Phylogenetic evidence for the origin and diversification of whale-fall fauna

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The first discovery of a chemosynthetic faunal assemblage on a whale-fall in 1987 was significant not just in advancing our understanding of deep-sea ecology and succession, but in also generating new hypotheses for the evolutionary origin of the deep-sea fauna. Could these remarkable habitats also provide avenues for dispersal and speciation over evolutionary time? The early phylogenetic studies provided some support for this controversial hypothesis. But more recent and comprehensive research has shown that the picture is more complicated. Here I review evidence for what I see as three possible hypotheses: the ‘evolutionary stepping-stone hypothesis’ where whale-falls have actually created a pathway for radiation into other chemosynthetic habitats, the ‘ecological stepping-stone hypothesis’ in which whale-falls play a role only in aiding dispersal in ecological time, and the ‘hotspots of adaptive radiation hypothesis’ in which whale -falls act as a biodiversity pump for fauna that originally evolved at hydrothermal vents or seeps.

ウミガメ遺骸の腐敗過程と遺骸に成立する生態系の解明
The deacay process of and the biological community on sea turtle-falls at the Tsukumo Bay, Noto Peninsula, Jpan

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The whale-fall community is one of the unique biological community formed on decaying whale carcass on the sea floor. The community thought to be changed at least four stages of ecological successions, i.e. the mobile scavenger stage, the opportunist enrichment stage, the sulphophilic stage and the reef stage. Molecular studies on some organisms included in the community suggested that the origin of the vent-and/or seep-restricted animals have come from through environments formed around such organic-falls. In this point of view, the reptile-falls would be more important than the whale-falls because of its longer fossil record than the marine mammals. Although the ecosystem on the whale-fall has been studied well, the ecosystem on the reptile-fall hasn’t been studied in details. Thus, we examined the decaying process of four sea turtles deployed on shallow sea floor (11 to 14 m in depth) in Tsukumo Bay, Noto Peninsula, Japan. The carcasses were observed by scuba, and some bones of the carcasses were recovered time to time to examined organisms which lived on/in the bones.

5 days after deployment, the sea turtle carcasses were covered by white microbial mat (*Bggiatoa* spp., indicator of sulphophilic stage). 21 days after deployment, the carcass was eaten by fish (indicator of mobile scavenger stage). *Zoothamnium* sp. (indicator of sulphophilic stage) was observed on the carcass. 36 days after deployment, dorvilleid and nereidid polychaetes (indicator of opportunistic stage) lived in the bones and barnacles (Crustacea; indicator of the reef stage) were attached to the bone. Thus, all four stages of ecological succession observed on whale-falls have also been observed on the sea turtle falls within 36 days after deployment. It is noteworthy that the sea turtle-fall sustained chemosynthetic community as same as whale-falls.

To examine sustainability of opportunistic and sulphophilic stages, we compared faunal assemblages in/on the recovered bones of the sea turtle carcasses with different body size and deployment period. Organic matrix was still remained in the bones of 2016ST-1(green turtle, carapace length (CL) = 42 cm, 144 days after deployment) and 2013ST-L (loggerhead turtle, CL = 72 cm, 3 years after deployment). There were *Beggiatoa* microbial mats, *Zoomthamnium* sp. and dorvilleid polychaetes in/on the bones. In contrast, there is no organic matrix in the bones of 2013ST-S (green turtle, CL = 36 cm, 3years after deployment), and there were no *Zoothamnium* sp. and dorvilleids. Thus, the smaller sized carcass exhausted within 3 years, but the larger carcass sustained opportunistic and sulphophilic stages more than 3 years.

