Morphological changes in kleptochloroplasts after ingestion in the unarmored dinoflagellates

Ryo Onuma\textsuperscript{1,*}, HORIGUCHI, Takeo\textsuperscript{2}


Dinoflagellates are ubiquitous unicellular protists and the evolutionary scenario of their chloroplast evolution is quite complex one. About half of the dinoflagellates are photosynthetic, while rests are heterotrophic species, and the latters are thought to have evolved from the photosynthetic ancestors by losing their chloroplasts. Additionally, some dinoflagellates have replaced their original chloroplasts with those of haptophyte, diatom or green alga. In addition, some dinoflagellates possess 'kleptochloroplast', which is the temporary chloroplast 'stolen' from other photosynthetic algae.

The unarmoured dinoflagellate \textit{Amphidinium poecilochroum} (marine) and \textit{Gymnodinium aeruginosum} (freshwater) are closely-related to each other, and both possess kleptochloroplasts derived from cryptomonads. These dinoflagellates ingest cryptomonad cell and retain its chloroplast temporarily, but eventually lose the chloroplast due to cell division or digestion. Previous studies revealed that several differences exist between marine and freshwater representatives with regard to the cryptomonad-dinoflagellate specificity and the dynamics of kleptochloroplast processing. \textit{A. poecilochroum} is capable of ingesting any species of cryptomonads, and synchronised division of kleptochloroplast with the host cell has never been observed. By contrast, \textit{G. aeruginosum} can accept only members of the genus \textit{Chroomonas} as prey and the kleptochloroplast is simultaneously divided with the host cell and being inherited by each daughter cell. Thus, the kleptochloroplastidy in \textit{G. aeruginosum} seems to represent much more advanced stage toward acquisition of 'true chloroplast' within the linage. Therefore, unraveling the differences between the two species in detail might give us clue to understand evolutionary significance and contribution of kleptochloroplast during the quest for true chloroplasts. Although the general ultrastructure of these dinoflagellates has been studied, the morphological changes from ingestion of cryptomonad to disappearance of kleptochloroplast have never been focused and remain unclear. In this study, we observed the morphological changes of kleptochloroplast in \textit{A. poecilochroum} and \textit{G. aeruginosum} using light and transmission electron microscopes, and compared the differences between the two species.

The both species ingested cryptomonad chloroplast, nucleus, nucleomorph, mitochondria and ejectosomes with surrounding cytoplasm directly into the dinoflagellate cytoplasm. In \textit{A. poecilochroum}, cryptomonad mitochondrion and ejectosomes were removed together with cytoplasm, by transferring them into the food vacuole within 1 h after ingestion. The kleptochloroplast was enlarged gradually, and the cryptomonad nucleus was digested after 3 h. In \textit{G. aeruginosum}, the cryptomonad cytoplasm, containing cryptomonad nucleus and mitochondria, was retained around the chloroplast. The chloroplast was enlarged drastically after 6 h, and eventually occupied most of the host cytoplasm by the 3rd day, forming a cup shape with several pyrenoids. The cryptomonad nucleus was positioned inside the cup-shaped chloroplast. By the day 5, the nucleomorph has undergone multiplication at the vicinity of the cryptomonad nucleus. This study revealed that \textit{G. aeruginosum} can expand its kleptochloroplast more extensively and is capable of retaining the cryptomonad nucleus for a longer period than \textit{A. poecilochroum}. Previous study on the kleptochloroplastidic ciliate \textit{Mesodinium rubrum} showed that the endosymbiont nucleus plays an important role to maintain its kleptochloroplast. The diatom-harboring dinoflagellates possess diatom nucleus, and can divide the latter nucleus simultaneously with the host cell division. The differences between \textit{G. aeruginosum} and \textit{A. poecilochroum} indicated in this study also support that retention of endosymbiont nucleus is advantageous to maintain its chloroplast stably.

