vent, Metabolism

太陽系岩石惑星の冥王代の歴史
HADEAN EVOLUTIONAL HISTORY OF ROCKY PLANET IN SOLAR SYSTEM

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隕石学および数値計算モデルに基づくこれまでの太陽系惑星形成論は、系外惑星探査、特にホットジュピターとスーパーアースの発見によって大きな変革を求められる時代となって久しい。古典的京都モデルに対してグランドタックモデルの提案に問題のありかが如実に示されている。これらの論争から一歩抜け出して次の時代へと導く鍵は、小惑星帯のサンプルリターンを含む系統的物質科学にある。本講演ではこれまでの小惑星帯の研究を要約して、地球の起源、初期進化、地球史をまとめる。
１）小惑星帯（２－５ＡＵ）の内側から外側までの化学的組成累帯とその起源、
２）隕石母天体形成までの物質分化とそれに要した時間
３）月と火星の表層地質と年代学、特にマグマオーシャンの固化年代とＬＨＢが起きた時刻とその期間
４）それらから導かれる地球の初期進化と表層環境、特に冥王代地球の復元
これらの課題の研究結果を元に、現在提案されている冥王代における原始太陽系惑星形成史を検証する。検証内容は以下のとおり。
１）地球―月系は、エンスタタイトコンドライト類似の物質から4567Ｍａに形成され、無海洋・無大気の状態で生まれた。
２）ジャイアントインパクトは、４４億年前ごろに起き、月は43億年前までに固化した。ジャイアントインパクトによる地球固体核の融解はなかった。
３）月と地球のマグマオーシャンは43.40億年前ごろまでに固化した。その後、約43億年前ごろをピークにＬＨＢがおきて、大気海洋が生まれた。このときに約４ｋｍの厚さの海洋が誕生し、プレート運動は42.66億年前に開始した。表層を覆った原初大陸はマントル対流および構造浸食によってマントル深部に崩落し、原始生命が４１億年前までに誕生した。地球生命の誕生は３段階で起きた。

キーワード：地球の起源、太陽系惑星形成論、アステロイドベルトにおける化学組成累帯構造
Keywords: origin of Earth, Planetary formation theory, Chemical zoning in asteroid belt

Organism-resolved Metagenomics using ggKbase: Recovering and analyzing thousands of genomes from metagenomic samples

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Metagenomics has the potential to recover near complete and complete genomes for the majority of microbial members present at > 0.2 % abundance level in natural communities, to track changes in community composition across space and time, and to document evolution *in situ*. The field has advanced tremendously since the first community metagenomic study of an acid mine drainage biofilm, more than a decade ago. Metagenomics is now a tool widely used by microbial ecologists. Thousands of research groups worldwide are now collecting complex metagenomic datasets, yet expertise in how to effectively and efficiently use the information is lacking. Currently most metagenomic data analysis methods yield only fragmented, partial genomes, or worse, they attempt to analyze only the read data from a sample and forego any genome assembly. Although such studies provide information about the representation of genes in an environment, much information is also lost. The result is often unsuitable for the development of useful, organism-resolved metabolic models.
Here we describe a multi-faceted approach for genomic analyses using ggKbase. ggKbase is a platform for storing, integrating, managing and analyzing metagenomic data. ggKbase provides intuitive visual binning tools which display key binning traits in a dynamic fashion allowing for the quick creation and assessment of organism bins. ggKbase provides a rapid functional profiling of genomes from a community and generates a detailed analysis of the overall community composition. ggKbase integrates multiple sources of annotation (e.g. KEGG, UniRef etc.) and provides high quality metabolic pathway information. Using ggKbase we have analyzed tens of thousands of genomes from almost 1000 metagenome samples. We will present the ggKbase framework and highlight several use cases.

Keywords: metagnomics

軟体動物の貝殻微細構造形成に関与する有機基質に関する研究

Studies on the functions of organic matrices to make the molluscan shell microstructures.