キーワード：ウミガメ、遺骸、鯨骨群集
Keywords: sea turtle, carcass, whale-fall

メタン酸化古細菌のバイオマーカー炭素同位体比による古冷湧水メタンの起源推定

Origin of methane at ancient seeps inferred from carbon isotopic signatures of biomarkers of methane-oxidizing archaea

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メタンは有機物の微生物分解または熱分解により生成し，その起源はメタンの炭素安定同位体比などから推定できる．海洋へのメタンの主要な放出場であるメタン湧水では，湧出するメタンの起源を知ることで海底下の生物地球化学プロセスや水循環について知ることができる．地質時代の古メタン湧水は，微生物が起こす嫌気的メタン酸化によって形成されたメタン起源炭酸塩岩として地層中に保存される．メタン起源炭酸塩岩はメタン由来の炭素を引き継いでいるが，形成時に海水中の溶存無機炭素などメタン以外の炭素も取り込むため，炭酸塩岩の炭素同位体比から過去に湧出していたメタンの同位体比を推定することは難しい．本研究では，メタンの同位体組成をより直接反映していると考えられるメタン酸化古細菌の脂質バイオマーカーの炭素同位体比をもとに，古メタン湧水のメタンの起源推定を試みた．分析には日本海側陸域11か所の下部中新統〜中部更新統より採集した古メタン湧水炭酸塩岩と，上越沖海底の熱分解メタンの湧出域で採取された現世の炭酸塩ノジュールを用いた．すべての炭酸塩の初生的な組織は−64.7〜−4.7‰（vs. VPDB）の幅広いδ^{13}C値を示し，微生物または熱分解メタンの両方が起源として考えられる．古メタン湧水炭酸塩岩より抽出したバイオマーカーであるペンタメチルイコサン（PMI）はほとんどが−100‰より低いδ^{13}C値を示したのに対し，上越沖の現世炭酸塩ノジュールから抽出したPMIは−80‰というより高いδ^{13}C値を示した．上越沖で湧出するメタン（−36‰）と炭酸塩中のPMIとの炭素同位体分別は−44‰であり，この分別が過去も同じであったと仮定すると，対象とした日本海側地域の古メタン湧水ではδ^{13}C値が−50‰より低い微生物起源のメタンが湧出していたと推定できる．このことは，対象とした古メタン湧水では海底下浅部で生成したメタンが供給されており，断層などの経路を通じた深部起源の熱分解ガスの海底への湧出はなかった可能性を示唆する．過去の湧水中のメタンの同位体組成をより制約するため，炭酸塩中に残留しているメタンを抽出する試みも進行中である．今後は炭酸塩の微量元素組成などの流体の起源指標と合わせて，古メタン湧水のメタンの起源を推定する必要がある．

キーワード：メタン、冷湧水、バイオマーカー、新生代、日本海

Keywords: Methane, Cold seep, Biomarker, Cenozoic, Japan Sea

Mussel genomes provide insights into adaptation to deep-sea chemosynthetic environments

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The environment of deep-sea hydrothermal vents and methane seeps is characterised by darkness, lack of photosynthesis-derived nutrients, high hydrostatic pressure, variable temperatures and high concentrations of heavy metals and other toxic substances. Despite this, these ecosystems support dense populations of specialised macrobenthos such as giant tubeworms, mussels, limpets, clams and shrimps. Lack of genome information hinders understanding of the adaptation of these animals to such inhospitable environment. Here we report the genomes of a deep-sea vent/seep mussel *Bathymodiolus platifrons* Hashimoto & Okutani, 1994 and a shallow-water mussel *Modiolus philippinarum* (Hanley, 1843). Phylogenetic analysis shows that these mussel species diverged approximately 110.4 million years ago (MYA). Many gene families, especially those for stabilising protein structures and removing toxic substances from the cell, are greatly expanded in *B. platifrons*, indicating adaptation to extreme environmental conditions. The *B. platifrons* innate immune system is considerably more complex than that of other lophotrochozoan species including *M. philippinarum*, with significant expansion and high expression of gene families related to immune recognition, endocytosis and caspase-mediated apoptosis in the gill, revealing presumed genetic adaptation of the deep-sea mussel to the presence of its chemoautotrophic endosymbionts. A follow-up metaproteomic analysis of the gill of *B. platifrons* found methanotrophy, assimilatory sulfate reduction, and ammonia metabolic pathways in the symbiont, providing energy and nutrients to allow the host to thrive without dependent on photosynthesis derived food. Our study of the genomic composition allowing symbiosis in extremophile molluscs gives wider insights into the mechanisms of symbiosis in other organisms such as deep-sea tubeworms and shallow-water corals.

