

## Phylogenetic composition of picophytoplankton in the Oyashio and Kuroshio transition regions

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Eukaryotic picophytoplankton (less than 3  $\mu\text{m}$ ) is ecologically and biogeochemically significant component in the marine microbial food web. Recently, studies about marine microbial diversity have been accelerated using molecular techniques, but basic information of picophytoplankton about diversity is still limited because of (i) lacking the 18S rDNA data in public database and (ii) fragile trait of the cell preventing sample collection. In this study, we investigated the phylogenetic diversity of surface community in one of the productive region of Japan, Oyashio and Kuroshio transition region. For the spatiotemporal comparison, seawater samples were collected from four geographically different sites with seasonal replicates (five seasons): Oyashio, Oyashio — Kuroshio transition regions, and mouth and head of the Sendai Bay. In order to better analyze the picophytoplankton community, we applied an efficient approach based on pyrosequencing of the 18S rDNA amplicon using flowcytometry sorting of cryopreserved cells. From the cleaned 10,000 reads came from the sorted 2,500 cells, 90 — 120 operational taxonomic units (OTUs: 95% cut off) were observed in each site and dominated by three higher level taxonomic groups: Stramenopiles (31 — 43%), Alveolata (16 — 35%) and Rhizaria (7 — 12%). Of the total of 217 OTUs, 40 OTUs were common among sites, and those included 21 OTUs common among five seasons, indicating spatially and temporally widespread distributing OTUs in this area. On the other hand, 21 — 38 OTUs were detected only in a site, indicating the local population. Multivariate analyses of OTUs compositions showed seasonal change of the community in each site (nMDS) and showed that the compositions were grouped by seasons ( $p < 0.01$ ) rather than by geographical difference ( $p = 0.5$ ). Thus, the phylogenetic composition of picophytoplankton in the Oyashio — Kuroshio transition region were composed of widespread and local phylotypes, and dynamically changed among seasons.

Keywords: Picophytoplankton, Flowcytometry, Pyrosequencing, 18S rDNA, Spatiotemporal distribution, Oyashio-Kuroshio transition region