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Biominerals are biogenic mineralized tissues containing not only inorganic compounds, but also a small amount of organic matrices that play an important role in biomineral formation. The mollusk shells which are typical biominerals consisting of calcium carbonate and organic matrices, have various microstructures. The organic matrices promote the nano-cluster formation of minerals to regulate the nucleation, crystal growth, crystal orientation and crystal morphology. We want to introduce two molecular formation mechanisms of shell microstructures in two molluscan species using organic matrices.

The shells of gastropods have spiral in shape around the central axis. As the living body grows up, the shell thickness in the internal side of spiral becomes thin to expand interior space. These observations suggested that a dissolution process, working as the remodeling mechanism, changes the shell shape in molluscan shells. The molecular mechanisms of remodelling processes in the vertebrate bone have been studied well. The function of both osteoblast and osteoclast cells orchestrate the bone formation and remodeling. Although various proteins associated with shell calcification have been identified in molluscs, no organic molecules related to the dissolution of molluscan shells have been identified and the remodeling mechanism of molluscan shells is unclear.

To reveal the dissolution mechanism for the remodeling of the spiral shells in gastropod, we used the fresh water snail, *Lymnaea stagnalis*, as an experiment material and focused on chitinases of the organism. Chitinase activity was observed in the acetic acid-soluble fraction from the shell and the buffer extract from the mantle, indicating that the shell and mantle may have a function to degrade the chitin scaffold in the shell. The chitinase activity in both fractions was disappeared by the heat treatment. Allosamidin, a specific inhibitor of family 18 chitinases completely inhibited the chitinase acitivity of both fractions indicating that the enzyme activities in the shell and mantle were from only the family 18 chitinases. Homology cloning and transcriptome analyses from the mantle revealed five genes encoding family 18 chitinases (*chi-I, chi-II, chi-III, chi-IV and chi-V*). GH18 domain for the activity of chitin degradation was conserved in all chitinases. All chitinases were expressed not only in the mantle, but also in other tissues, suggesting that chitinases in the mantle have multiple-functions. We injected the allosamidin into living snails to inhibit the chitinase activity in the mantle. Although the chitinase activity in the mantle was strongly suppressed by allosamidin injection, the shell microstructure before and after injections was not changed. However, treatment of chitinase from *Trichoderma viride* by a commercially available altered the shell microstructure of *L. stagnalis* suggesting that the chitinase was associated with the shell dissolution process.

On the other hand, the “scaly foot” gastropods (*Chrysomallon squamiferumuse*) use the organic matrices to make the scales of iron sulfide on the foot and shell surface. The “scaly foot” was discovered in the Kairei deep-sea hydrothermal field of the Central Indian Ridge. The black scales consist of nano-crystal of iron sulfide minerals within a laminated organic matrix. Although iron sulfide mineralization is known in the metabolic sulfate reduction from prokaryotes, the formation mechanism of iron sulfide nano-crystal is unclear. In this study, we tried to extract the key

organic components that interact with iron in the scale. Such organic components may keep the small size of iron sulfide crystals on the foot and shell surface.

キーワード：バイオミネラリゼーション、軟体動物貝殻、有機基質
Keywords: biomineralization, molluscan shell, organic matirces

海底堆積物中の生物源マグネタイトの分布と化学的環境による結晶形態の違い
Distribution of bacterial magnetites in deep-sea surface sediments and variations of magnetosome morphology with chemical conditions