In addition, we would also like to take this opportunity to introduce a large-scale program on “U-Shape” area that targets at the vents along the Mid-Ocean Ridge of both South Atlantic and Western Indian Ocean, to be launched by China Ocean Mineral Resource Research and Development Association, for which we call for international collaboration in next 15 years.

Keywords: Genome sequencing, Bathymodiolus, Symbiosis

One, two, or many species? Morphological and genetic analyses of vent and seep pectinodontid limpets reveal extreme morphological plasticity

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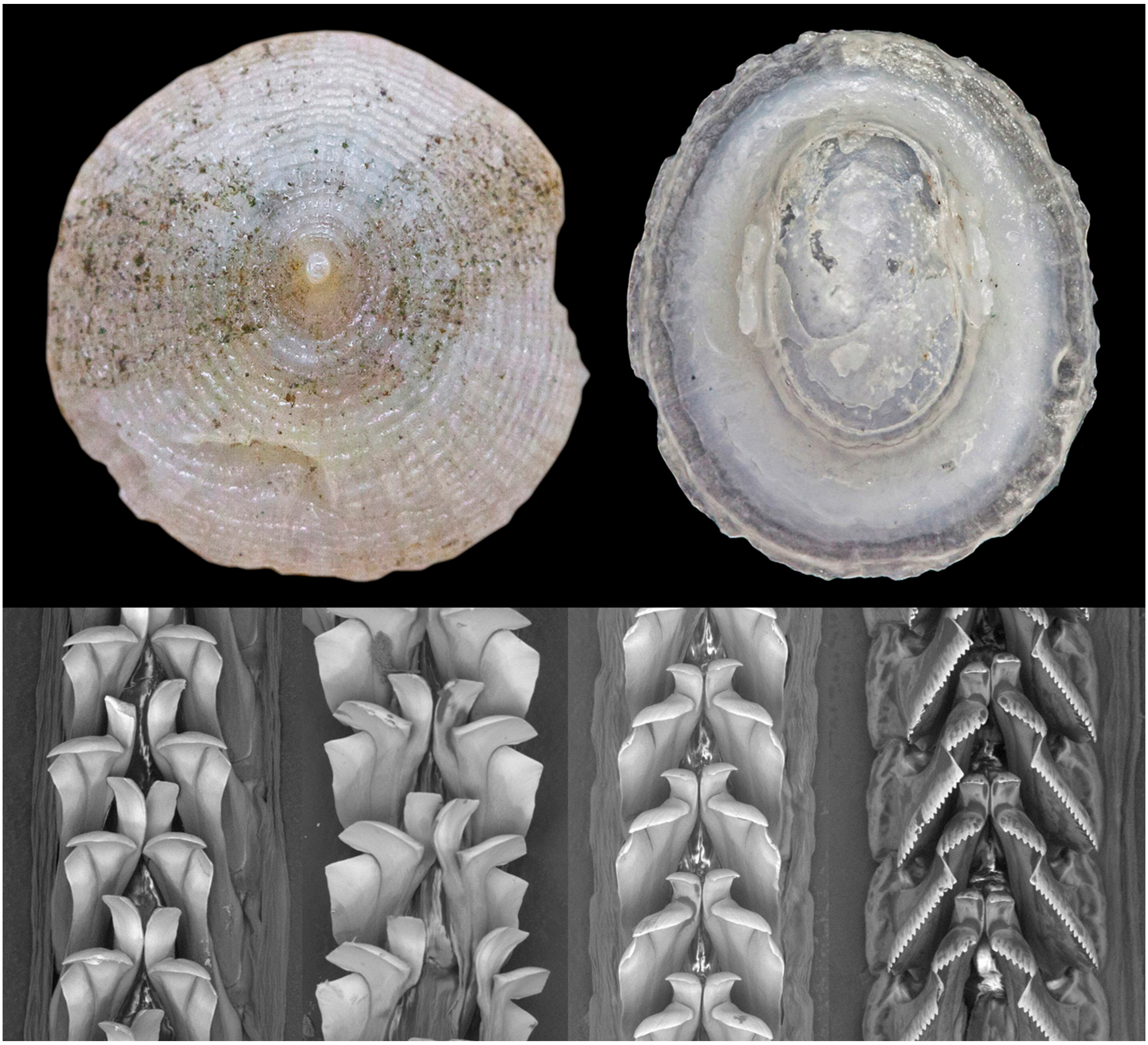
Chemosynthetic ecosystems harbour rich megafauna communities, of which gastropod molluscs comprise a major component and have received considerable taxonomic efforts. Pectinodontid limpets, characterised by a white shell with cancellate sculpture and a radula with a single trifurcating lateral teeth on each side, are a common constituent of vents and seeps in the western Pacific. Thus far, two genera (*Bathyacmaea* and *Serradonta*) totalling eight species have been described based on shell and radula characteristics. However, no data on their intraspecific variation or genetic characterisation have been published. In the present study, numerous pectinodontid specimens from Sagami Bay and Okinawa Trough were investigated morphologically, revealing great disparity in both shell and radula in each locality, rendering existing species and even genera boundaries questionable. Changes in shell form according to substrate shape was confirmed through live-rearing in a controlled aquarium. Furthermore, phylogenetic and population genetic analyses of *Bathyacmaea* and *Serradona* specimens from Sagami Bay to the South China Sea clearly demonstrated that most specimens belonged to one single molecular operational taxonomic unit regardless of their morphological affinity. Although a number of individuals from Minami-Ensei and Hatoma Knoll fields in Okinawa Trough were found to be genetically divergent, these did not exhibit obviously morphological differences and are likely cryptic. Altogether, these results strongly suggest that most (if not all) currently described vent and seep pectinodontids are actually mere forms of a single extremely morphologically plastic species. As a case study, the present study serves to raise awareness against splitting and describing species solely based on hard part morphology without carefully assessing the reliability of characteristics used.

