

Microbial eukaryotes living in the coastal marine of Tokyo bay insights from the metagenome

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Progresses in sequencing technique makes it possible to reveal the existence and to detect the diversity of pico-planktonic organisms, and also decide the taxonomic position of uncultured organisms, rapidly and easy way. Metagenomic approaches show that the huge amounts of pico-planktonic organisms are living in various environments. It means that eukaryotic microorganisms play important roles as a producer, consumer or reducer in the biosphere such as microbial loop or biogeochemical cycle. There are so many taxonomically unknown organisms, even though their phylogenetic positions have been determined. It would not be an exaggeration to say that we just reach at the start line to reveal the eukaryotic diversity. Furthermore, there are less physiological or ecological information about them. In this study, we determined the 18SrDNA sequences using filter captured microbial eukaryotes collected every month from the sea water in Tokyo Bay.

Throughout the investigation period, the sequences belonging to Opisthokonta, Stramenopiles and Alveolata, were respectively obtained in each quarters of the total. The residual one quarter were the mixture of Rhizaria, Cryptophyta, Chlorophyta, Rhodophyta, Katablepharid, Telonemia and Haptophyta. When *Heterosigma akashiwo* made the bloom, the half of the determined sequence comes from the surface bloom water were originated from this alga, and the one from the lower layer under the bloom was mainly composed by Ciliophora and/or parasitic Dinophytes. In summer, centric diatoms, and the Opisthokonta in sometime, became dominant taxa. Most of the Opisthokonta sequences were originated from Metazoa. Notably, Chytridiomycetes were the dominant taxa in August. The sequences identified as Picobiliphyta or MAST(MARine STRamenopiles) were infrequently detected. These findings indicates the existence of many unidentified or missing link organisms in the universal aquatic ecosystems, and the importance of our studies. For the further understandings of the unknown organisms, we are developing the technique to get the both profiles of the phylogenetic position and morphological features together.

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