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Magnetotactic bacteria (MTB) have attracted interest of paleo- and rock magnetists as a source of magnetic minerals in sediments and from a viewpoint of remanent magnetization acquisition processes. Furthermore, MTB should also play an important role for biogeochemical cycles of iron. MTB are considered to be microaerophilic and most commonly live near or below the Fe-redox boundary. However, their actual distribution within natural deep-sea sediments was little studied. Recent progress in rock magnetic techniques has enabled semi-quantitative detection of fossil biogenic magnetites (magnetofossils) in sediments. Common occurrence of magnetofossils in Pacific red clay (Yamazaki and Shimono, 2013), which contains abundant dissolved oxygen and does not have a Fe-redox boundary, may conflict with the widespread interpretations of MTB ecology mentioned above. For better understanding of the ecology of MTB in deep-sea sediments, we have conducted rock-magnetic, biogeochemical, and microbiological analyses of surface sediments taken from the Japan Sea with a multiple corer. From dissolved oxygen and Fe (II) contents of interstitial water and color reflectance of the sediments, the Fe-redox boundary was clearly detected at 7 to 25 cm below the seafloor at three sites (1770 to 2710m in water depth). Rock magnetic proxies and TEM observations indicate that magnetofossils occur throughout the sediment columns regardless of the distance from the Fe-redox boundary, even at the sediment-water interface. We found that the proportion of magnetofossils with tear-drop morphology increases near the Fe-redox boundary. On the other hand, the morphology of magnetofossils in oxic red clay is dominantly (>90%) octahedral. These results suggest that some species of MTB that produce magnetosomes of tear-drop morphology prefer a chemical condition near the Fe-redox boundary, whereas other species may live in microaerophilic microenvironments around organic particles near the water-sediment interface. Even some species of MTB that yield octahedral magnetosomes might be aerotolerant and prefer oxic environments. To strengthen the notion above, pyrosequencing of 16S rRNA gene sequences was conducted for the corresponding sediments. Among diverse bacterial lineages known to produce magnetosomes, 16S rRNA gene sequences phylogenetically affiliated within the lineages of Nitrospirae known to produce magnetosomes with tear-drop morphology were distributed only around the Fe-redox boundary, whereas those affiliated within the family Rhodospirillaceae (Alphaproteobacteria) and known to produce octahedral magnetosomes were distributed in all investigated sediments regardless of the Fe-redox boundary. Taken together, it is strongly suggested that the dependency on the Fe-redox boundary is different among phylogenetically and morphologically diverse magnetotactic bacteria.

キーワード：走磁性バクテリア、磁石化石、岩石磁気
Keywords: magnetotactic bacteria, magnetofossil, rock magnetism

鉄安定同位体を用いた熱水噴出孔生物の鉄代謝評価
Stable isotope signature of Fe to understand the Fe-biocycle in the hydrothermal-vent