Keywords: dinoflagellate, kleptochloroplast, ultrastructure
Algivore or Phototroph? Plakobranchus ocellatus (Gastropoda) Continuously Acquires Kleptoplasts and Nutrition

Taro Maeda1∗, Euichi Hirose2, Yoshito Chikaraishi3, Masaru Kawato3, Kiyotaka Takishita3, Takao Yoshida3, Heroen Verbruggen4, Jiro Tanaka5, Shigeru Shimamura3, Yoshihiro Takaki3, Masashi Tsuchiya3, Kenji Iwai6, Shuji Shigenobu1, Tadashi Maruyama2

1National Institute for Basic Biology, 2University of the Ryukyus, 3Japan Agency for Marine-Earth Science and Technology, 4The University of Melbourne, 5Tokyo University of Marine Science and Technology, 6Okinawa Prefectural Fisheries and Ocean Research Center

The sea slug Plakobranchus ocellatus (Sacoglossa, Gastropoda) retains photosynthetically active chloroplasts from ingested algae (functional kleptoplasts) in the epithelial cells of its digestive gland for up to 10 months. While its feeding behavior has not been observed in natural habitats, two hypotheses have been proposed: 1) adult P. ocellatus uses kleptoplasts to obtain photosynthates and nutritionally behaves as a photoautotroph without replenishing the kleptoplasts; or 2) it behaves as a mixotroph (photoautotroph and herbivorous consumer) and replenishes kleptoplasts continually or periodically. To address the question of which hypothesis is more likely, we examined the source algae for kleptoplasts and temporal changes in kleptoplast composition and nutritional contribution. By characterizing the temporal diversity of P. ocellatus kleptoplasts using rbcL sequences, we found that P. ocellatus harvests kleptoplasts from at least 8 different siphonous green algal species, that kleptoplasts from more than one species are present in each individual sea slug, and that the kleptoplast composition differs temporally. These results suggest that wild P. ocellatus often feed on multiple species of siphonous algae from which they continually obtain fresh chloroplasts. By estimating the trophic position of wild and starved P. ocellatus using the stable nitrogen isotopic composition of amino acids, we showed that despite the abundance of kleptoplasts, their photosynthates do not contribute greatly to the nutrition of wild P. ocellatus, but that kleptoplast photosynthates form a significant source of nutrition for starved sea slugs. The herbivorous nature of wild P. ocellatus is consistent with insights from molecular analyses indicating that kleptoplasts are frequently replenished from ingested algae, leading to the conclusion that natural populations of P. ocellatus do not rely on photosynthesis but mainly on the digestion of ingested algae.

Keywords: kleptoplasty, sacoglossan, ulvophyceae, symbiosis
Evolution of symchlorosomes driven by endosymbiosis of zoochlorellae in freshwater protozoa and metazoa

Masashi Hayakawa¹*, Suzaki Toshinobu¹

¹Department of Biology, Graduate School of Science, Kobe University

Freshwater micro-predators bearing zoochlorellae (intracellular symbiotic green algae) have been reported in various protozoan and metazoan groups. In order to extract common features among endosymbiosis of zoochlorellae in various host organisms, four ‘green’ species, *Mayorella viridis* (amoeboid protozoan), *Paramecium bursaria* (ciliated protozoan), *Stentor polymorphus* (ciliated protozoan), and *Hydra viridissima* (Cnidaria) were observed with a transmission electron microscope by freeze-substitution technique. Their endosymbiotic zoochlorellae formed very regulative membrane-bound photosynthetic organelles, which we named symchlorosomes. Symchlorosomes can be found in many freshwater micro-predatory species with a very wide genetic variety, which are ecologically important as they can provide a new niche for such mixotrophic organisms in freshwater microenvironment. We are going to introduce a possibility of ecological and evolutional researches on symchlorosomes through our resent ultrastructural study.