キーワード：熱水噴出孔、冷水湧出域、軟体動物、表現型可塑性、分類学、集団遺伝学
Keywords: Hydrothermal vent, Cold seep, Mollusca, Morphological plasticity, Taxonomy, Population genetics



Locomotion and move tracking of "*Calytogena*" clams *in situ* and in patented H_2S controlling tanks

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Vesicomyid clams are one of the representative chemosynthetic animals, which have flourished in seep and vent sites during the Cenozoic. We report locomotion and behavior patterns of “*Calytogena*” clams to examine their adaptability to fluctuation of seep activity and disturbance of rapid burial. We analyzed time-lapse image data of *in situ* Real-time Deep Seafloor Observatory off Hatsushima Island in Sagami Bay, 1174 m in depth (3 min. interval) and patented H_2S controlling tanks in JAMSTEC (30 sec. interval) and Enoshima Aquarium (3 min. interval).

The “*Calytogena*” clams usually show semi-infaunal standing position with anterior side down and foot penetrating into underground sulfide layer, but sometimes crawl laying their shells with ventral side down. In standing position, the clams rearrange their postures swaying and obliquely rotating shells with foot as an axis. The clams sometimes push one another maybe quarreling over their favorite seep spots.

In crawling mode, they move forward by repeating the following steps: 1) laying shell down, 2) extending and penetrating foot in anterior direction, 3) maybe forming an anchor by foot expansion, and 4) pulling shell forward by foot contraction. In cases, the clams gathered into one spot and stranded one another, but could restore their postures into normal semi-infaunal position by extending and bending foot, which has wide movable range and high flexibility. During foot re-penetrating into the sediment, we observed that mass of sediment particles travels on whole surface of foot from its tip to root. Our SEM observation confirmed that the foot surface is densely covered by mucous cilia. The ciliary movement maybe enables the sediment conveying backward, which helps foot penetration.

In patented H_2S controlling tanks of Enoshima Aquarium, the “*Calytogena*” clams migrated keeping their track along the outer margin of bacteria mat. The average time and distance of one move action is about 15 min and 3.22 cm, so the average speed is about 0.38 cm/min. “*Calyptogena*” clams have been reported to form a ring colony surrounding bacteria mat, and this ring colony is a result guided by best condition of chemical subbottom profile. The positions and areas of bacteria mats in the Enoshima Aquarium tank have been rather stable but the margin fluctuated. The Enoshima clam tracks seem to be a result of tracing the best spot for getting subbottom hydrogen sulfide. In contrast, the “*Calyptogena*” clams of *in situ* the Hatsushima observation seem to move breaking bacteria mats, which were newly formed just after turbiditic rapid burial. In emergency where they lost their favorite seep spots just after such physical disturbance, the clams also repeated round trips from one position, back and forth in various directions, with maximum speed about 12 to 14 cm/min.