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Recent progresses in isotope analysis based on the mass spectrometry technique enabled us to detect small changes of the many elements in the periodic table. Among the elements, stable isotope studies using Fe has been widely adopted to understand both the mechanism of Fe metabolism in marine organisms and the bio-cycling of Fe in marine environment. Iron is typical essential inorganic nutrients for all plants and animals. For the land organisms, the Fe isotope ratios varies significantly with increase of the trophic level (Walczyk and Blanckenburg, 2002, 2005). In strike contrast, for marine organisms, because of very limited availability of Fe in seawater, the intake efficiency for Fe could be higher than those for the terrestrial animals. Higher intake efficiency of Fe can results in smaller magnitude of isotopic fractionation through dietary process, and therefore, the difference in the Fe isotope ratios for marine organisms of lower trophic levels were close to the seawater sample (Jong et al., 2007; Bergquist and Boyle, 2006). Moreover, there were no significant difference in the Fe isotope ratios (<0.5‰) for high trophic level marine organisms between muscle and liver (Yamagata, in prep). These studies revealed that magnitude of the isotope effects on Fe can reflect both the nutritional status of Fe in animals and the availability of Fe in marine environments. To investigate this, we have measured the $^{56}Fe/^{54}Fe$ and $^{57}Fe/^{54}Fe$ for deep-sea organisms in hydrothermal field for understanding Fe bio-cycle which has both characteristics of environment, terrestrial and marine.
In this study, *Chrysomallon squamiferum* called “Scaly-foot“ gastropod (n=5) and *Gigantopelta aegis* (n=5) from a deep-sea hydrothermal field at the Longqi vent field, Southwest Indian Ridge, were subsidized to the Fe isotope ratio analysis. The *Chrysomallon squamiferum* has unique scale made of iron sulphide on its foot (Suzuki et al., 2006). The *Gigantopelta aegis*, collected in the identical locations for the *Chrysomallon squamiferum*, has a thick iron oxide coating on the shell. Both the *Chrysomallon squamiferum* and *Gigantopelta aegis* has sulphur-oxidizing bacteria in oesophageal gland to form a symbiotic relation. Sclerite samples and soft body samples of muscle, ctnidium, blood, heart, and oesophageal gland were decomposed, and the Fe was extracted by anion-exchange chromatography. The Fe isotopic ratios were analyzed by a multiple collector-ICP-mass spectrometer (MC-ICP-MS) technique (Nu Plasma II) equipped with a desolvating sample introduction system and pseudo high resolution mode.
The resulting Fe isotope ratios demonstrated the distinct variations in the $^{56}Fe/^{54}Fe$ and $^{57}Fe/^{54}Fe$ ratios for Chrysomallon squamiferum and Gigantopelta aegis samples. The resulting $\delta^{56}Fe$ values for all soft body samples collected from the *Chrysomallon squamiferum* were systematically higher than those for the *Gigantopelta aegis*, whereas no significant difference in the $\delta^{56}Fe$ values could be found for oesophageal gland samples collected from *Chrysomallon squamiferum* and *Gigantopelta aegis* samples. It should be noted that the $\delta^{56}Fe$ for all the soft body samples from the *Chrysomallon squamiferum* was rather higher than those for symbiotic bacteria. This can reflect both very high intake efficiency of Fe from marine environments and the small contribution of Fe intake through the symbiotic bacterial for the *Chrysomallon squamiferum*. The Fe isotope signature obtained here demonstrate the clear difference in the Fe metabolism between *Chrysomallon squamiferum* and

sulphur-oxidizing bacteria. The details of the mechanism why separate the $\delta^{56}Fe$ values of these two samples will be discussed in this presentation.

キーワード：鉄安定同位体、生物鉄代謝、深海生物、多重検出器型ICP質量分析計
Keywords: Iron stable isotope, Fe bio-cycle, deep-sea organisms, multiple collector-ICP-mass spectrometer

Coupling of multi-range imaging mass spectrometry and isotope chronology for multidisciplinary study on life and environmental sciences

Coupling of multi-range imaging mass spectrometry and isotope chronology for multidisciplinary study on life and environmental sciences

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Images of trace-elements or isotopes can provide key information to evaluate the contribution of metamorphic events or movements of elements through secondary heating events. The LA-ICPMS technique is a useful tool to obtain image data of major to trace-elements from samples. Elemental and isotope images can be obtained by repeated analysis of line-scanning measurements using the LA-ICPMS technique. Time resolved-signal intensity profile obtained by laser rastering can be converted to a position based-signal intensity profile via the relationship between the rastering rate and the elapsed time. The resulting spatial resolution and the elemental sensitivity is dependent upon several key operational parameters such as, size of laser beam, raster rate as well as time slice of the data acquisitions (ie., dwell time for each analytes). The LA-ICPMS technique is highly sensitive to determine the abundance of the trace elements. One of the main advantages to use the LA-ICPMS technique for imaging analysis is that the sample is placed under atmospheric pressure, and neither evacuation of the sample housing nor coating with conductive materials is required. Moreover, because of both the minimum sample preparation and the post-ionization system configurations, the LA-ICPMS technique represents a fast and accurate method for quantitative imaging technique for trace-elements from biochemical or geochemical samples.
Another important feature of the elemental imaging using the LA-ICPMS technique is the analytical capability for large-sized samples (>10 mm). This is of crucial importance to secure a bridge between the microscopic and macroscopic realm in geochemical studies. The elemental imaging for trace-elements is an essential tool to derive inherent information from samples. Difference in the distribution pattern of the isotopes can reflect the geochemical and cosmochemical features of the elements. Moreover, the images suggests possible contribution of a re-distribution or secondary movement of these elements through heating or weathering. In addition, difference or similarity in the distribution pattern of the elements may provide key information concerning the status of system closure for chronologies. Thus, the coupling of the elemental imaging and the isotope chronology can become a major analytical tool to obtain reliable and precise age data from the geochemical samples, including biochemical or even micro-fossil samples. Analytical capability of the imaging mass spectrometer using the LA-ICPMS technique will be demonstrated in this presentation.

