

Paleogenomics: a review

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Paleogenomics concerns reconstruction of genome sequences of past life. It may be achieved by sequencing ancient DNA preserved in fossils or by comparisons of genome sequences of living organisms. The former approach is restricted in time scale (0-1 Ma), but allows us to have a direct grasp of past genomes. The latter approach is indirect, but allows us to infer the genome sequence of the last common ancestor between any living organisms, and to theoretically go back in time to the origins of life (0-4 Ga). Although theories for this approach have existed at least since 1963, and a number of reconstructions of ancestral gene sequences or even resurrection of ancient proteins have been achieved since then, no one appears to have reconstructed a full genome sequence for a hypothetical ancestor that existed in the geological past. In the context of earth and planetary sciences, the reconstructed genome sequences of past life shall be a basis for understanding the interplay between life and environments throughout earth history. This is because they can be used to deduce ancestral metabolic pathways, developmental cascades, and other genomic features (such as GC content), that reflect the environmental status at the time.

Photosynthetic activity and community structure in intertidal microbial mats revealed by taxon-specific rRNA SIP method

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Microbial mats are a multi-layer of diverse benthic microorganisms, commonly dominated by photosynthetic bacteria. Those in marine intertidal flats often experience strong fluctuation of oxygen/sulfide concentrations, hence may serve as a modern model system for the study of organismic response to the redox shift in the past. Here we integrated stable isotope probing (SIP) and magnetic-bead capture hybridization and assessed diversity and physiology in coastal microbial mats, with special focus on how cyanobacteria respond to redox change in the environment.

Microbial mats were sampled from two locations, distinct in position along the littoral gradient, in the sandy beach facing the North Sea in the Dutch barrier island Schiermonnikoog in summers of two successive years. In order to investigate effects of the environmental factors on photosynthetic activity, the collected mats were incubated with [¹³C]sodium bicarbonate under varied oxygen/sulfide conditions in a temperature- and light-controlled room, and were freeze-stored until total RNA extraction. Taxon-specific rRNAs were captured using magnetic beads with biotin-modified probes and analyzed for molecular phylogeny and for ¹³C labeling, to directly link taxonomic diversity and physiological property of active microbes under each tested condition.

Analysis of 16S rRNA clone libraries confirmed high taxon specificity of the oligonucleotide probes used in this study. The phylogenetic study showed that the microbial mats from both sampling sites were predominated by cyanobacteria, most of which were non-heterocystous filamentous species (Oscillatoriales), with minor fraction of coccoid (Chroococcales) and heterocystous ones (Nostocales). Although the oscillatorialean *Microcoleus* occupied a major part in both, the two sites presented marked difference in response to the growth conditions as well as in overall taxonomic diversity. Continuing study of microbial communities together with detailed investigation of isolate cultures, will provide us a clue to a better understanding of not only ecological characteristics of photoautotrophs, but also their evolutionary background in the earth's changing environments.

Keywords: cyanobacteria, redox condition, 16S rRNA, stable isotope, diversity, microbial mats

Evaluation the Effect of Environmental Factors in Foraminiferal Test Chemistry by the Precise Laboratory Experiments.

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The environment controlling culture system is managed in order to evaluate the effect on deep-sea foraminiferal test chemistry and stable isotopic compositions by pH. Chemical and isotopic compositions of foraminiferal tests have played a major role in geochemical proxy to reconstruct paleoenvironmental information. A laboratory culture experiment has great potential to evaluate these geochemical proxies, because broad conditions are reconstructive in laboratory. Recently, oceanic acidification is in progress in proportion to a rapid increase of artificial carbon dioxide (CO₂) emissions. There are, however, no direct tracers of atmospheric CO₂ in sedimentary records. So, paleoceanographers are trying to reveal oceanic pH history, because oceanic pH should be mirror of atmospheric pCO₂ in geologic time scale. The seawater pH can be adjusted from 5.5 to 8.4 in this system with CO₂. Lower pH will be able to maintain with injection of such acid solution as hydrochloric acid. The system could maintain the pH of 7.519 and the DO of less than 10% during a month in preliminary experiments.

Keywords: calcification, culture, foraminifera

Molecular phylogeny of *Mycalesis* and *Ypthima*, its vicariant speciation in Ryukyu

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I analyzed molecular phylogenetically the butterflies, *Mycalesis* (bushbrown) and *Ypthima* (ring), using mitochondrial COI gene, by myself. There live localized species in Ryukyu. The phylogenetic trees indicate that the vicariant speciation, due to 1.55 Ma simultaneous isolation of islands of Ryukyu. I will show these data and discuss these relations.

Keywords: *Mycalesis*, *Ypthima*, Ryukyu islands, 1.55 Ma isolation, molecular phylogenetic tree, vicariant speciation

Synchrotron X-ray micro-CT analyses of the early Cambrian microfossils: Decoding of the early evolution of Metazoa

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Cambrian Explosion is the most drastic event in history of life on Earth. Chemopaleontological studies are very important to reveal early evolution of Metazoa. Recent X-ray micro-CT analyses of microfossils yielded new methods to observe the internal structures (e.g. Donoghue et al., 2006). Compared with microscopic and SEM observations of cutting planes of the microfossils, the technique has two advantages of **nondestructive** analyses on **any** cross-sections of internal structures. This work presents observations of three-dimensional structures of about 60 specimens of the Early Cambrian microfossils, interpreted as embryo, larvae, and adult species of cnidarian with a Synchrotron X-ray micro-CT at SPring-8, Japan (BL47XU). The fossils occur in Kuanchuanpu Formation at Shizhonggou area, Shanxi Province, China, together with Anabarites and Protohertzina (Yao et al., 2011).

Yao et al., (2011) proposed various *Olivoides* fossils as each stage of Gastrulation based on the external morphology (Epi-boly). Our direct observation of the interiors reveals a blastopore, supporting the interpretation. In addition, their other cross-sections display ten-fold radial structures. Cheng and Dong (2008) showed five-fold structures on top of *Punctatus*. Our observations show the five or ten-fold structures are present even in the *Gastrula*. Micro-CT observations of internal structures of sea anemone-like microfossils display digestive systems of mouth, gastrovascular cavity and partitions. In addition, the Micro-CT analyses show that microfossils, interpreted as polyps of cnidarians, have pentaradial symmetry, apparently inconsistent between the external and internal morphology. The pentaradial structures are very common in the embryo and larvae fossils in the Kuanchuanpu Formation. In addition, their symmetry is very good, and directive axis can be defined in many microfossils. Recent molecular biological studies revealed that even cnidarians possess HOX/paraHOX clusters related to the bilateral symmetry (e.g. Martindale, 2005, *Nature Reviews Genetics*, 6, 917-927; Baguna et al., 2008, *Philos. Trans. R. Soc. B*, 363, 1481-1491). Our paleontological studies support that the cnidarians had bilateral structures in the early evolution, and lost the structures later. Alternatively, the fossils provide a stem group with a bilateral structure and diploblastic. High-resolution observations of internal structures of microfossils with the Synchrotron X-ray micro-CT possibly help in developing insight into early biological evolution from diploblastic to triploblastic organisms and from radial to bilateral symmetry.