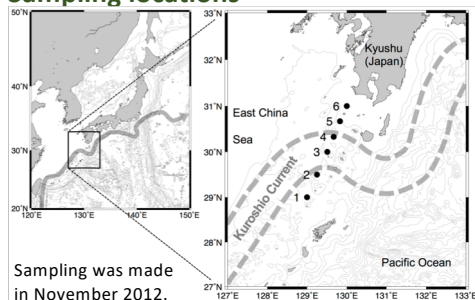


Hisashi Endo<sup>1,2</sup> and Koji Suzuki<sup>1,\*</sup> (\*kojis@ees.hokudai.ac.jp)<sup>1</sup>Faculty of Environmental Earth Science, Hokkaido University, Sapporo, Japan<sup>2</sup>Institute for Chemical Research, Kyoto University, Uji, Japan

## SUMMARY

- We present a fine-scale community structure and diversity of haptophytes in the Kuroshio waters off southern Japan in November 2012.
- Haptophytes were the most dominant eukaryotic phytoplankton group in the current axis and offshore side of the Kuroshio as estimated by algal pigments.
- Water samples were divided into surface and deep chlorophyll maximum (DCM) layers on the basis of community structure of haptophytes, which was estimated from high-throughput Ion Torrent 18S rDNA gene (rDNA) metabarcoding.
- The redundancy analysis (RDA) suggests that haptophyte community composition was constrained mainly by depth at both operational taxonomic unit ( $\geq 97\%$  sequence similarity) and genus levels.
- Haptophyte diversity was greater in the DCM waters than in the surface waters. Additionally, diversity, richness, and evenness indices tended to increase around the Kuroshio axis, possibly due to the advection of haptophyte taxa from the upstream region.
- Our results underscore the importance of physical properties such as light intensity and advection and diffusion of water mass on regulating haptophyte community structure in Kuroshio ecosystems.

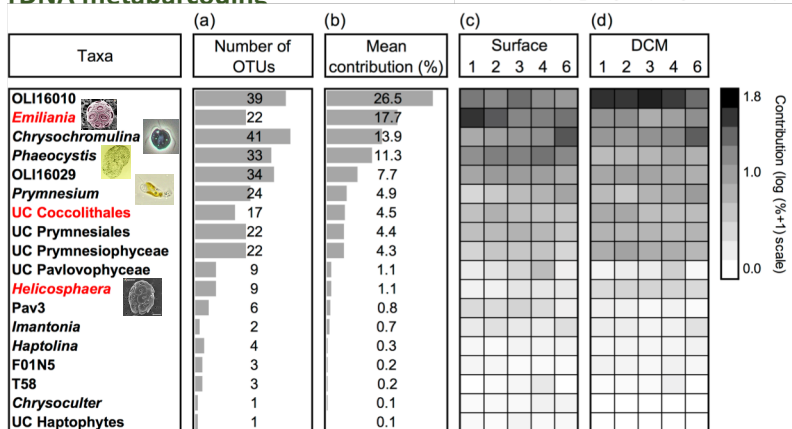
## Sampling locations



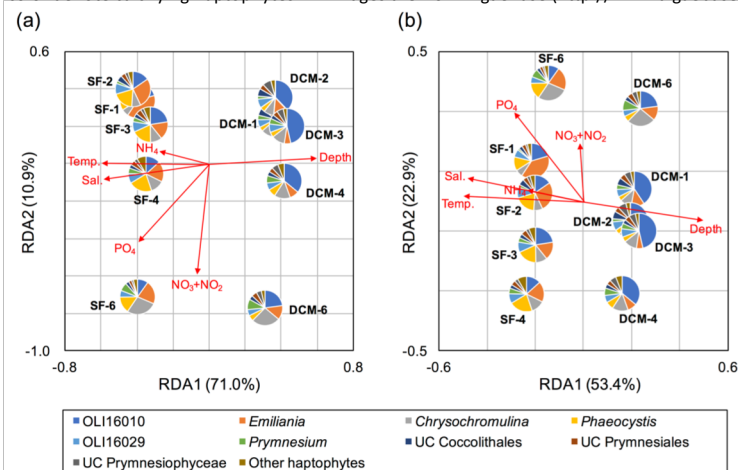
Sampling was made in November 2012.

