Conodonts and other microfossils from the Omi Limestone of the Akiyoahi Belt, Niigata Prefecture

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Although pelagic seas occupy the widest biosphere on earth, we have limited information concerning the Paleozoic ecosystem in the pelagic sea environment. We are now conducting a study to clarify the late Paleozoic ecosystem in pelagic sea environments using microfossils, including conodonts, foraminifers, ostracods, and others. Here we present our preliminary results on the microfossils obtained from the Omi Limestone of the Akiyoshi belt, Niigata Prefecture. The Akiyoshi belt is an accretionary complex that formed in the Permian period. It has a sporadic distribution from northern Kyushu (Fukuoka Prefecture) to the northern part of central Honshu (Niigata Prefecture) (Kanmera et al., 1990). The Akiyoshi belt is characterized by the presence of huge limestone blocks associated with basaltic rocks, which are inferred to have accumulated on a seamount. These limestone blocks are generally massive with no clear stratification and a complete lack of coarse quartz grains (Sano and Kanmera, 1991), which means that deposition occurred at a great distance from the continents. Seamounts are gradually sinking because of cooling of oceanic plates, and associated biota are growing upward to maintain their optimal environmental conditions. Therefore, seamount limestones are presumed to have a record of environmental and biotic changes over the last 100 ma, from the Early Carboniferous to the Middle Permian period. Based on their lithological and biostratigraphical characteristics, these limestones were generally constructed by reef builders, such as corals, bryozoans, algae, brachiopods, ammonites, and others. The organic reef has topographically diversified environments, such as the outer and inner reef, and various species are associated with each environment (Kitsukawa, 1994).

The Omi Limestone is located around the Omi Town, Niigata Prefecture, which is the most northeastern extension of the Akiyoshi belt. It is distributed along the Omi River with a length of approximately 8 km and a width of approximately 2 km (Nagamori et al., 2010). Many previous paleontological investigations have been conducted on the microfossils of the Omni Limestone, including foraminifers (Igo, 1960; Watanabe, 1973; Kobayashi, 1988; Ueno and Nakazawa, 1993), conodonts (Igo and Koike, 1964; Watanabe, 1975), corals (Rowett and Minato, 1968; Yoshida et al., 1987; Yoshida and Okimura, 1992; Niko and Hasegawa, 2000; Niikawa, 2001), brachiopods (Hayasaka, 1918; Tazawa et al., 1983; Tazawa et al., 2004), bryozoans (Sakagami, 1962, 1963), conuralia (Makiguchi, 1993), and others. This aim of this study was to re-examine the conodont biostratigraphy and investigate the Late Paleozoic microfossil fauna recovered from the limestone using the acetic acid method. Limestone samples were systematically collected from the Tomi (Myojyou Cement Co., Ltd.) and Omni mines (Denkikagaku Kogyo Co., Ltd.).

We recovered conodonts, fish teeth, ostracods, smaller foraminifers, bryozoans, sea urchin spines, holothurian sclerites, calcareous algae, and other unidentified fossils. The following conodont genera, indicative of the late Carboniferous Bashkirian–Moscovian time scale, were identified: *Declinognathodus*, *Idiognathoids*, *Idiognathodus*, *Streptognathodus*, *Neognathodus*, *Mesogondolella*, and others. With respect to the limestone lithology, limemudstone and grainstone predominated based on the thin section analysis. Lime mudstone consists of very fine calcareous mud and often contains fossil fragments. Grain stone is characterized by a concentration of fragments and ooids within a sparitic matrix. As these lithological microfacies are continuously observed laterally and stratigraphically, these limestones seem to have been deposited in a back reef environment during the late Carboniferous period. This indicates that the microbiota were diversified in pelagic back

reef environments during this time.

