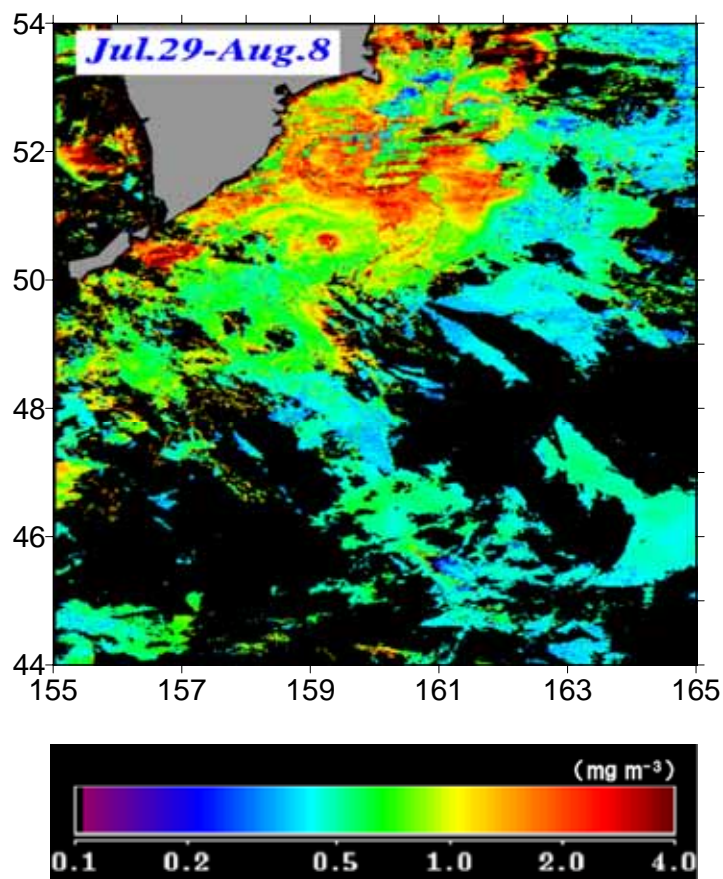
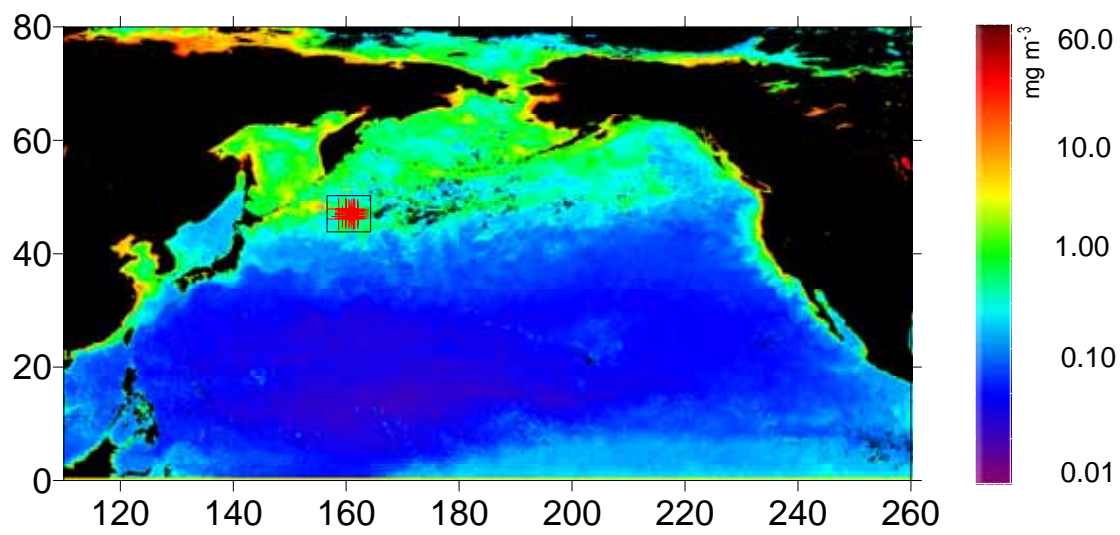


VERTIGO Picoplankton @ K2 (NW Pacific)

