Japan Geoscience Union Meeting 2012
(May 20-25 2012 at Makuhari, Chiba, Japan)

BPT26-01 Room:301B Time:May 23 15:30-15:50

Earthquake Biosphere

KAWAGUCCI, Shinsuke[1*]

[1] JAMSTEC

A novel concept, Earthquake Biosphere, will be introduced in the meeting.

Keywords: Earthquake Biosphere

Japan Geoscience Union Meeting 2012
(May 20-25 2012 at Makuhari, Chiba, Japan)

BPT26-02 Room:301B Time:May 23 15:50-16:05

Impact by the mega-earthquake: the 2011 Mw 9.0 Tohoku-Oki Earthquake, on deep-sea ecosystems in Japan Trench

FUJIKURA, Katsunori[1*], Hiromi WATANABE[1], Norio MIYAMOTO[1], Yasuo FURUSHIMA[1], Hidetaka NOMAKI[1], Ken TAKAI[1], Hiroshi KITAZATO[1], Takeshi TSUJI[2], Kazuno ARAI[3], Onboard Party[1]

[1]JAMSTEC, [2]Kyoto University, [3]Chiba University

The tremendous March 2011 Tohoku earthquake (Mw 9.0) ruptured a wide area along the plate interface off the Pacific coast of Tohoku, Japan. The tsunami induced by earthquake was extremely huge. Earthquake, after shocks and tsunami have been variously affected to not only coastal marine ecosystems but also deep-sea ecosystems. Expected impacts to deep-sea ecosystems were following:

1) The extinction of deep-sea organisms by turbidity currents,

2) The extinction and/or new occurrences of chemosynthesis-based ecosystems by chemicals such as CH_4 and H_2, discharge from seafloor,

3) Change of faunal composition and distribution patterns of deep-sea organisms by numerous suspended matters.

To estimate and make clear for above expected impacts by the earthquake, we conducted deep-sea investigations using the HOV Shinkai 6500 and Deep-towing TV Camera systems in the Japan Trench from June to August, 2011. Several fissures on the seafloor, new occurrences of bacterial mats associated with CH_4 and H_2S seepages, other bacterial mats associated with decay of dead benthic organisms aggregations, decreasing of Calyptogena phaseoliformis colonies and new occurrences of single species holothurian dense aggregations were observed. These phenomena have never found before the March 2011 Tohoku earthquake. So far, we have investigated using some deep-sea research gears. So, we believe, to describe these impacts by the huge earthquake is our important task.

Keywords: the 2011 Mw 9.0 Tohoku-Oki Earthquake, deep-sea ecosystems, bacterial mat, Japan Trench

Japan Geoscience Union Meeting 2012
(May 20-25 2012 at Makuhari, Chiba, Japan)

BPT26-03 Room:301B Time:May 23 16:05-16:20

Growth pattern of the chemosynthetic bivalve Lucinoma annulatum based on growthline and isotopic analysis

NAKASHIMA, Rei[1], Mizuho Sato[2], SAKAI, Saburo[3], MAJIMA, Ryuichi[2]*

[1]Geological Survey of Japan, AIST, [2]Yokohama National University, [3]JAMSTEC

Lucinid bivalve has sulfur-oxidizing bacteria in their gills and are known as a member of cold-seep community. Though they are known as edible in Southeast Asia and a large number of fossil records, their growth process are not revealed at all. Therefore, we examined shell structural and stable isotopic analysis using *Lucinoma annulatum* shells to clarify the growth pattern, physiology, and its relationship with environmental changes.

Shell materials are collected by dredge at 50m in depth of Beppu Bay, West Japan, in November 2005. We observed shell structure of polished section along growth direction using acetate peel method. The shell consists of the outer, middle, and inner shell layers. Width and positions of the growthlines in the middle shell layer and concentric rib and growth disturbance rings in the outer shell layer are measured. Powder samples for stable isotope analysis are milled with 80-500 um intervals in the middle shell layer along shell growth direction by high precision micromill system (GeoMill 326).