The position of the Kuroshio at the sampling period was obtained from the Quick Bulletin of Ocean Conditions on the website of the Japan Coast Guard (<http://www1.kaiho.mlit.go.jp/jhd-E.html>)

## Community composition and diversity of haptophytes with 18S rDNA metabarcoding



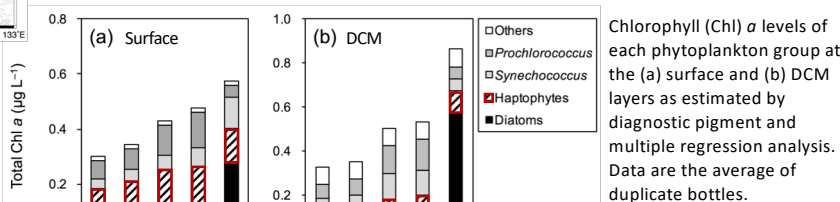
Summary of the operational taxonomic unit (OTU) classification and the distribution of haptophyte taxa as measured by 18S rDNA sequences. (a) Number of OTUs within each clade. (b) Mean contribution of each clade to the total haptophyte community. (c and d) Heatmap showing the distribution of haptophyte taxa across stations in the surface and DCM layers. The taxa in red color denote calcifying haptophytes. All images are from AlgaeBase (<http://www.algaebase.org/>).



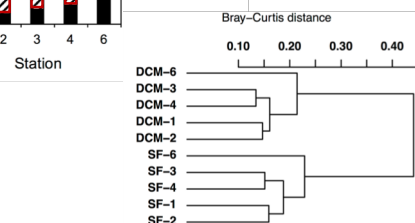
RDA ordinations of (a) OTU-level and (b) genus-level community compositions of haptophytes as estimated from 18S rDNA metabarcoding. Pie charts indicate the relative contribution of major taxa to the total haptophytes.

## Hydrography

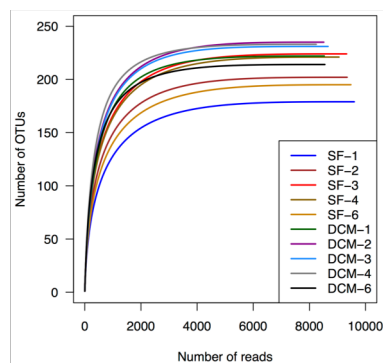
Station	Sample ID	Depth (m)	Temp. (°C)	Salinity	NO <sub>3</sub> +NO <sub>2</sub> (μmol L <sup>-1</sup> )	NH <sub>4</sub> (μmol L <sup>-1</sup> )	PO <sub>4</sub> (μmol L <sup>-1</sup> )	Si(OH) <sub>4</sub> (μmol L <sup>-1</sup> )
1	SF-1	5	24.15	34.51	0.03	0.27	0.11	1.94
	DCM-1	60	24.18	34.51	0.00	0.26	0.10	1.80
2	SF-2	5	24.08	34.52	0.09	0.13	0.09	1.93
	DCM-2	60	24.09	34.52	0.08	0.41	0.09	1.77
3	SF-3	5	24.32	34.47	0.09	0.20	0.09	1.64
	DCM-3	60	24.34	34.46	0.12	0.34	0.06	1.82
4	SF-4	5	23.75	34.32	0.54	0.21	0.11	2.28
	DCM-4	40	23.65	34.29	0.46	0.23	0.10	2.05
6	SF-6	5	21.83	34.31	0.84	0.26	0.15	3.42
	DCM-6	35	21.49	34.37	1.78	0.16	0.20	3.87



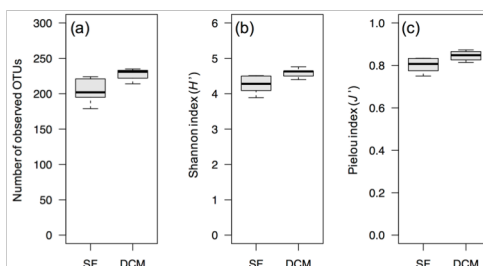
Chlorophyll (Chl) *a* levels of each phytoplankton group at the (a) surface and (b) DCM layers as estimated by diagnostic pigment and multiple regression analysis. Data are the average of duplicate bottles.



Cluster analysis based on haptophyte OTU composition, which estimated from 18S rDNA fragments. Sample abbreviations as in Table.



Rarefaction curves of haptophyte OTUs at 97% sequence similarity for each sample. Sample abbreviations as in Table.



Box plots summarizing the (a) number of observed OTUs, (b) Shannon diversity, and (c) Pielou evenness indices in the surface and DCM layers.

Acknowledgement: We gratefully acknowledge the captain, officers, and crew of the R/V *Tansei-Maru* for their generous support during the cruise. Our acknowledgement is also extended to Drs. Koji Sugie and Jun Nishiohira. This study was conducted within the framework of the Study of Kuroshio Ecosystem Dynamics for Sustainable Fisheries (SKED), Ministry of Education, Culture, Sports, Science and Technology (MEXT), Japan. Also, the work was partly supported by the Grant-in-Aid for Specifically Promoted Research (#24121004) from MEXT and Japan Society for the Promotion of Science (JSPS).