Yao Zhang & Nianzhi Jiao*

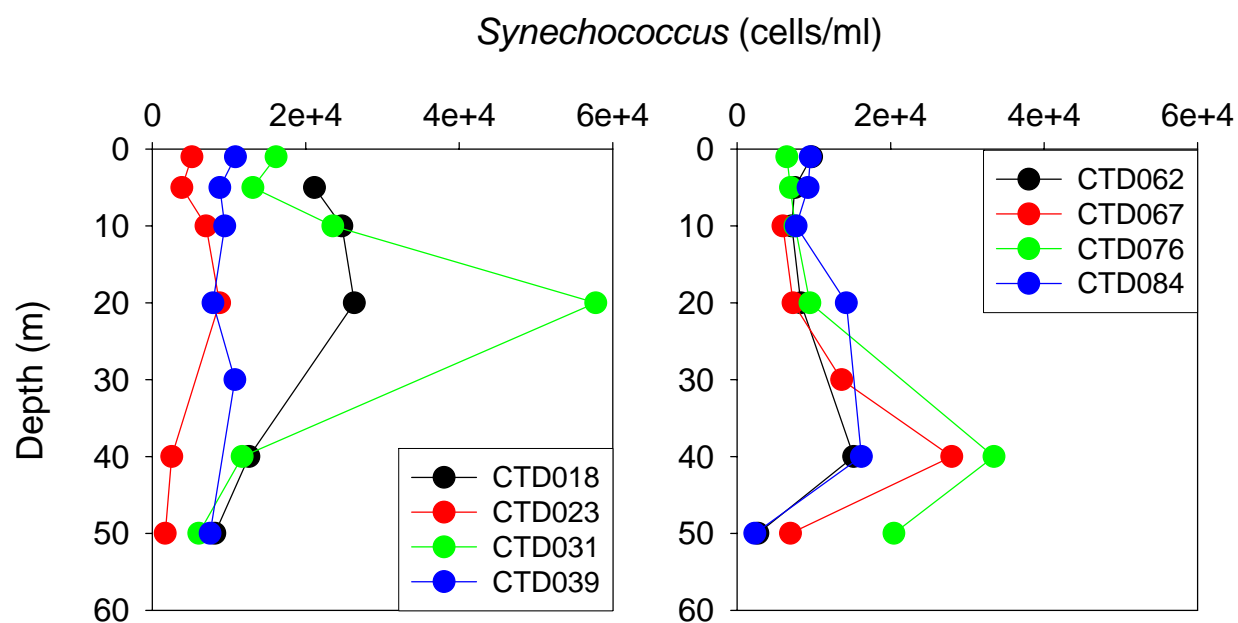
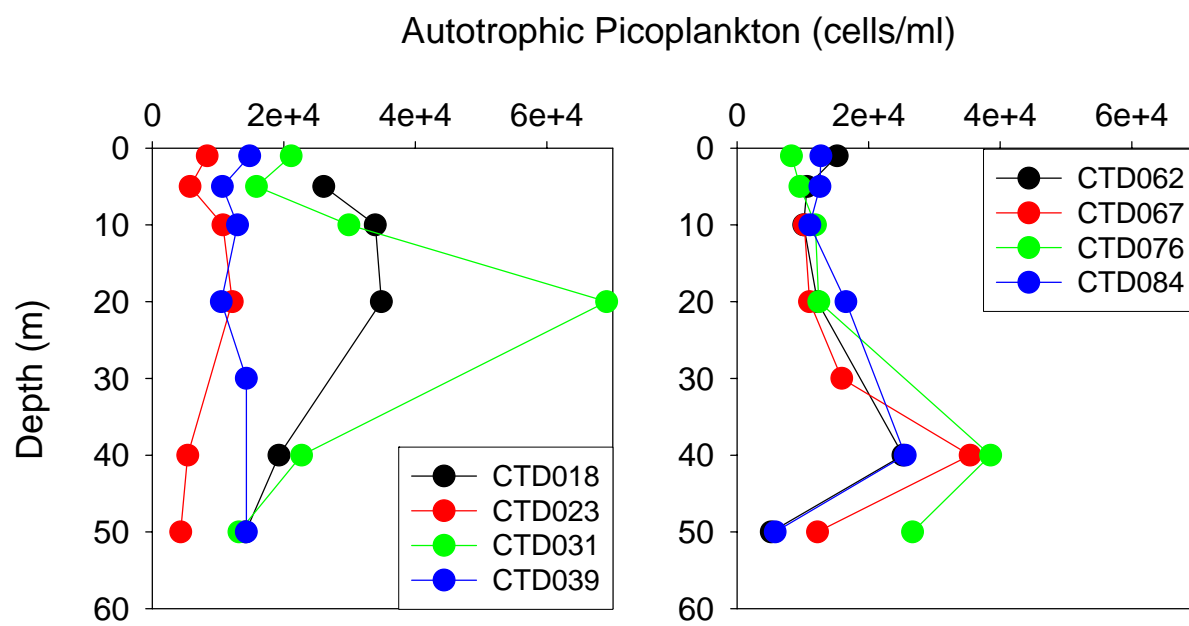
State Key Laboratory for Marine Environmental Sciences, Xiamen University

Remote sensing images of Chl. *a* (Aug. 2005)

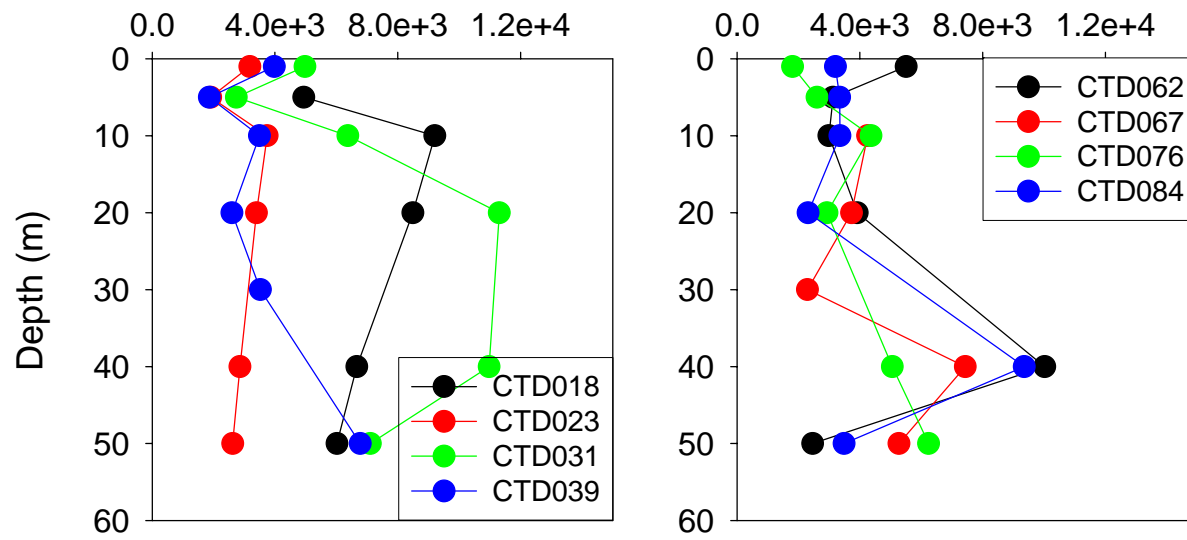


Vertical profiles of autotrophic picoplankton and heterotrophic bacteria at K2 (by Flow Cytometry)