キーワード：Elemental imaging、Elemental Metabolism、Isotope Chronology
Keywords: Elemental imaging, Elemental Metabolism, Isotope Chronology

トラバーチン堆積物に見られる微生物遷移と縞状構造：北部スマトラ島の例

Transition of microbial communities and laminated structures in travertines: a case study in northern Sumatra, Indonesia

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トラバーチンとは，CO_2とCa^{2+}に富む温泉水から沈殿する炭酸塩堆積物である．太古代～原生代に発達したストロマトライトと類似した縞構造を持つことから，当時のモダンアナログとされている．先行研究ではシアノバクテリアとストロマトライトの関連性が強調されてきたが，これはストロマトライトが既に存在していた太古代の極めて低い酸素濃度と矛盾する．酸素を発生しない微生物群集もストロマトライトを作る可能性がある．この問題を解決するため，本研究ではインドネシア共和国スマトラ島北部のDolok Tinggi Rajaで調査を行なった．ここでは，約62℃，無酸素で硫化水素と二酸化炭素に富む源泉からアラゴナイトとカルサイトで構成されるトラバーチンが長径約50mのマウンド状の地形を作る．水質分析の結果は，湧出直後の急速な二酸化炭素と硫化水素の脱ガス，溶存酸素濃度の上昇，pHと炭酸カルシウム過飽和度の上昇，流下経路での炭酸塩鉱物沈殿を示している．この水質条件の変化を反映するように，上流から下流にかけて微生物の優先種が化学合成細菌→紅色硫黄細菌→緑色非硫黄細菌→緑色硫黄細菌と遷移する．シアノバクテリアは下流部で認められるものの優先しない．遺伝子解析で検出された硫黄細菌の中には，紅色硫黄細菌*Chromatiaceae*科の様な明らかな非酸素発生型光合成細菌も認められた．おそらく，硫化水素が豊富にある環境では，水を用いる酸素発生型光合成（シアノバ゛クテリア）よりも硫化水素を用いる非酸素発生型光合成（硫黄細菌）のほうが有利となるのだろう．微生物マットが発達している場所では，トラバーチンは縞構造を形成していることが多く，硫黄細菌でも大分県長湯温泉やジャワ島Pancuran Pituと同様の日輪組織を形成できる．したがって，太古のストロマトライトは必ずしもシアノバクテリアによって作られたものとは言えない．

キーワード：トラバーチン、硫黄細菌、ストロマトライト
Keywords: travertine, sulfur bacteria, stromatolite

日本海東縁深海堆積物中におけるメタノールの生物地球化学的物質循環
Biogeochemical cycle of methanol in anoxic deep-sea sediments of the eastern Japan Sea

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Methanol is one of the most important carbon and energy sources in anoxic environments. However, the biological flux and lifetime of methanol in anoxic marine sediments are largely unknown. In this study, we report quantitative methanol removal rates in subsurface sediments for the first time. Methanol concentrations in pore water from Japan Sea sediments gradually increased with depth below the sulfate-methane transition zone. Based on anaerobic incubation experiments with radiotracers, high rates of microbial methanol consumption were detected in the sediments. Our experiments also showed that the methanol oxidation to CO_2 surpassed methanol assimilation and methanogenesis from CO_2/H_2 and methanol. Nonetheless, a significant decrease in methanol was not observed after incubation, likely because of the microbial production of methanol in parallel with its consumption. This study suggests that microbial reactions play an important role in the sources and sinks of methanol in subseafloor sediments.