“*Calytogena*” clams have high ability of moving and restoring of their postures, as noted above. This ability is one of the keys of their adaptability to fluctuation of seep activity and disturbance of rapid burial, leading to their flourishing since the Cenozoic.

キーワード：化学合成、メタン湧水、オトヒメハマグリ科、ロコモーション

Keywords: chemosynthesis, methane seep, Vesicomyclae, locomotion

室戸岬沖南海トラフにおける深海底長期映像のアーカイブ
Archives of long-term deep seafloor video image offshore of Cape Muroto in Nankai Trough

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　高知県室戸岬沖南海トラフの水深3572mの深海底に海底ケーブル型観測システム「海底地震総合観測システム」の先端観測ステーションが1997年に設置された．先端観測ステーションは，数個体のシロウリガイが存在する冷湧水域に位置しており，ビデオカメラ，CTD（電気伝導度，水温，深度）センサ，地中温度計，電磁流向流速計及びADCP（音響層別流速計）が搭載されている．ビデオカメラによる海底の目視観察は1997年4月以降，全ての水中ライトの断やビデオカメラが故障する前の2003年1月までの間実施された．目視観測の概要は，2002年に製作されたビデオ「深海3572mに生きるー室戸沖南海トラフ4年間の記録」（岩崎・岩井，東京シネマ新社）に紹介されている．ビデオ映像は，800本に及ぶS-VHSビデオに収録されており，今回その全てのビデオテープをMPEG-2フォーマットでデジタル化し，電子ファイルに保存した．

　ビデオカメラは，パン・チルト（首振り）機能を有しているが，シロウリガイが2個体，観測期間の大半を通して存在した特定の場所をホーム・ポジションとしている．ライトが順次故障していったため，撮影条件は全観測期間で同一ではないが，これらのシロウリガイの変化が観察されている．シロウリガイのうち1個体は2001年5月に死んだとみられ，もう1個体は2001年8月に視野外に移動した．また，観測期間の初期の段階では，一方の個体の脇に小規模なバクテリアマットが周期的に消長する現象が見られる．

　これらのMPEG-2ファイルのオンライン公開は現在のところ計画していないが，オフラインでの提供は近い将来に可能になると考えており，化学合成生態系の研究への寄与を期待している．

キーワード：室戸岬沖南海トラフ、長期ビデオ観察、ビデオアーカイブ
Keywords: offshore of Cape Muroto in Nankai Trough, long-term visual observation, archives of videos

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深海化学合成環境に生息する蔓脚類の分類再考

Revision of taxonomy of barnacles in deep-sea chemosynthetic environments

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Barnacle is one of the abundant animals associated with deep-sea hydrothermal vent in the northwestern Pacific, Indian and Southern Oceans. Currently each of four suborders of thoracican barnacles is reported from deep-sea hydrothermal vent fields, although recent molecular phylogenetic analyses on the barnacles in deep-sea chemosynthetic environments provided new insights into barnacle phylogeny. Molecular phylogenetic analyses showed; 1) molecular phylogeny of the stalked eolepadid barnacles was not correlated to genus-level taxonomy, 2) hydrothermal vent barnacles of genus Neoverruca is not belong to the lineage of suborder Verrucomorpha, and 3) the solitary brachylepadomorph, *Neobrachylepas relica* is not consist a monophyletic clade, but consist a part of scalpellomorph, as same as the genus *Neoverruca*. Shell morphology, that is important morphological characters of barnacles, is not always appropriate characters for taxanomy, because it is variable according to density of the population.

