

# Genome biological studies on marine microbial eukaryotes

Ryoma Kamikawa (Graduate School of Agriculture, Kyoto University)

kamikawa.ryoma.7v@kyoto-u.ac.jp

## Abstract

Microbial eukaryotes play primary roles in marine environments. Photosynthetic microbial eukaryotes are responsible for major parts of the annual net primary production in the ocean. On the other hand, heterotrophic microbial eukaryotes function as intermediate “connectors” in the marine food web. Importantly, some of microbial eukaryotes form toxic and/or harmful blooms called red tides that would cause mass mortalities of cultivated fish and bivalves in the coastal areas of Japan. Unveiling genetic and genomic diversity in microbial eukaryotes would contribute not only to deeper understanding of material circulations in the ocean but also to development of useful genetic resources as well as of methods for accurate and rapid identification and quantification of toxic and/or harmful bloom-forming species.

Cysts (or resting spores) of those toxic/harmful species present in the marine sediments on the Japanese coastal areas function as a seed population for the next generation red tides and highly useful to evaluate potential of occurrence of toxic and harmful red tides. However, it is difficult to accurately identify cysts of toxic and harmful species on the basis of morphological characters under microscopy. Therefore, I developed a method to rapidly and accurately detect and quantify cysts of toxic species from marine sediments, by using the real-time quantitative PCR targeting that species-specific gene sequences<sup>1)</sup>. I was also engaged in accumulation of genetic resources in microbial eukaryotes of which genomic and transcriptomic data have not been fully analyzed. Many microalgal species are known to have lost photosynthesis secondarily and have shifted their lifestyles to heterotrophy. I have isolated such non-photosynthetic microalgal species from environmental samples and analyzed their genomes and transcriptomes to reveal their evolutionary background and cellular functions. Especially, the genomic and transcriptomic analyses unveiled that the non-photosynthetic microalgal species still retain plastids that are incapable of photosynthesizing but capable of biosynthesizing various compounds including fatty acids and carotenoids, some of which are well known as useful anti-oxidants<sup>2)</sup>. I also focused on anaerobic microbial eukaryotes that are capable of thriving in low oxygen or anaerobic environments such as marine sediments and human intestines. Genomic and transcriptomic analyses allowed us to obtain gene sequences that encode proteins for hydrogen gas production in their anaerobic mitochondrion-related organelles<sup>3)</sup>.

## References

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