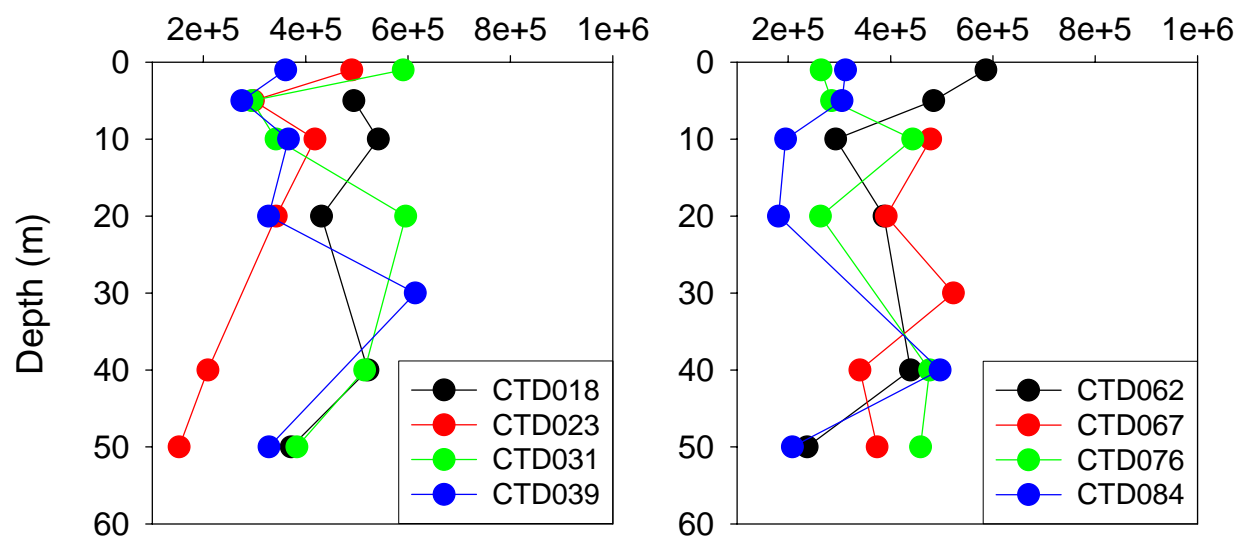
- Autotrophic picoplankton = *Synechococcus* + picoeukaryote
- *Prochlorococcus* didn't occur in the high latitude sea area, limited by low temperature.
- Interestingly, the depths of autotrophic picoplankton max were deeper for the second deployments (40m) than for the first (20m).
- The abundance of autotrophic picoplankton (mainly *Synechococcus*) at CTD031-20m was extremely high.
- No distinct inerratic stratification for heterotrophic bacteria, at least above 50m.



Picoeukaryote (cells/ml)

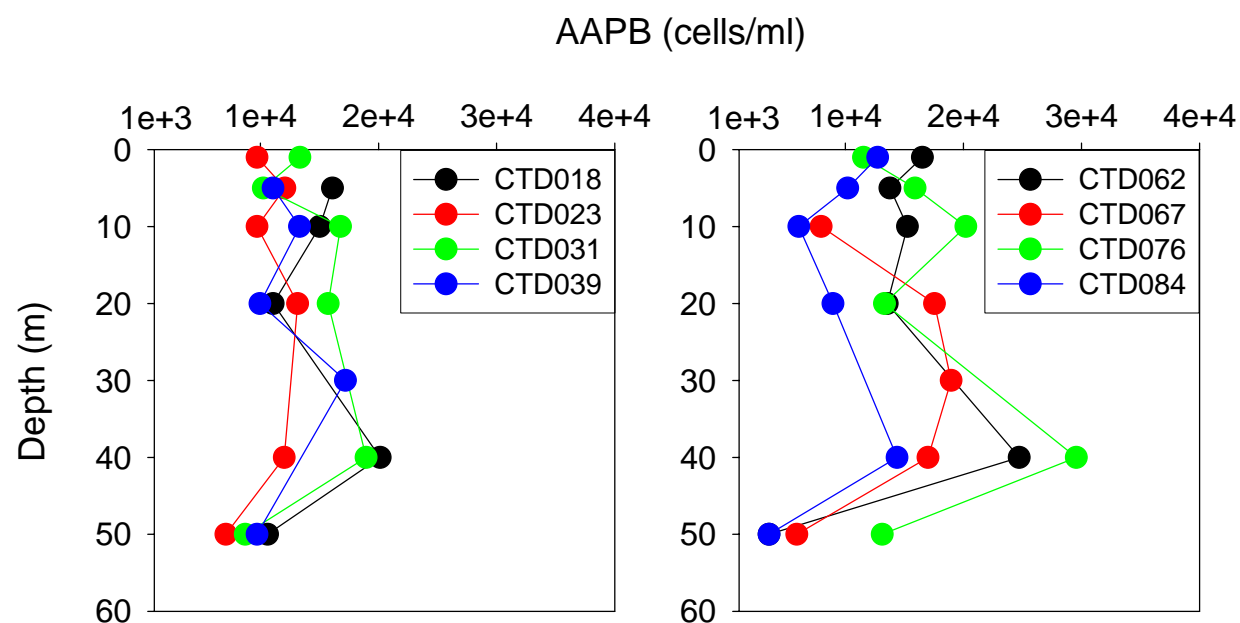


Bacteria (cells/ml) (FCM)