Keywords: protozoa, algae, endosymbiosis, zoochlorella, symchlorosome
Marine, holoplanktonic protist radiolarians retain the algal symbionts within the cytoplasmic bodies. The majority of modern symbionts-bearing radiolarians appear to depend on their symbionts to provide photosynthetically fixed carbon and to maintain the radiolarians in low nutrient environments (e.g., Anderson 1978). Therefore, acquisitions of the photo-symbionts have may have had their survival under low nutrient condition in the geologic time. During symbiotic state, algal symbiont within radiolarians generally appear as yellow-brown minute spheres, several micrometers in diameter. Cyanobacteria, dinoflagellates, prasinophytes, and haptophytes have all been identified as symbionts of radiolarians (e.g. Anderson 1983; Foster et al. 2006; Yuasa et al. 2012). However, the accurate taxonomic affiliation of these symbionts has not been clarified by the lack of diagnostic morphological features, such as theca or flagella, during the symbiotic state. Among them, I was able to establish cultures of the symbiotic dinoflagellate and compared the motile cell morphology and the molecular phylogeny of the SSU rDNA sequences with those of related species. The features of the thecal plate pattern and the molecular phylogenetic analysis indicate that the symbiotic dinoflagellate belongs to the peridinioid genus and species. In addition, based on the ultrastructural features by scanning electron and transmission electron microscopy and the molecular phylogenetic analyses of non-motile cells of other symbiotic algae, I found that radiolarian species contained some other partners; Synechococcus sp. (Cyanobacteria), Chrysochromulina sp. (Haptophyte) and Chlorophyta gen. sp. This symbiont diversity is in contrast to many corals, which host only dinoflagellate (Symbiodinium spp. and others). On the other hand, the symbionts have never co-occurred in a single host radiolarians, so the notion of only one kind of symbiotic algae per individual host has been maintained. A hypothesis would be that radiolarian symbions originated from some free-living algae. This hypothesis is in agreement with the concept that radiolarians can easily acquire cyanobacteria symbionts Synechococcus sp. and Prochlorococcus sp. from environmental pools (Foster et al. 2006; Yuasa et al. 2012). Very little is known, however, about the distribution of free-living dinoflagellate, and, as far as we know, there is no evidence for the presence of radiolarian specific dinoflagellate symbionts in the natural environment.

Keywords: Radiolaria, Symbiosis, algae, ultrastructure, molecular phylogeny
Symbiotic relationship between *Braarudosphaera bigelowii* and cyanobacteria

Kyoko Hagino\(^1\)\(^*\), Masanobu Kawachi\(^2\)

\(^1\)Institute for Study of the Earth’s Interior Okayama University, \(^2\)National Institute for Environmental Studies

*Braarudosphaera bigelowii* (Haptophyta, Prymnesiophyceae) is a single-celled coastal coccolithophores, which is characterized by regular dodecahedral exotheca consists of regular pentagonal calcareous scales called pentaliths. Fossil records of the Family Braarudosphaeraceae and *B. bigelowii* extend back to the early and late Cretaceous, respectively. Living and fossil *B. bigelowii* have significant variation in size of pentaliths. Molecular phylogenetic study of living *B. bigelowii* revealed that morphotypes of living *B. bigelowii*, which was classified based on the size of pentaliths, can be related to the 18S rDNA genotypes. Therefore, it is thought that living *B. bigelowii* is a species complex consists of at least four discrete species which can be differentiated from each other based on size of pentaliths and of 18S rDNA sequences (Hagino et al. 2009). A recent study revealed close phylogenetic relationships among *B. bigelowii* sensu stricto (morphotype Intermediate form B, 18S rDNA Genotype III), *Chrysochlomulina parkeae* (Prymnesiophyceae) and a prymnesiophyte cell that has symbiotic association with a nitrogen-fixing cyanobacterium UNYN-A. The prymnesiophyte host cell receives nitrogen from the cyanobacterium in exchange for transferring fixed carbon (Thompson et al., 2012). It was an unexpected relationship since *B. bigelowii* dissimilar to *C. parkeae* in general morphology, and *B. bigelowii* differs from UCYN-A in geographic distribution; living *B. bigelowii* is a notable coastal-neritic dweller, while the UCYN-A were abundantly reported from oligotrophic open ocean. In order to examine their relationships, we have conducted transmission electron microscopic and molecular phylogenetic studies of *B. bigelowii* and *C. parkeae*. In this talk, we will present an overview of geological history of the Family Braarudosphaeraceae, and morphological and genetic diversity in living *B. bigelowii*. We will also discuss about relationships among *B. bigelowii*, *C. parkeae* and the prymnesiophyte host of the UCYN-A based on the results from our morphological and molecular phylogenetic studies.