Keywords: microfossil, Paleozoic Era, Akiyoshi Belt, Omi Limestone, conodont

Marine strata and fossils of the Kuwajima Formation, Itoshiro Subgroup of the Tetori Group, in the Setono area, Hakusan City, Ishikawa Prefecture, central Japan

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The presence of marine strata in the Itoshiro Subgroup of the Tetori Group has attracted much attention recently. The marine deposits within the Kuwajima Formation of the Itoshiro Subgroup in the Setono area, Hakusan City of Ishikawa Prefecture, was recognized based on the sedimentary facies analysis and the occurrence of ichnofossils of limuloids (Matsuoka et al., 2009). A tuff bed overlying limuloid ichnofossils indicated an U-Pb age of 130±0.8 Ma (Kusuhashi, 2008). Thus, the marine Kuwajima Formation in the Setono area is one of a few horizons where their stratigraphy, sedimentary environments, and numerical age have been recognized. We conducted the sedimentary facies analysis in this area, and extracted radiolarians and sponge spicules from 2 marine horizons. Radiolarians show drop-like outlines, which are common in the Jurassic and Cretaceous intervals, under an optic microscope. Sponge spicules are mainly composed of diactinal megascleres with blunt to rounded ends. This is the first record of marine microfossils of the middle Early Cretaceous age from the Tetori Group, suggesting the future contribution of radiolarian biostratigraphy and/or paleoenvironmental reconstruction using these fossils to the Itoshiro Subgroup. Other marine to brackish water megafossils from this area are also examined: a shell accumulation of *Myrene* (*Mesocorbicula*) *tetoriensis* with a small amount of Ostreidae gen. et sp. indet. in the studied sequence, and a belemnite fossil in sandstone float boulder, which probably suggests the presence of another marine horizon in this area.

Keywords: Tetori Group, Kuwajima Formation, radiolaria, belemnite

Geology and geological age of Upper Cretaceous seqence in the Hobetsu Inasato area, Hokkaido, Japan

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The Cretaceous Yezo Group distributed in the Hobetsu area, Hokkaido, Japan was geologically mapped based on newly surveyed lithological and micropaleontological data. Though the Inasato Formation in this area correlated to Cenomanian, our preliminary study found planktonic foraminiferal species that indicate Turonian or later from the localities previously mapped as the Inasato Formation. Geological map published by Takahashi (2002) is needed to be renewed.

Thirty seven planktonic foraminiferal species belonging to eleven genus were identified in this study. Lithostratigraphic classification shown in the previous study was basically followed but the chronological information from the foraminifera is reflected to renew the map of the west of Hobetsu Dam. The mudstones had been assigned to the Inasato Formation but divided into three formations, as follows: Inasato, Nutapomanai and Osawa formations. They are fault-bounded and some new faults are distinguished and mapped. Occurrence of *Praeglobotruncana delrioensis*, *Rotalipora cushmani*, *Thalmaninella globotruncanoides* among others from the Inasato Formation show that this formation is correlated to the Cenomanian. *Dicarinella canaliculata* and *Marginotruncana marginata* collected from the Nutapomanai Formation show Turonian age of this foramtion. *Contusotruncana fornicata*, *Globotruncana arca* and *Hedbergella holmdelensis* from the Osawa Formation indicate Coniacian to Santonian, or Campanian age.

Planktonic foraminifera observed here were highly diversified. Many specimens has white or pale yellow in color and were not filled with recrystallized calcite showing good preservation. They are especially preserved in the Osawa Formation. This is exceptional feature in southern Hokkaido. For example, specimen of *C. fornicata* have clear double keels on the peripheral side and opened pore on the surface of the chambers indicating very low degree of recrystallization. Many occurrence of *Dicarinella hanzawai* (Takayanagi) and *Dicarinella japonica* (Takayanagi), which is known as endemic species in Japan were also observed in the formation. Re-description of these species appears to be needed as their morphologies are highly diversified. Exceptionally well preserved nature of the specimen (even umbilical structures can be recognized) indicates the Inasato area suits for such descriptive study.

Keywords: Hokkaido, Hobetsu Inasato, Upper Cretaceous, Inasato Formation, planktonic foraminifera

Variability of *Ciconia boyciana*'s footprints on the homogenious sediment.

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An ichnological experiment using *Ciconia boyciana* was carried out to reveal morphological variability of tracks left on a potter sediment by 2 individual birds. We obtained a total of 56 tracks, for each of which the area, length, width, depth, and volume were measured. The average value of the track area was almost equal to its median value. *Ciconia boyciana* generally left morphologically uniform tracks, suggesting that it controls digit-substrate interaction to keep body balance. A unique anatomical feature is that *Ciconia boyciana* does not leave metatarsal impression, unlike other wading birds. This feature will be useful to identify *Ciconia boyciana* from other trackmakers being similar in body weights and habitats. Track width has a wide range of variability up to 40 %, which can be caused by the linkage of muscles between leg and foot being characteristic to birds. The co-efficient analysis of track geometry reveals that the width and depth of a track have a trade-off relationship to keep a same volume. Application of the theoretical morphology analysis to the track data reveals that the outer digits take a lot of the body weight in *Ciconia boyciana* while walking.

