

Eukaryotic phytoplankton contributing to a seasonal bloom and carbon export revealed by tracking sequence variants

*Takuhei Shiozaki^{1,2}, Yuu Hirose³, Koji Hamasaki¹, Ryo Kaneko⁴, Kazuo Ishikawa¹, Naomi Harada²

1. Atmosphere and Ocean Research Institute, The University of Tokyo, 2. Japan Agency for Marine-Earth Science and Technology, 3. Toyohashi University of Technology, 4. National Institute of Polar Research

Greater diversity of eukaryotic phytoplankton than expected has been revealed recently through molecular techniques, but little is known about their temporal dynamics or fate in the open ocean. Here, we examined size-fractionated eukaryotic phytoplankton communities from the surface to abyssopelagic zone (5,000 m) throughout the year, by tracking sequence variants of the 18S rRNA gene in the western subtropical North Pacific. The oceanographic conditions were divided into two periods, stratification and mixing, between which the surface phytoplankton community differed. During the mixing period, the abundance of large phytoplankton ($> 3 \mu\text{m}$) increased, with diatoms and putative *Pseudoscurfieldia marina* dominating this fraction. Picophytoplankton ($< 3 \mu\text{m}$) also increased during the mixing period and were dominated by Mamiellophyceae. Taxa belonging to prasinophytes (including *Ps. marina* and Mamiellophyceae) were observed in the epipelagic zone throughout the year, and thus likely seeded the seasonal bloom that occurred during the mixing period. In contrast, diatoms observed during the mixing period mostly represented taxa unique to that period, including coastal species. Numerical particle backtracking experiments indicated that water masses in the surface layer could be transported from coastal areas to the study site. Gene sequences of coastal diatoms were present in the abyssopelagic zone. Therefore, allochthonous species drove the seasonal bloom and could be transported to deep waters. In the abyssopelagic zone, the relative abundance of *Ps. marina* in deep waters was similar to or higher than that of diatoms during the mixing period. Among picophytoplankton, Mamiellophyceae made up a significant fraction in the abyssopelagic zone, suggesting that prasinophytes are also involved in carbon export. Our molecular survey showed that these previously overlooked phytoplankton species could contribute significantly to the seasonal bloom and biological pump in the subtropical open ocean.

Keywords: 18S rRNA, eukaryotic phytoplankton, biological pump, coastal diatoms, prasinophytes