キーワード：メタノール、深海堆積物、海底下生命圏
Keywords: methanol, deep-sea sediment, subseafloor biosphere

大陸地殻内生命圏における第三のエネルギー源

Co-occurrence and Metabolic Consequences of Candidate Bacterial Phyla and Anaerobic Methane Oxidizing Archaea in the Deep Crustal Biosphere

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The terrestrial crust is known to harbor deep microbial life energetically dependent on organic matter and/or H_2. Recent studies have provided fragmented pieces of evidence suggesting that anaerobic oxidation of methane (AOM) is microbiologically mediated in the terrestrial subsurface as well as the deep oceanic crust. As the abundance of methane is extremely common in the deep aquifers, the existence of subsurface microbial ecosystems capable of harvesting the energy from AOM can dramatically change our view of the Earth's biosphere. Here we show the integrated evidence of the anaerobic methanotrophy based on geochemical, stable isotopic, molecular phylogenetic and metagenomic data from the deep granitic aquifer. High-quality groundwater was collected from two adjacent boreholes drilled into highly and sparsely fractured domains at a 300-m deep stage of the Mizunami underground research laboratory (URL), central Japan. The highly fractured domain was associated with groundwater dominantly colonized by AAA (AOM associated Archaea) and the candidate phyla OD1 and OP3, neither of which were detected from the sparsely fracture domain with groundwater enriched with H_2 (~10-100 nM) and depleted in sulfate (<5 μM). Consistent with 16S rRNA gene sequences, methyl-coenzyme M reductase gene sequence analysis revealed the habitat segregation of AAA and methanogens corresponding to the fracture domains. As the strong correlation of AAA and sulfate was statistically indicated by canonical correspondence analysis (CCA), anaerobic methane oxidation coupled to sulfate reduction was experimentally demonstrated by the amendment of $^{13}CH_4$ of, and the subsequent detection of ^{13}C-enriched dissolved inorganic carbon from, microbial cells incubated in groundwater with and without the molybdate inhibition of dissimilatory sulfate reduction. Heatmap of 16S rRNA gene abundance in the boreholes within the two domains over two years showed the highly correlated distributions of AAA and the candidate phylum OP3, the nearly completed genome of which has functional genes involved in sulfur metabolisms such as a potential reductase gene of nitrite and sulfite. Although the syntrophic partnership among AAA and the candidate phyla needs to be further investigated, our results clearly demonstrate that the deep methanotrophy coupled to sulfate reduction is microbiologically mediated, which leads to the reconsideration of the biomass production and the cycling of hydrogen, carbon and sulfur in one of the largest microbial habitats on Earth.

キーワード：地殻内生命圏、瑞浪超深地層研究所、嫌気的メタン酸化
Keywords: Deep biosphere, Mizunami underground research labolatory, Anaerobic oxidation of methane

深海堆積物中に記録された真核生物DNAに堆積物酸化還元状態が与える影響
Effects of sedimentary redox conditions on Eukaryotic DNA recorded in deep-sea sediments