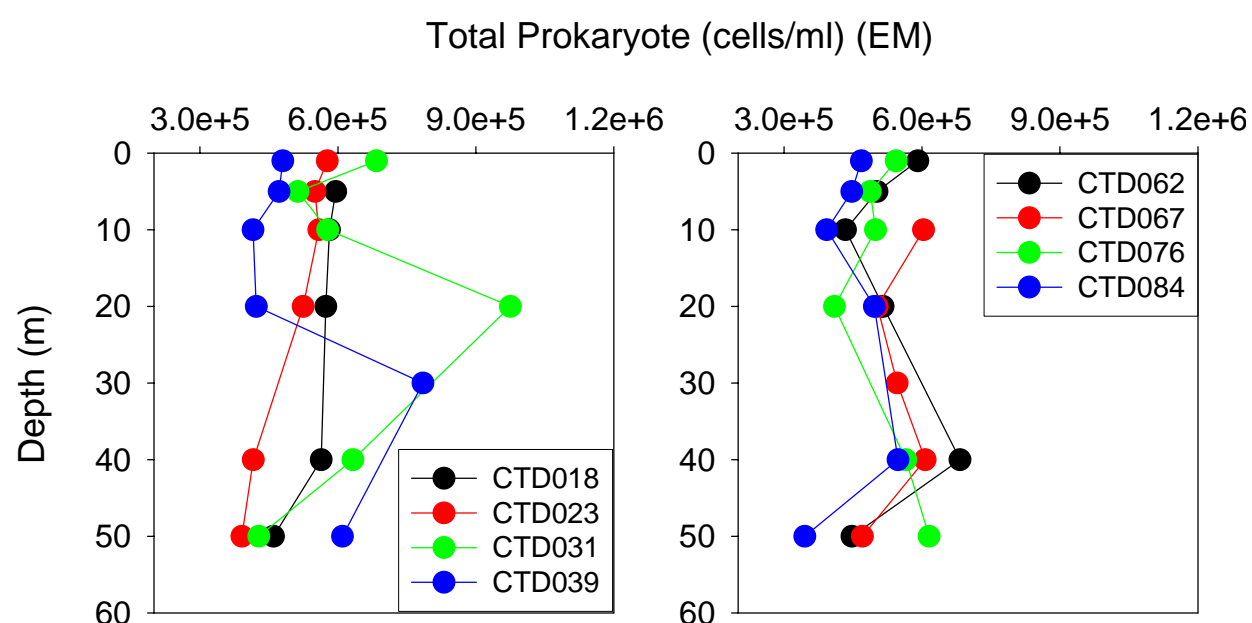


Vertical profiles of Aerobic Anoxygenic Photosynthetic Heterotrophic Bacteria (AAPB) and their rate to total Prokaryote at K2 (by Epifluorescence Microscopy)

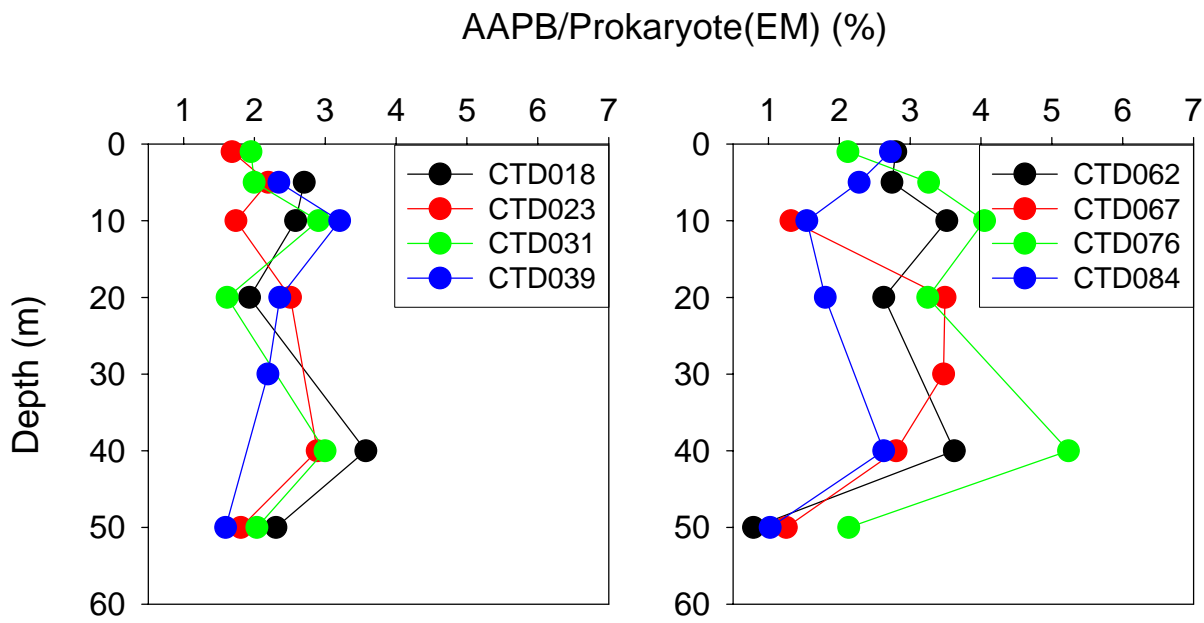
- AAPB are a functional group of microorganisms containing Bacterial Chlorophyll *a*.
- Different from autotrophic picoplankton, the depths of AAPB max were similar (40m) for the second deployments and for the first, though the max depths for the first were less obvious.
- The depths of AAPB max were close to DCM.



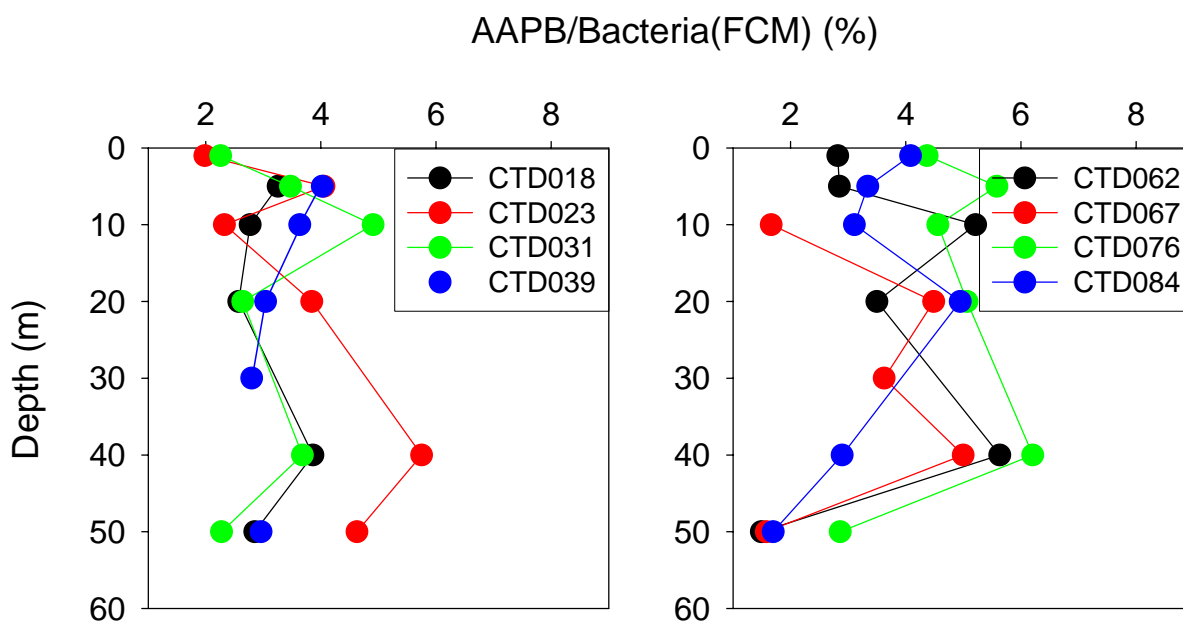
- The depths of prokaryote max were deeper for the second deployments than for the first, though the variations in the abundances from different layers were small.