Keywords: foot morphology, Ciconia boyciana, classification, track fossils, limb anatomy

Species identification of Spumellaria (Radiolaria) on the basis of the small subunit and internal transcribed spacer region of ribosomal DNA

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Radiolaria are one of the best candidates for time- and environmental-indicators in the modern and past, because their tests have been preserved and the diversity of these morphological species has reflected the water ecosystem in the long Earth history. Although the significance of radiolarian ecology and evolution is well-known issue in paleontology and paleoceanography, the biological studies of radiolarians have been poorly studied so far, especially for the genetics. For the better understanding of the ecology and evolution, the diversity and distribution on the basis of biological species is essential data. However, there is no criterion to identify the biological species of radiolarians by molecular approach. The motivation for this study is setting the delimitation to identify the biological species of radiolarians by molecular data, for the future ecological study.

Identification of the biological species by molecular technique is different among the organisms in consideration of the various types of the reproduction systems: sex and hybridization. Some species identification by genetics are based on molecular distance of the small subunit ribosomal DNA (SSU rDNA) or the secondary structure of the internal transcribed spacer region of ribosomal DNA (ITS1 and 2). In the present study, 232 individuals of five morphological species of spumellarian radiolarians were collected from various environments. I amplified the three gene regions (SSU, ITS1, and ITS2 rDNA) from all collected individuals and examined whether molecular distance of rDNA or secondary structure of ITS2 sequences is useful to identify species in radiolarians. Comprehensive SSU and ITS rDNAs survey clearly show that molecular distance of ITS rDNA is good to identify the species, though it is difficult to set the common delimitation to identify the biological species, among all the spumellarian radiolarians. On the other hand, the secondary structure of ITS2 rDNA have the common threshold for the species identification: below 4 hemi-CBCs (HCBCs: base changes occurring on one side of a double-stranded portion) in a single biological species. The results show that the secondary structure of ITS 2 rDNA could be the criterion for radiolarian species identification.

Keywords: Radiolaria, Internal Transcribed Spacer region, biological species

Robustness of coverage estimators for assessing the completeness of paleontological sampling

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The study on global diversity change requires an adequate method to correct diversity estimates that are readily affected by unevenness of sampling density. The diversity estimates depend on true diversity as well as sampling effort. Therefore, rarefaction to a uniform sample size causes overcorrection of diversity measures which results in an underestimate of diversity particularly when true diversity is high. Alroy (2010) introduced the shareholder quorum subsampling (SQS) method which allows to remove only the effect of sampling intensity without overcorrection. The SQS method needs to estimate the proportion of the total number of individuals belonging to an already observed species in the sample, or sample coverage. The sample coverage can be accurately estimated using Good-Turing frequency estimation when the number of occurrences for each species follows a binomial distribution and the sample size is large enough. In natural community, however, individuals are not evenly distributed among species and often a few species predominate in a community. In addition, a small sample size is common in paleontological studies, especially if we focus on regional or local diversity of a particular taxonomic group. Chao and Jost (2012) proposed coverage-based rarefaction and extrapolation methods using an improved version of the Good’s estimator of coverage. The sample coverage can also be estimated using a rarefaction curve calculated from the sample of interest: the final slope of the rarefaction curve represents the probability of encountering an individual hitherto unseen in the sample which is equal to one minus the sample coverage. However, precision and accuracy of the coverage estimators have not yet been fully verified for samples with various sizes from populations with a variety of statistical distribution.

Here I assessed the robustness of the above estimators of sample coverage through a simulation study. 10,000 bootstrap samples with various sizes were taken from the populations that follow logarithmic normal distributions with various sets of parameters. The three kinds of coverage estimators as well as a true coverage were computed for each bootstrap sample. The random error of estimation of the sample coverage was assessed by calculating the standard deviation of true coverage at a fixed value of each coverage estimate. The result of the simulation shows that the precision of any of the estimators examined tends to decrease with decreasing the sample coverage. The random error of estimation is considerably great in the case with a low coverage even if the sample size is pretty large. It also increases fairly as the median of the population increases.

Keywords: paleobiodiversity, completeness of fossil record, rarefaction