References:

Keywords: coccolithophores, cyanobacteria, symbiosis
Putative functions of kleptoplast in Planoglabratella opercularis (foraminifera)

Masashi Tsuchiya\textsuperscript{1,}, Seiji Miyawaki\textsuperscript{2}, Yoshito Chikaraishi\textsuperscript{1}, Kazumasa Oguri\textsuperscript{1}, Akihiro Tame\textsuperscript{3}, Katsuyuki Uematsu\textsuperscript{3}, Hiroshi Miyake\textsuperscript{2}, Tadashi Maruyama\textsuperscript{1}, Naohiko Ohkouchi\textsuperscript{1}

\textsuperscript{1}Japan Agency for Marine-Earth Science and Technology, \textsuperscript{2}Kitasato University, \textsuperscript{3}Marine Works Japan Ltd.

A rocky-shore benthic foraminifera, \textit{Planoglabratella opercularis}, constructs specific host-symbiont relationships that has chloroplast as kleptoplast. Host organisms may have some benefit from kleptoplast, such as organic matters, or amino acids. To understand the functions of kleptoplast, we conducted culture experiment, ultrastructural observations, oxygen micro-sensor observations and nitrogen stable isotope of amino acid analyses. The trophic positon of individuals with or without kleptoplast, we measured stable isotopic composition of amino acid to understand whether their nutritional requirements come from kleptoplast or not. As a result, trophic position (TP) of the individual with kleptoplast shows 1.2. In contrast, TP of cultured individual specimens that digested kleptoplast shows 2.0. It is possible that \textit{P. opercularis} behave as a primary producer, phyto-benthos, in nature.

Keywords: Kleptoplast, benthic foraminifera, nitrogen isotope of amino acid, oxygen micro-sensor, transmission electron microscope
The effect of temperature on the composition of lipid biomarkers produced by *Chrysotila lamellosa*

Hideto Nakamura¹, Ken Sawada¹, Hiroya Araie², Iwane Suzuki², Yoshihiro Shiraiwa²

¹Faculty of Science, Hokkaido University, ²Graduate School of Life and Environmental Science, University of Tsukuba, ³CREST, Japan Science and Technology Agency (JST)

Long chain alkenones are synthesized by several species of Haptophyte, and used for quantitative paleo-sea surface temperature reconstructions. Alkenones have also been found in many lakes around the world, although their origin is not clear. Recent phylogenetic study suggested that typical lake alkenones with high content of tetra-unsaturated compounds are possibly produced by *Chrysotila lamellosa*, *Isochrysis garbana* or their intimately-associated species. However, only two investigations hitherto reported the lipid composition for *C. lamellosa* as a function of culture temperature. Intraspecific variation in the physiological response are noted by culture experiments of *Emiliania huxleyi* strains (Conte et al., 1998), which is less understood in coastal/limnic species including *C. lamellosa*. Here, we report $U^{K,37}$ and $U^{K,37}$ values for a *C. lamellosa* strain which no alkenone composition ever studied.