キーワード：生物多様性、形態、分子系統
Keywords: Biodiversity, morphology, molecular phylogeny

Meta-transcriptomic analysis unveils the symbiotic relationship between methane seep tubeworm and its symbiont

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Deep-sea chemosynthetic ecosystems are known for abundant reduced chemicals and thus support extensive megafauna including tubeworms (Annelida, Siboglinidae) which are mouthless and gutless and reliant on their symbiotic sulphide-oxidizing bacteria (SOB) as an energy and nutrient source. Most studies of chemosynthetic tubeworms have focused on *Riftia pachyptila* and *Lamellibrachia* spp., while other tubeworms have received little attention. We analyzed the meta-transcriptome of *Paraescarpia echinospica* collected from a newly discovered methane seep in the South China Sea to understand the molecular mechanisms of symbiosis between the tubeworm and its symbionts by sequencing three tissues, i.e. plume (a gill-like organ), vestimentum and trophosome (the organ that harbors the symbionts). The transcriptome sequences were assembled, annotated, and species sorted. The bacterial transcripts were involved in chemoautotrophy activities which were characteristics of SOB, such as sulphide oxidation, ion-regulation, and sulfurtransferase activity, etc. Host genes that were highly expressed in trophosome were represented by chitin metabolism, oxygen transport, hemoglobin complex and cell adhesion. These results suggest mutual benefits between *P. echinospica* and its symbionts. Our study has revealed the importance of thioautotrophy regulatory pathways in the symbionts, the dominant regulatory pathways in the host, and demonstrated the utility of meta-transcriptome sequencing in unveiling the relationship between deep-sea invertebrate hosts and their uncultured symbionts.

Keywords: Deep-sea, Chemosynthetic, Tubeworm, Symbionts

Paleoecology of serpulid worm tubes in the Late Cretaceous Sada Limestone seep deposits in southwestern Shikoku, Japan

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The Sada Limestone consists of a group of seep carbonate deposits enclosed in the Late Cretaceous slope mudstone facies of the Northern Shimanto Belt, Shikoku, SW Japan. The seep deposits are characterized by mass occurrence of large-sized chemosynthetic thyasirid bivalves and serpulid worm tubes, but the taxonomy and paleoecology of the worm tubes has not yet been fully examined. We report tube shell characters, lithology of the surrounding sediments, and the detail mode of fossil mass occurrences.

The tube fossils are slightly curved with circular cross section, 2.11 to 8.00 mm in diameter, over 10 cm in length, often attached to each other. The outer surface is ornamented with straight or corrugated growth lines and perpendicular ridges. The attached part forms a widened base with single thick keel or three keels. The tubes lumen contains few to numerous irregularly spaced septae, concave in cross section. The tube wall is moderately thick, and consists of a thin inner layer and a thick outer layer with chevron growth pattern, which suggests the worm tube to be assigned to serpulids. The inner layers are composed of two organic(?) sheets binding carbonaceous fill. The septae also have similar structure to inner layers, but sometimes form multiple stacking, between which elliptical pellets were often sealed. The inner layers and septae were under flexible deformation and delamination during calcification in early diagenesis. Such delamination has been often confirmed in other tubes having organic walls in several seep deposits.

The tubes occur in muddy micrite, sometimes mixed with thyasirid fossils, but the exclusive mass occurrence of tubes is lithorogically characterized with rich sparitic fabrics enclosing abundant undeformed pelloids. The δ^{13}C values of the micritic matrices are not so depleted (-10 to -15 ‰). The mass of tubes forms beds and mounds, over 1 m thick, composed of well-preserved tubes standing vertically to beddings in matrix-supported condition. Such autochthonous tube concentration directly covers turbiditic sandy layers rich in shell fragments, indicating that abundant serpulids simultaneously settled by attaching to shell fragments or coarse clastics just after the physical disturbance. Top of the mass occurrences is often truncated by sandy flow deposits, which broke and pushed down upper parts of the tube individuals. Thin sandy layers also sometimes abut tube-cluster mounds, which maybe formed slight topographic rises.

On the basis of the mode of fossil occurrence noted above, the Sada serpulids were opportunistic and semi-infaunal sessiles, forming colonial mounds in seep site. Abundant pellets sealing between the septae suggest the possession of digestive system, and suspension feeding maybe on high production of chemosynthetic seep ecosystem.