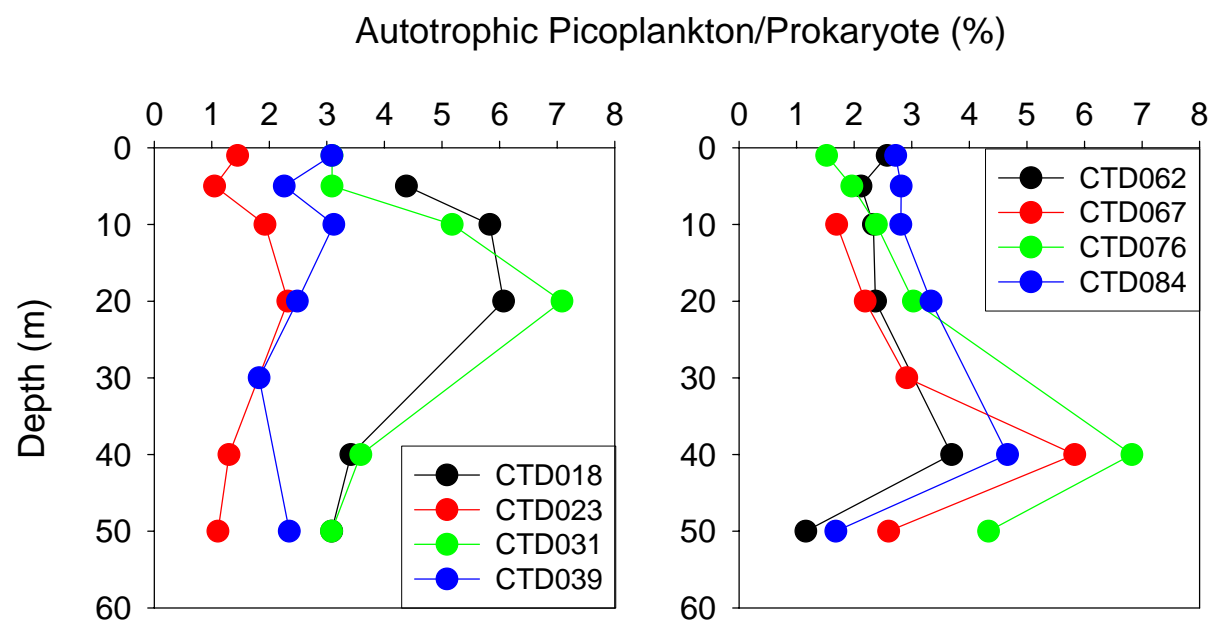
- Vertical profiles of rate of AAPB in total prokaryote were coincident to their abundance profiles.
- AAPB accounted for more important portion of the total biomass at 40m for two deployments.



- Vertical profiles of rate of AAPB in heterotrophic bacteria were coincident to the above profiles.