Keywords: Alkenone, Alkene, Haptophyte, Chrysotila lamellosa, UK’37, UK37
The ecological role of green sulfur bacteria in the chemocline of Lake Suigetsu

Yumi Mori, Ryuji Kondo

Department of Marine bioscience Fukui Prefectural University

Phototrophic sulfur bacteria are characterized by their oxidation of reduced sulfur compounds, which serve as electron donors during carbon fixation and anoxygenic photosynthetic growth in aquatic environments when the anoxic layers containing reduced sulfur compounds are exposed to light. Phototrophic sulfur bacteria often form dense blooms in the oxic-anoxic interfaces of stratified lakes. Furthermore, a high level of carbon fixation was detected at the oxic-anoxic interface in some meromictic lakes, indicating that phototrophic sulfur bacteria contribute significantly to primary production during the anaerobic carbon cycle. However, there is no evidence about in situ CO$_2$ fixation by phototrophic sulfur bacteria and the importance of CO$_2$ fixation by phototrophic sulfur bacteria in environment is still speculative. Lake Suigetsu is a meromictic lake, which is characterized by a permanent chemocline at a depth of 3-8 m that separates the oxic low salinity mixolimnion from the anoxic saline sulfidogenic monimolimnion. Green sulfur bacteria dominated at the chemocline of the Lake Suigetsu through the year. In this study, we evaluate the contribution of phototrophic sulfur bacteria to carbon fixation in the Lake Suigetsu.

The identity of active CO$_2$-fixing bacteria in the chemocline was assessed by DNA-stable isotope probing. The water at the chemocline was incubated with $^{13}$C-labelled sodium bicarbonate and under light or dark condition. The community composition of active CO$_2$-fixing bacteria was revealed by analysis of $^{13}$C-labelled DNA fractions. The diversity of 16S rRNA gene was analyzed using clone libraries. And productivity was measured in light or dark conditions by $^{14}$C method.

Chemotrophic carbon fixation accounted for about 80% of the carbon fixation rate in the chemocline. This indicates the contribution of chemotrophic bacteria to carbon fixation was larger than phototrophic bacteria in the chemocline. Clone sequences related to sulfide-oxidizing *Thiomicrospira* and sulfur-reducing *Thioreductor* were frequently recovered from $^{13}$C-DNA fraction library under dark condition, suggesting that these bacteria assimilate CO$_2$ using sulfur compounds in the water in the dark. Most of 16S rDNA sequences amplified from $^{13}$C-DNA under light condition were related to the genera *Chlorobium*. This indicated green sulfur bacteria assimilate CO$_2$ in the light. And sulfur-disproportionating *Desulfocapsa* also recovered from $^{13}$C-DNA fraction library under light condition. Although *Desulfocapsa* grow chemolithotrophically, clones related to *Desulfocapsa* did not detect from in dark incubation. In light condition, green sulfur bacteria also main bacteria and they accumulate elemental sulfur on its cell surface coupled with photosynthesis. We speculated *Desulfocapsa* use sulfur deposited on green sulfur bacteria as energy source for CO$_2$ fixation.

This study indicated that green sulfur bacteria fix carbon in the chemocline. And chemolithotrophic bacteria also play a significant role in the anaerobic CO$_2$ fixation in the chemocline of Lake Suigetsu. Our results suggest new ecological role of green sulfur bacteria serving energy for chemotrophic bacterial CO$_2$ fixation.

Keywords: meromictic lake, CO2 fixation, green sulfur bacteria, stable isotoping method
Steroid analysis in culture samples of Parmales: Search for Parmales biomarker

Chisato Kanou1, Ken Sawada1,∗, Akira Kuwata2, Shinya Yoshikawa3, Mutsuo Ichinomiya4

1Faculty of Science, Hokkaido University, 2Tohoku National Fisheries Res. Inst., 3Fukui Prefectural University, 4Prefectural University of Kumamoto

Palmales is picoplankton that has siliceous tests, and may be closely related to diatom, which is a main important primary producer in the Cenozoic ocean. There have been no reports for siliceous fossil of Palmales. It is known to well preserve siliceous diatom fossil in ancient sediment, and however, such fossil is frequently lost through its dissolution by diagenesis during postdeposition. Therefore, very small siliceous tests of Palmales must be easily dissolved by diagenesis, and it cannot evaluate the timing of first appearance and reconstruct productivity of Palmales by using its siliceous fossil. Thus, we clarified the Palmales biomarkers and their compositions, and these biomarkers are used as molecular fossils for giving understanding evolution processes and historical variations of productivity of this alga. In the present study, we try to search lipid biomarkers, especially steroid, of the Palmales, and to give understanding for taxonomic variability for steroid composition and concentration.

