

# 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－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

## 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 relicha* 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 lithologically characterized with rich sparitic fabrics enclosing abundant undeformed pelloids. The  $\delta^{13}\text{C}$  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 epibiotic 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 ( $\text{BaSO}_4$ ), Sphalerite ( $\text{ZnS}$ ), Chalcopyrite ( $\text{CuFeS}_2$ ), Pyrite ( $\text{FeS}_2$ ), Marcasite ( $\text{FeS}_2$ ), Argentite ( $\text{Ag}_2\text{S}$ ) and Hematite ( $\text{Fe}_2\text{O}_3$ ) 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

## Biom mineralization 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 $\text{CaCO}_3$ 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