キーワード：化学合成、冷湧水、チューブワーム、カンザシゴカイ科、四万十帯
Keywords: chemosynthesis, cold seep, worm tube, Serpulidae, Shimanto Belt

Population genetic connectivity and natural selection in deep-sea mussels: insights from mitochondrial genes and genome-wide SNP markers

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Understanding the genetic connectivity among hydrothermal vent and methane seep ecosystems can help to develop informed-management for these deep-sea resources. Nevertheless, little is known about the genetic connectivity of these special chemosynthesis-based ecosystems in the Western Pacific Province. Here, we applied a combination of three mitochondrial genes (i.e., *cox1*, *nad4* and *atp6*) and 7227 genome-wide SNPs identified based on restriction site-associated DNA genotyping-by-sequencing (RAD-seq) approach, to study the genetic connectivity of seven *Bathymodiolus platifrons* populations totaling 130 individuals in the Northwestern Pacific. These populations are distributed over a distance of 3486 km, and are between 858 m and 1482 m in water depth. Among them, two populations in the South China Sea (SCS) and one in Sagami Bay inhabit methane seeps, and four populations in Okinawa Trough inhabit vent fields. The mitochondrial markers showed that these populations were clustered into two genetic groups with one represented by the South Hainan (SH) population and another represented by the rest. In contrast, the genome-wide SNP markers showed that these populations were clustered into three distinct groups represented by the SH, the Jiaolong Ridge (JR) and the Okinawa Trough-Sagami Bay (OT-SB) populations. This pattern of genetic divergence revealed the importance of the Kuroshio Current and its intrusion into the SCS from the Luzon strait, rather than the water depth or types of habitat (vents vs. seeps), in shaping the genetic structure of this deep-sea mussel with a long pelagic larval period. Furthermore, an analysis of the SNP outliers detected 162 genes under natural selection, including genes with detoxification, endocytosis and apoptosis functions. Overall, our study has revealed the key role of the Kuroshio Current in maintaining the high genetic connectivity of the deep-sea mussel populations along its main course, the importance of the SCS as a marginal sea in promoting genetic divergence of deep-sea mussels, and highlighted the potential of high-throughput SNP discovery in resolving the fine genetic structure of deep-sea invertebrates with long-distance larval dispersal capabilities.

Keywords: Genetic connectivity, natural selection, hydrothermal vent, methane seep, Bathymodiolus, RAD-seq

Distribution pattern of minerals and iron-oxides in hydrothermal vent shrimp *Rimicaris* with special focus on its gut contents

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The vent shrimp *Rimicaris*, dominated at many vent sites along the Mid-Atlantic Ridge and the Central Indian Ridge, harbors episymbiotic bacteria in their gill chamber. Because of those microbes, surface of the *Rimicaris* in gill chamber is fully covered by iron-oxides, and thus the *Rimicaris* has been considered one of the animals which do bioaccumulation of metals. In contrast to their gill chamber, however, gut contents haven’t been investigated well. Here, we examined distributions of iron-oxides and minerals in digestive tract and in gill chamber of the *Rimicaris kairei* from the Edmond hydrothermal vent field on Central Indian Ridge.

We found Barite ($BaSO_4$), Sphalerite (ZnS), Chalcopyrite ($CuFeS_2$), Pyrite (FeS_2), Marcasite (FeS_2), Argentite (Ag_2S) and Hematite (Fe_2O_3) on the surface and in the gut of the *Rimicaris.* Nano- to micron sized iron-oxides were dominated in everywhere we examined, i.e. the surface, mouth part, stomach and gut. Relative amount of the iron-oxides largely increased between mouth and gut. In contrast, sulfide minerals decreased between them. Maximum diameters of those mineral particles drastically decreased through the digestive tract, especially at the mouthpart and the stomach. Those features suggest that the *Rimicaris* crushes the mineral particles at the mouthpart and within the stomach, and the sulfide minerals are consumed and/or deserted at the stomach.