As a result of measurement of the width of growthlines, disturbance rings, and concentric ribs, shell growth patterns of the species are divided into early, middle and late growth stages. The early, middle and late growth stages are characterized by narrow intervals of concentric ribs and disturbance rings, wide intervals of concentric ribs and disturbance rings, and drastic decreasing width of growthlines, respectively. The positions (about 25mm from umbo) of boundary between the middle and late growth stages are common to examined specimens. The shell structural change indicates that physiological change from juvenile to adult probably happened at this position.

Oxygen isotope value ranging from 0.5 per mil to 1.5 per mil are calculated to seawater temperature between 15 and 20 degree Celcius. It means that shell growth interruptions are occurred during high and low water temperature extremes, considering temperature range at 50m in Beppu Bay. And the profile of the oxygen isotope shows seven cycles of fluctuations, indicating seven years temperature records during shell growing period.

Keywords: growthline, growth pattern, chemosynthetic community, bivalve, stable isotope

Japan Geoscience Union Meeting 2012
(May 20-25 2012 at Makuhari, Chiba, Japan)

BPT26-04 Room:301B Time:May 23 16:20-16:35

Genetic Population Structure of Alvinocaridid Shrimps in the Okinawa Trough and the Izu-Ogasawara Arc

YAHAGI, Takuya[1*], WATANABE, Hiromi[2], KOJIMA, Shigeaki[1]

[1]The University of Tokyo, [2]JAMSTEC

In hydrothermal vent fields and cold seep areas, most faunal communities are comprised of endemic species (Tunnicliffe and Fowler, 1996). In addition, the hydrothermal vent fields are unstable environments and patchy distributed. Therefore, vent endemic species are thought to have high dispersal ability to maintain gene flow among local populations.

In the northwestern Pacific, the Okinawa Trough and the Izu-Ogasawara Arc are sea areas in which many hydrothermal vent fields are distributed. Species composition of vent faunas and geological background in these two sea areas are strikingly different from each other. Therefore, it seems to be difficult for most species to disperse and maintain gene flow between the two areas. Actually, neoverrucid barnacles in the both fields have been shown to be genetically differentiated by population genetic analysis based on nucleotide sequences of a mitochondrial cytochrome oxidase c subunit I (COI) gene (Watanabe et al., 2005). Although an interspecific comparison of genetic population structures will provide important information to understand the relationship of the communities in the two sea areas, such researches are yet limited.

The purpose of this study is to clarify the population connectivity of alvinocaridid shrimps between the Okinawa Trough and the Izu-Ogasawara Arc by genetic population structure analyses.

An alvinocaridid shrimp, *Alvinocaris* sp. was collected at the Irabu Seamount in the southern Okinawa Trough and the Suiyo Seamount in the Izu-Ogasawara Arc during the NT11-09 and NT11-20 cruises of the R/V ’Natsushima’ and the ROV ’Hyper Dolphin’, respectively. We determined nucleotide sequences of the COI gene of *Alvinocaris* sp. for 20 individuals of each site.

Alvinocaris sp. populations in the both sites were shown to consist of two genetically deviated lineages. They, however, showed no significant genetic differentiation between two sea areas. In this presentation, we discuss the population connectivity and history of *Alvinocaris* sp. based on the population genetic analyses, ecological information, and geological background of the two sea areas.