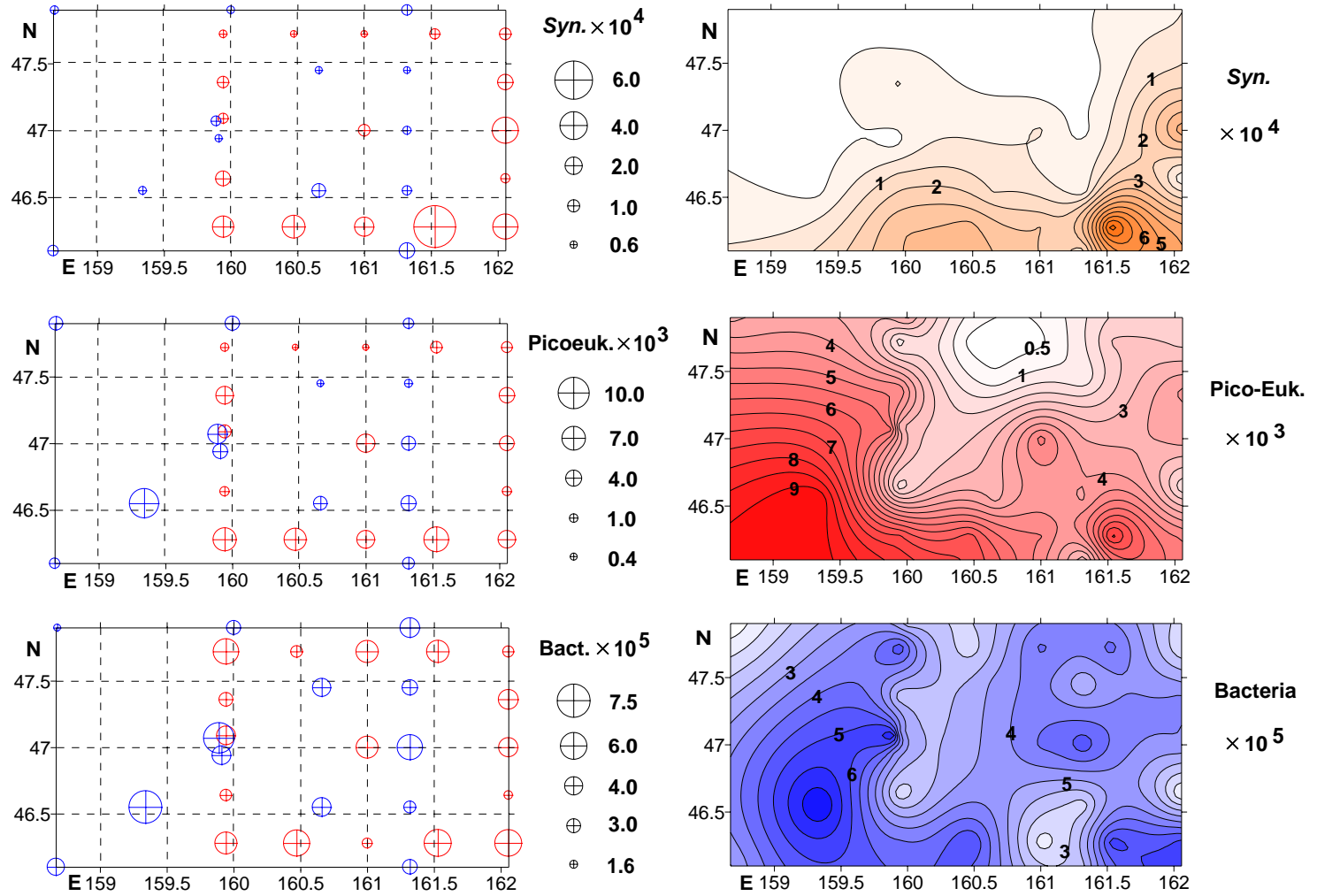


- **Autotrophic picoplankton accounted for more important portion in total prokaryote communities at 10-20m for the first deployments, while did at 40m for the second.**



Distributions of *Synechococcus*, Picoeukaryote and bacteria at the survey sites around K2

Left Figure: Blue indicated CTD #004-016; Red indicated CTD #042-058
Sampling depth: 10m (5m at seven sites)

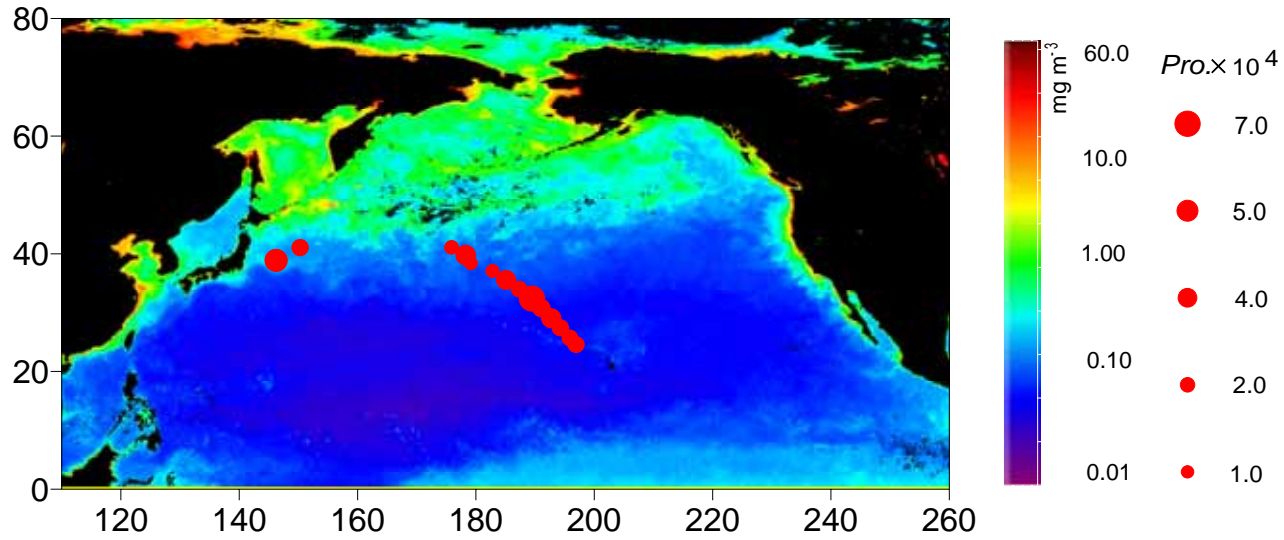


Distributions of picoplankton in Northwest Pacific (Yokohama-K2-Honolulu)

Sampling depth: about 1m

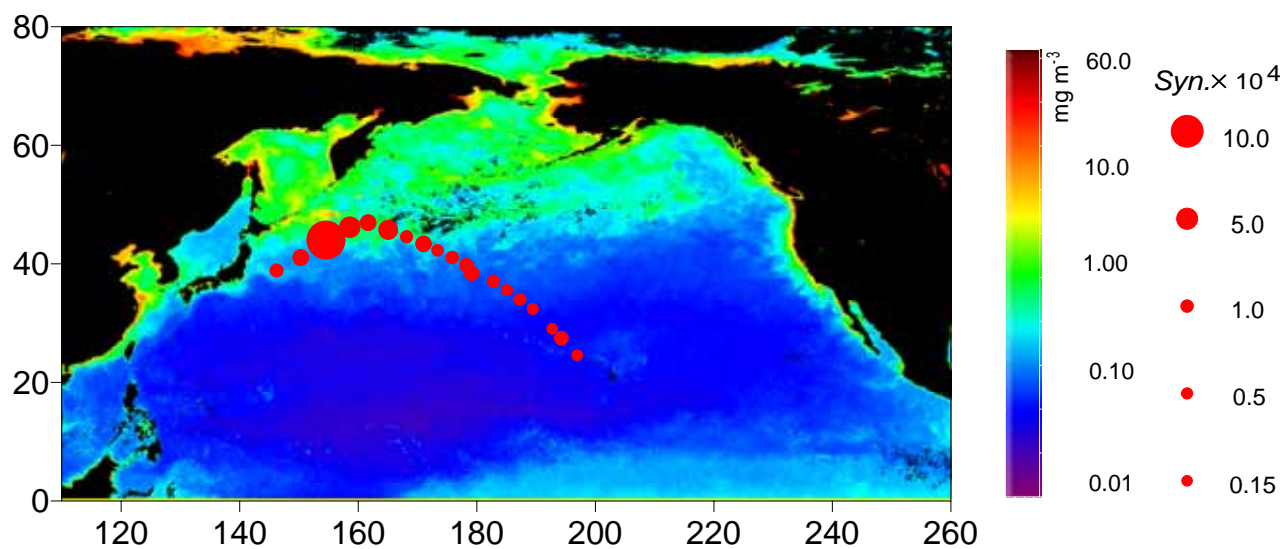
Prochlorococcus:

- *Prochlorococcus* didn't occur in the high latitude sea area, limited by low temperature.
- They are typical oligotrophic species, and dominant in oligotrophic ocean.
- The high value at the site nearest to Japan was caused by Kuroshio.