We use culture strains of Triparma laevis, Triparma laevis f. longispina and Triparma strigata for analysis of lipid biomarker. Wet culture samples were extracted with methanol/ dichloromethane, and the extracts were fractionated by silica gel chromatography. Polar fraction was silylated by BSTFA before analyses using GC/MS (Sawada and Shiraiwa, 2004, Phytochem. 65, 1299).

We can identify $C_{21:6}$ n-alkene, $C_{20:5}$ and $C_{22:6}$ n-alkenoic acids as well as $C_{27-C_{29}}$ sterols as Palmales biomarkers. These lipids have been detected from diatom cultures as reported previously (e.g. Rampen et al., 2010, Limnol. Oceanogr. 55, 91). In particular, T. laevis strain is found to be characterized by overwhelmingly abundance of $C_{29}$ beta-sitosterol. However, $C_{28}$ sterol as ostreasterol is more abundant rather than $C_{29}$ sterols in T. strigata. These results indicate that there is possibly interspecies variability in sterol composition within Triparma genus. In addition, we can detect a number of unknown polar compounds with higher molecular weight. These unknown compounds may have potential as specific Triparma biomarkers.

Keywords: Parmales, biomarker, culture, steroid, evolution of diatom, chemotaxonomy
Chlorophyll detoxification catabolism associated with protistan phycophagy and evolution of phototrophic symbiosis

Yuichiro Kashiyama¹, Akiko Yokoyama², Hitoshi Tamiaki³

¹JST PRESTO; Ritsumeikan Univ., ²Life Environ. Sci., Univ. Tsukuba, ³Grad. Sch. Life Sciences, Ritsumeikan Univ.

Chlorophylls are highly phototoxic and thus potentially problematic during their biosynthesis, organization, and degradative processes [1]. We have recently reported that metabolic conversion of chlorophyll to 13²,17³-cyclopheophorbide enol ("cyclo-enol") is a major detoxification mechanism for phycophagic protists (i.e., unicellular eukaryotes feeding on algae).[2] Significantly, a cyclo-enol is completely non-fluorescent and proven to be non-photosensitive in spite of their intact cyclic tetrapyrrole structure exhibiting green color in a solution. We cultured a series of phycophagic protists feeding on uniclonal algae and identified cyclo-enols as a sole major chlorophyll derivative presenting in extracts of the cultures. In addition, we demonstrated in microscopic observations of phycotrophic protists a quick disappearance of the autofluorescence of chlorophylls in the chloroplasts of ingested algae in an early stage of their digestion in phagocytosis, suggesting very rapid and nonradiative quenching of the presumable chlorophyll degradative product therein. We also infer that the cyclo-enol catabolism would be significant for the evolutions of algae that possess chloroplasts originating in secondary symbionts.

References

Keywords: phototoxicity of chlorophyll, protists, phototrophic symbiosis, evolution of secondary algae, cyclopheophorbide enol
Spatio-temporal relationship between chlorophyll derivatives and eukaryotic microorganisms in a coastal water.

Akiko Yokoyama¹, Yuichiro Kashiyama², Shigeharu Moriya³, Hitoshi Tamiaki⁴, Isao Inouye¹

¹Fac. Life Environ. Sci., University of Tsukuba, ²JST PREST, ³ASI, RIKEN, ⁴Grad. Sch., Life Sci., Ritsumeikan University

Chlorophylls (Chls) are essential components of photosynthetic organism (algae), which include Chls-a, b, c, d, and f. The composition of the photosynthetic pigments including Chls as well as cartenoids and phycoobiliproteins can be used as the taxonomic character or the biomarker to distinguish the dominant species in the aquatic ecosystems. While various Chl metabolites are known, their sources in the nature are not clear. Recently, ubiquitous occurrence of cyclopheophorbide a enol (cPPB-aE) is reported, and its producers, herbivorous protists, were elucidated. Therefore, we inspected that cPPB-aE can be able to be the biomarker to detect the feeding activity of protists. To understand the spacial-temporal relationships between the Chl derivatives and microorganisms, pigment analysis by HPLC, calculation of the cells and quantitative analysis using the environmental sequencing were performed.