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Eukaryotic DNA in marine sediments can be a useful indicator of both ancient marine ecosystem in water column and living microbial eukaryotes in sediments. However, the environmental factors that influence the composition and preservation of eukaryotic DNA in marine sediments are poorly characterized. In this study, we examined effects of sedimentary redox conditions on the diversity of eukaryotic communities recorded in deep-sea surface sediment samples from 8 sites of the Japan Sea (from oxygenated abyssal sediments to sulfidic sediments in methane seeps) using a combination of various geochemical and molecular-biological tools. Sedimentary redox conditions were characterized by depth profiles of pore water (oxygen, nitrate, iron, sulfide, etc.) and bulk sedimentary organic matter (TOC, TN, $\delta^{13}C$, $\delta^{15}N$). The concentration and diversity of 18S rDNA in the sediment samples were investigated by qPCR and pyrosequencing. Decreases in 18S rDNA concentration with sediment depth were rapid in the oxic sediments, while decreases were moderate in the anoxic sediments and the sulfidic sediments. The community composition based on 18S rDNA sequences also varied with the sedimentary redox conditions. These results suggest that redox conditions of surface sediments can be important factors controlling the composition and preservation of eukaryotic DNA in deep-sea sediments.

キーワード：酸化還元状態、海洋堆積物、生物多様性、DNA、真核生物
Keywords: Redox condition, Marine sediments, Biodiversity, DNA, Eukaryote

南極氷床下の水-鉱物相互作用と氷河湖の生物地球化学：氷床下の伏流水によるシリカ流入と微生物生態系のレスポンス

Biogeochemistry and subglacial meltwater limnology in East Antarctica: insight from microbial response with subglacial silica input in a perennially ice-covered lake at Rundvagshetta

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南極氷床下には，基盤岩に接する氷の部分融解により液体の水（subglacial meltwater）が存在することがある。そのような氷床下の水は，地底湖を形成するほか，一部は伏流水となり，水脈に沿い，大陸縁辺部に向かって流れてゆく（e.g., [1]）。氷床下の水脈は，基盤岩との物理的削剥や化学的な水-鉱物相互作用（subglacial weathering）を経て，無機態の炭素（relic ^{14}C）のほか，窒素，鉄，シリカ等の栄養塩をわずかに供給・運搬する。氷床下の伏流水の恩恵を受けるのが，氷床縁辺部の微生物生態系である。南極全体の約１％程度は，完新世の氷床後退により，かつて氷床に覆われていた場所が露岩域となっている。そのような氷床縁辺部には，かつての氷食作用の形跡が見られる他，氷河性の湖沼が存在する。では，水の収支や物理・化学的特徴が，そこに棲息している（棲息してきた）基礎生産者にどのような影響を与え，全体の微生物相は，どのように応答しているのだろうか。これらの全体像について，基礎的な記載が非常に少なかったため，我々は，東南極氷床のルンドボークスヘッダ地域の氷床縁辺部にある氷河湖を対象に，完新世の地史的背景と生物地球化学プロセスの記載を行った。永年的な氷に被覆された湖底には，少なくとも約6000年前から微細な氷河性砕屑物の堆積作用が始まっていた。初生的な基礎生産者は，同時期の海成湖沼（Lake Skallen [2]）でも観察された珪藻（*Chaetoceros*）であることが分かった。その後，氷床後退に伴うアイソスタティックリバウンドによる隆起と離水の後にも基礎生産者は，*Chaetoceros*に近縁な種が卓越しており，離水後に基礎生産者が，大気CO_2（modern ^{14}C）と大気N_2に依存したシアノバクテリアに変遷するスカーレン地域とは，対照的な結果となった。ルンドボークスヘッダでは，無機態の炭素（relic ^{14}C）を含む，氷床下の伏流水（窒素，シリカ等）に依存した独特の生態系を形成していることが明らかになった[3] 。