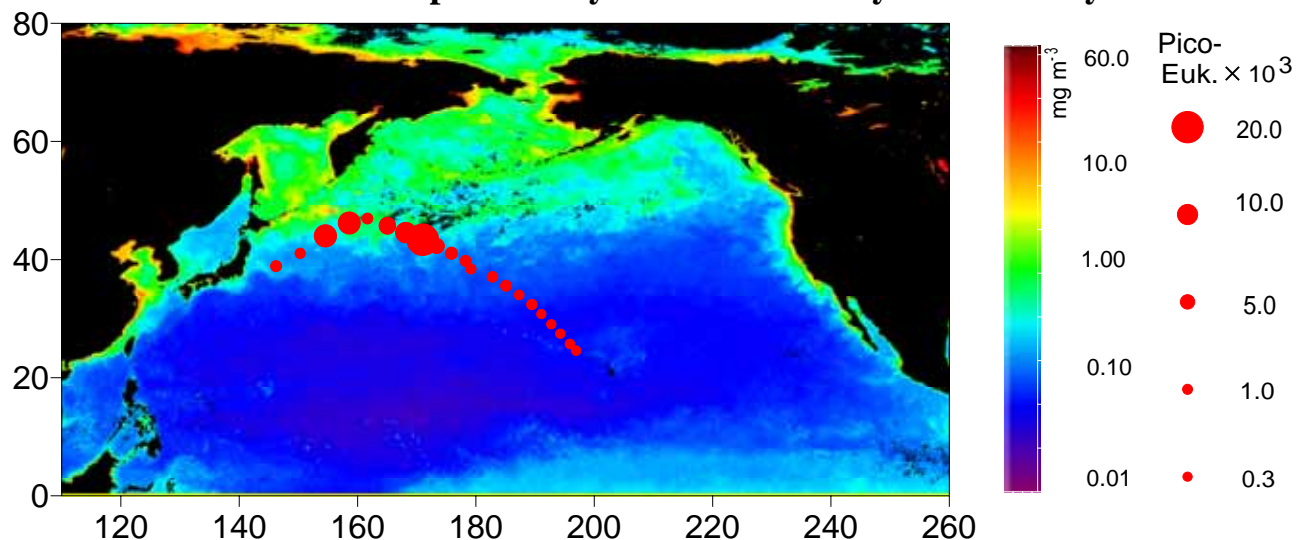
Synechococcus:

- *Synechococcus* is ubiquitous in marine environments.
- The higher values occurred in the area with high chlorophyll.



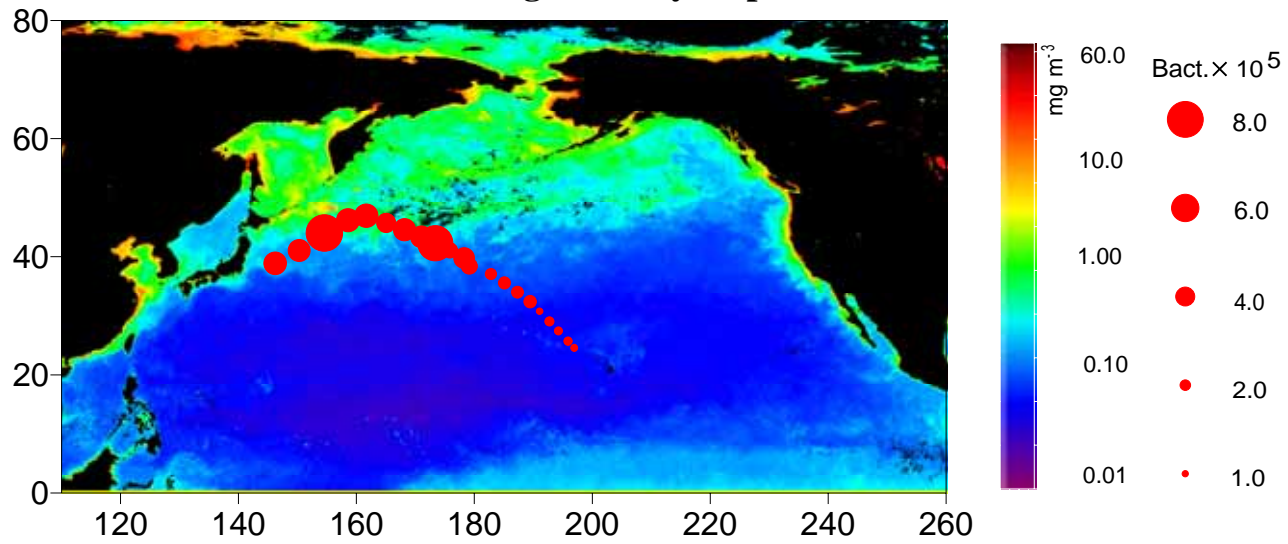
Picoeukaryote:

- The abundances of picoeukaryote were lower than other autotrophic picoplankton.
- Their distribution was regulated by trophic level.
- The low abundance of picoeukaryote about K2 may be caused by iron limitation?