Keywords: Okinawa Trough, Izu-Ogasawara Arc, Alvinocaridid shrimps, Genetic population structure

Japan Geoscience Union Meeting 2012
(May 20-25 2012 at Makuhari, Chiba, Japan)

BPT26-05 Room:301B Time:May 23 16:35-16:50

Cultivating approach for understanding symbiont-host linkage of invertebrates in deep-sea chemosynthetic ecosystem

KONISHI, Masaaki[1]*, WATSUJI Tomo-o[1], NAKAGAWA Satoshi[2], HATADA Yuji[1], TAKAI Ken[1], TOYOFUKU Takashi[1]

[1]Institute of Biogeoscience (Biogeos), Japan Agency for Marine-Earth Science and Technology (JAMSTEC), [2]Faculty of Fisheries Sciences, Hokkaido University

Chemoautotrophic ecosystem are supported by chemoautotrophs, which are organisms that are capable of fixing carbon by using chemical energy obtained from the oxidation of reduced compounds blowing up from hydrothermal vents, such as sulfuric compounds, methane, and hydrogen. Several benthic invertebrates are well known to be hosts of chemoautotrophic bacteria in cells of specialized tissues and on the surface and obtain nutrition from the bacteria. The behaviors of the symbiont and organisms have been estimated by evidences from the results by field works, phylogenetic analyses, and characterization of isolates related to the symbionts, named ’field work based approach’. However, the approaches are limited by unclear causal associations between environmental and physiological factors and their behaviors. We, therefore, developed a rearing tank system with feedback control system to provide hydrogen sulfide, which is strong reducing and toxic gas, in order to characterize the deep-sea organisms and their symbionts by ’cultivating approach’.

Using rearing tank system newly developed, we first examined the effect of low concentration H_2S on the episymbiotic bacterial communities of a deep-sea crab, *Shinkaia crosnieri*, by comparison of with/without H_2S feeding. The H_2S concentrations in tank were successfully maintained between 5 to 60 micro mol. per litter for 80 days with the exception of brief periods of mechanical troubles. The survivals of the crab were 44 individuals against initial 60 individuals (73.3%) for 84 days cultivation. On the other hand, the values were three individuals against initial 30 individuals (90.0 %)without the feeding. Even if additional effects of a trouble be considered, the survivals with H_2S feeding seemed to be less than that without the feeding. Busy setae were observed at few days after the continuous feeding of H_2S. Furthermore, white biofilm caused and increased on the surfaces of tank wall and of sea sand in the feeding unit. According to real-time PCR analysis, the copies of partial 16S rDNA of the episymbiont with feeding were three-orders of magnitude larger than those without the feeding. Based on a phylogenetic analysis of episymbiont, several phylotypes were detected in *alphaproteobacteria*, *ganmaproteobacteria*, *epsironproteobacteria* and *flavobacteria*, from the crab with H_2S feeding. The symbiont-related phylotypes would be grouped into four different groups; *gammaproteobacteria* in marine epibiont group I, *Sulfurovum*-affiliated *epsilonproteobacteria*, *Osedax mucofloris* endosymbiont-affiliated *epsilonproteobacteria*, and *flavobacteria* closely related to CFB group bacteria epibiont of *Rimicaris exoculata*. Based on the analysis of the biofilm, several phylotypes belong into the above results of epibionts. Growth of these bacteria would be dependent on only chemical and physical conditions except of pressure, and physiological host-symbiont interaction might not be necessary to be significant factor. On the other hand, marine epibiont group I in *ganmaproteobacteria*, which has been detected in epibiont phylotypes, was not detected. This fact implies a possibility that the marine epibiont group I tightly bind to their host by somewhat physiological interaction. Interestingly, one of major clades of phylotypes were *Sulfimonas*-affiliated bacteria, and closely related to endosymbiont of a snail, *Alviniconcha* sp. type II that was collected from Vienna Woods site, Manus Basin, where Iheya North field in Okinawa Trough, where *S. crosnieri* was collected, located approximately 3,700 km of geographical distance of Vienna Woods site. The significant growth factors of these bacteria would be also chemical and physical conditions, but not geographical factors. The results demonstrate possibility and clue that the behaviors are able to be discussed against chemical and physical factors, which distinguished from geographical and physiological factors.

Keywords: rearing tank, symbiont-host linkage, *Shinkaia crosnieri*, feed-back control, semiconductor gas sensor