キーワード：熱水噴出孔、生物濃縮、鉱床、大型動物相
Keywords: Hydrothermal vent, bioaccumulation, ore deposit, macrofauna

Biomineralization Toolkit in Deep-Sea Mussels: Insights from the Mantle Transcriptome and Shell Matrix Proteome of *Bathymodiolus platifrons*

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As calcium carbonate is more soluble at lower temperature and higher pressure, understanding how deep-sea mollusks form their shells through biomineralization can reveal their adaptation to the deep-sea environment. Shell matrix proteins (SMPs) are known to play a key role in the shell formation of shallow water mollusks but so far there is no report of the composition and roles of SMPs in shell formation of deep-sea mollusks. In the present study, we analyzed the mantle transcriptome and shell matrix proteome of the deep-sea mussel *Bathymodiolus platifrons*. GO enrichment analysis of the highly expressed genes of the mantle revealed the enrichment of genes that are related to ion transportation and extracellular regions, indicating that the mantle was active in biomineralization. Nineteen SMPs were identified and their methiothine residues were exclusively oxidized. Among these identified SMPs, homologs of the 2 Chitin-bd-like proteins, 1 Perlwapin-like and 2 MSI60-like proteins have been reported in the shallow-water mussels *Mytilus* spp.. The 19 SMPs also included 3 with homology to proteins from non-mytilid bivalves, 1 from a gastropod, 1 from a nematode, and 9 novel proteins. Protein functional domain analysis showed that domain shuffling and *de novo* generation could be the major mechanisms for the evolution of SMPs in deep-sea mussels.

Keywords: deep-sea, bivalves, shell matrix protein, evolution, proteomics

日本各地の貝殻内部の結晶形態と含有微量元素測定

Relationship between various elements in shells and crystal form of $CaCO_3$ constituting inside seashell All over Japan

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貝殻やサンゴなどは炭酸カルシウムを主成分とする無機物質と少量の有機物質を含み炭酸カルシウムの形態としてはカルサイト・アラゴナイトの結晶構造を有している。本研究では日本各地10地点の海岸にて採集した貝殻の結晶形態の解析と含有微量元素測定を行い結晶形態と微量元素量の関係、微量元素【Ca,Na,P,Si,Sr,Zr,Y,Rb,S】の関係から貝殻中の無機元素について考察した。その結果、カルサイトの結晶構造にはアラゴナイトの結晶構造に比べPとSが多く含まれ、アラゴナイトの結晶構造にはカルサイトの結晶構造に比べSrとZrが多く含まれた。更に貝殻中のSrとZrの元素間には強い相関が見られ、貝殻以外の試料であるサンゴやフジツボではSr・Zrが更に高い値を示した。貝殻試料の全般で海水中の含有量に比べZrの元素は高い値を示し

海水組成の約10^6倍の高度な濃縮が見られた。Yにおいても他元素との相関は見られなかったものの海水組成に比べ約10^5倍の高度な濃縮が確認された。このような元素の濃縮から貝殻のバイオミネラルゼーションの未知領域を推察した。

キーワード：生体鉱物、カルサイト、アラゴナイト、微量元素
Keywords: biomineral, calcite, aragonite, element

大船渡市日頃市地方に見られる坂本沢層と長岩層・叶倉層の地層境界について

Boundary of Sakamotozawa formation, Nagaiwa formation and Kanokura formation in a part of Hikoroiti district

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岩手県大船渡市日頃市町には基底礫岩・粘板岩・石灰岩・砂岩からなるペルム紀前期の坂本沢層が存在しており、長岩層(石炭紀中期)とは傾斜不整合、叶倉層(ペルム紀中期)とは整合で接している。日頃市町の西方では坂本沢層を中心に、叶倉層と長岩層を観察することができる。本研究では長岩層・坂本沢層・叶倉層三層のより正確な地層境界を求め、先行研究に新たな解釈を加えるべく調査を行った。

その結果、長岩層、叶倉層と思われていた一部で坂本沢層と同じTi-Nb比の砂岩を見つけた。また、坂本沢層の泥質石灰岩を溶解し、残渣の微量元素を測定したところ同地域の砂岩・泥岩には見られない量のCr・Niを検出した。このことから石灰岩堆積時に蛇紋岩にみられるようなCr・Niに富んだ後背地が存在したことがうかがえた。

キーワード：石灰岩、坂本沢層、長岩層、叶倉層、大船渡
Keywords: limestone, Sakamotozawa formation, Nagaiwa formation, Kanokura formation, Ofunato