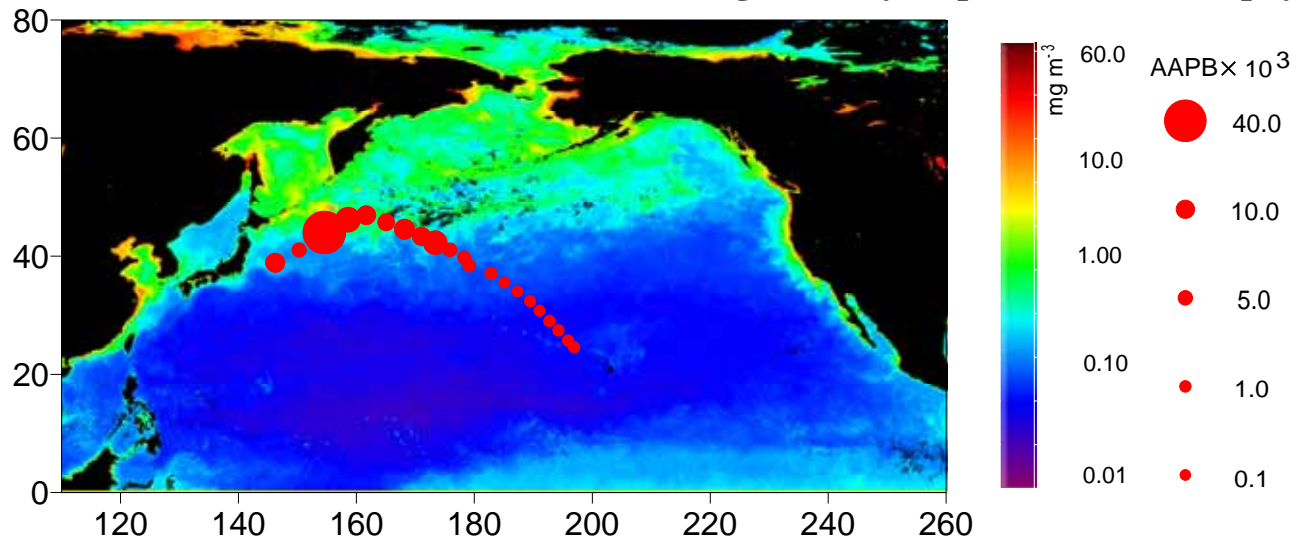
Bacteria:

➤ Bacterial distribution was regulated by trophic level.

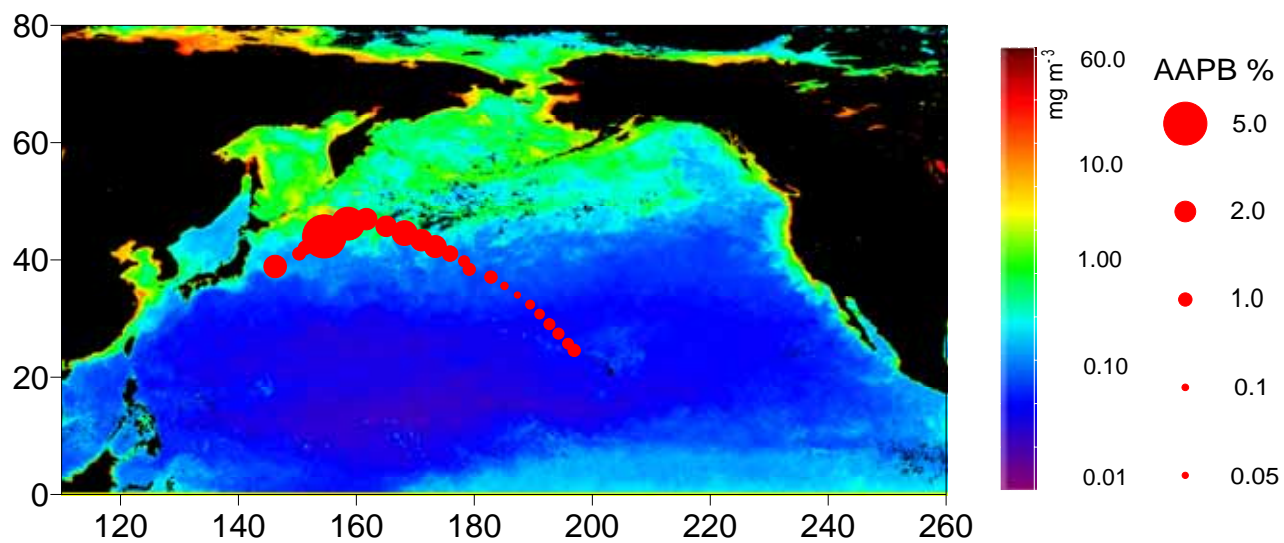


AAPB:

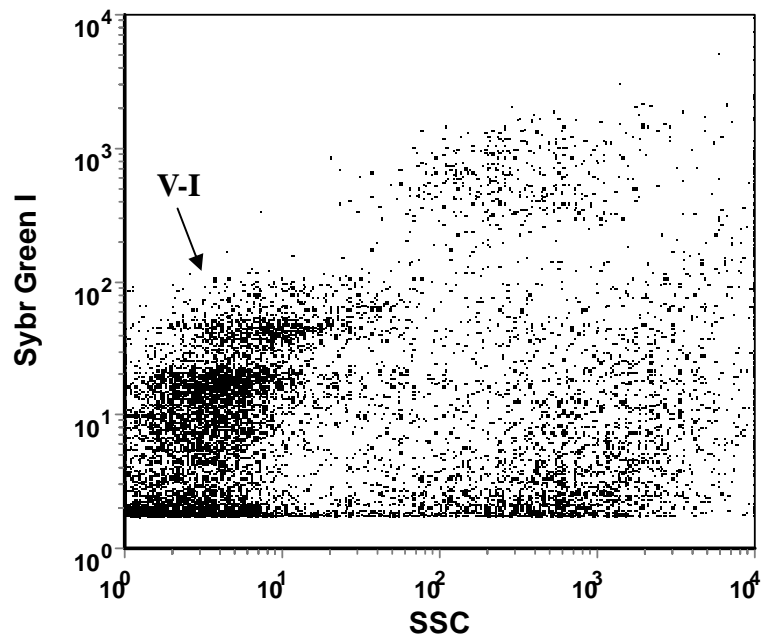
➤ The abundance and rate of AAPB were regulated by trophic level (Chlorophyll).



AAPB/Bacteria %:



Virioplankton populations were also detected by Flow Cytometry. The further study is going on.



Flowcytogram of a field sample (CTD023-40m) from VERTIGO shows the discrimination of the virioplankton populations. V-I with high fluorescence are considered as algal viruses, the majority below V-I as bacteriophages.