The results demonstrated that quantity of the Chls and microorganisms were co-related. Chl-a was an extremely abundant pigment and much detected in shallow water. A quantitative trend of the cPPB-aE was similar to Chl-a, but the quantity in deep water in mid summer to early winter was much larger than shallow water. Even though a considerable amount of Chl-a was detected, cPPB-aE in winter was less abundant than in summer. Those trend shown in cPPB-aE was consistent with the abundances of the heterotrophic protists indicated by the environmental sequences.

Keywords: Chlorophyll derivatives, Cyclopheophorbide a enol, Protist, Algae
Distribution of chlorophyll $f$ within hot spring microbial mat

Satoshi Ohkubo$^{1*}$, Hideaki Miyashita$^1$

$^1$Grad. Sch. of Human Environ. Stud., Kyoto Univ.

Chlorophyll (Chl) $f$ is a recently discovered photosynthetic pigment, which absorbs far-red (FR) light (700-750 nm) in vivo. The distribution and role of Chl $f$ in natural environments were still unclear. We have isolated Chl $f$-containing cyanobacteria from various habitats by cultivation using FR-LED as their sole light sources. These cyanobacteria produced Chl $f$ only when the cells were grown under FR-LED. Therefore, we hypothesized that Chl $f$ was distributed only in certain environments where FR light mainly existed, and it contributed to the oxygenic photosynthesis at those habitats. We thought that the inner layer of microbial mat was one of such environments, because photosynthetically active radiation (PAR 400-700 nm) was absorbed by phototrophs in surface layer. In this study, we aimed to reveal the vertical distribution of Chl $f$ and the light environment within hot spring microbial mats.

We collected 20 microbial mat samples at 6 hot springs in Nagano and Gifu prefectures in Japan. Chl $f$ was detected from 5 samples of them. Vertical profiles of Chl $f$ and downward spectral irradiance within microbial mats were measured by using HPLC and fiber optic spectrophotometer, respectively. Community structure analysis in mats was also performed by PCR-DGGE to reveal the vertical distribution of Chl $f$-producing cyanobacteria. In this poster, we discuss the adaptive significance of Chl $f$ in microbial mats.

Keywords: chlorophyll $f$, cyanobacteria, microbial mat
Spatio-temporal dynamics of chlorophylls and chlorophyll-derived catabolites in Lake Biwa

Yuichiro Kashiyama\(^1\), Kanako Ishikawa\(^2\), Hideaki Miyashita\(^3\)

\(^1\)JST PRESTO, \(^2\)LBERI, \(^3\)Human Environ., Kyoto Univ.

Chlorophylls in aquatic samples have been regarded as important biomarker for phototrophic microbes such as cyanobacteria and algae. Chlorophyll \(a\) (Chl-\(a\)) in particular has been treated as a proxy for photosynthetic production in oceans and lakes. Recently, Kashiyama, Yokoyama et al. (2012) [1] reported that \(13^2,17^3\)-cyclophoribide \(a\) enol (cPPB-\(a\)E), a pigment derived from Chl-\(a\), occurs ubiquitously from most of aquatic environments. cPPB-\(a\)E comprises 7-16% of total Chl-\(a\) derivatives in euphotic water column and 51% in the surface sediment at the center of Lake Biwa. We herein report monthly changes in pigment concentrations of vertical water column profile to discuss on year-around variations in activities of phototrophic and phycophagic microbes in Lake Biwa.

References

Keywords: Lake Biwa, Protists, cycloenls, algae, microbial loop