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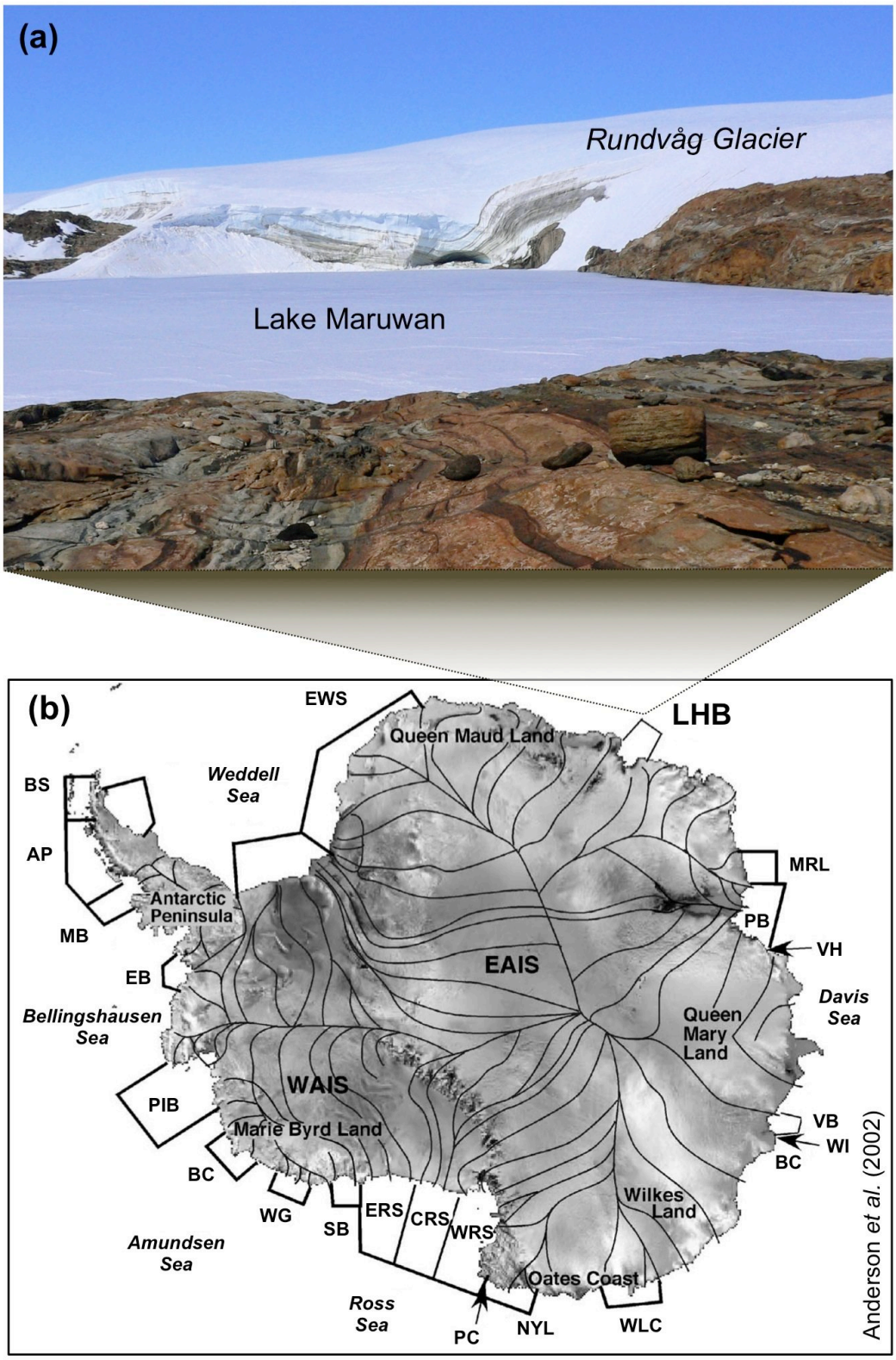
キーワード：氷床下の水-鉱物相互作用、氷床縁辺部の微生物生態系
Keywords: Biogeochemistry within subglacial weathering, Subglacial meltwater limnology and microbial ecology



(a) Lake Maruwan, a perennially ice-covered glacial lake at the Rundvågshetta on the Soya Coast of Lützow-Holm Bay (LHB), East Antarctica. **(b)** a drainage map of the Antarctic ice sheet. Modified after Anderson *et al., Quaternary Sci. Rev.*, 2002 and Takano *et al.*, this study.

