Biological production in the water off Cape Inubo and its influence on the biological environment of the Kuroshio Extention region

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The larvae of small pelagic fishes, e.g. Japanese sardine, Japanese anchovy, and Pacific saury, grows through the advection process in the Kuroshio and its surrounding waters. The environmental factors for fishes, which includes water temperature and food abundance, are expected to change geographically and thus process of biological production should be examined in each specific region. In this study, we examined the biological production and physico-chemical process around the Cape Inubo, where Kuroshio change its direction eastward, based on satellite data and oceanographic observation.

Satellite observation: Sea surface temperature (SST) and Sea surface chlorophyll concentration (SSChl) in the area bounded by 135°30’–142°00’ E and 30°00'–37°00' N was examined. We used OISST (AVHRR only) for SST and MODIS-Aqua for SSChl and calculated climatological 8 day-mean for 2003–2013. In the study area, the Izu Ridge area was recognized to have depths of 500–3000 m in the area bounded by 138°15'–141°15' E and 30°00'–34°30' N. The grids in the study area with depths of > 500 m, except for those allocated to the Izu Ridge, were divided at 140° E into the Suruga-nada region to the west and the Boso (< 35°42' N)and the Kashima-nada regions (> 35°42' N) to the east. The areas assigned to these four sub-regions were further divided based on the location of the Kuroshio Current into the slope (near the coast), the Kuroshio Current (within the current), and offshore of the Kuroshio Current (the subtropical gyre) areas. The highest SSChl in the slope waters of the Suruga-nada and the Boso area was 0.75 and 0.84 μg l^{-1}, respectively, in late March to April in the former and 1 month later in the latter. In the Kashima-nada, the SSChl kept high (> 0.8 μg l^{-1}) from the mid April to the mid June, with the highest value (1.10 μg l^{-1}) among regions.

Field observation: Oceanographic observations were conducted in April 2009 and April–May 2015. At each station, a conductivity-temperature-depth profiler (CTD) cast was made along with water collection from the surface to 1000 m (2009) or 500 m (2015) depth. Water samples for nutrient and chlorophyll analyses were collected and concentrations of nitrate and chlorophyll were determined in the laboratory. Zooplankton were collected by a NORPAC net with a diameter of 450 mm and mesh size of 100 μm. Plankton collected in net pulls from a depth of 50 m to the surface, preserved in 5% buffered formalin-seawater solution, and examined in the laboratory for major taxa. The oceanographic condition in 2015 observation corresponded to the "O–pattern" in the analysis by Kubo (1985), which defined 3 oceanographic patterns for the area. In 2015, the surface water around the Cape Inubo was covered by a water mass, which extends from off Boso to Kashima–nada, with density of 0.25–0.50 kg m^{-3} higher than the surrounding waters. High concentrations of nutrients and chlorophyll were observed around the water mass. The chlorophyll concentrations in stations along the line south of the Cape Inubo were generally less than 2 μg l^{-2}, while higher chlorophyll concentrations (>5 μg l^{-2}) were observed in a station north of the cape. The water mass with the high chlorophyll concentrations had lower salinity than the surface waters of other stations. The neritic copepod species, *Acartia omorii*, was occurred with a high density (> 40,000 inds. m^{-2}) in the station. Thus the water mass was suggested to be advected from the coast of Honshu Island by the cyclonic surface current in the Kashima-nada (Yagi et al, 2001).

The satellite and field observations suggest that advection of and organisms by the surface current and subsurface upwelling of nutrients should both lead to the enhancement of the biological production in the surface, which would contribute to the food conditions of fish larvae/juveniles in the Kuroshio Extension area.

Keywords: Plankton, upstream of the Kuroshio Extension, Kuroshio

Community structure of Archaea in the western North Pacific and the Arctic Ocean

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Archaea are ubiquitously found in various environments. Many issues on their biological functions and ecological roles still remain to be investigated because they are often hard to be cultivated. Four phylogenetic groups, Marine Group I (MG-I) belonging to the phylum *Thaumarchaeota* and MG-II, MG-III, MG-IV belonging to the phylum *Euryarchaeota*, have been found so far in seawater environment. Although their abundance in mesopelagic and bathypelagic layers is comparable to bacteria, their ecological roles are not fully understood. Analyses of limited number of cultured strains, single-cell genomics and metagenomics of marine archaea have revealed that their contribution to energy flows and biogeochemical cycles in pelagic ecosystems can not be negligible. However, even basic information about their distribution, diversity and community structure is still very limited comparing with bacteria. Here we report archaeal community structure in the western North Pacific and the Arctic Ocean based on the deep sequencing of 16S rRNA genes directly amplified from seawater filtrates. Totally 44 samples including multiple depths of 8 different locations (4 in the North Pacific and 4 in the Arctic) were analyzed. Two size fractions, particle-associated (>3.0 μm) and free-living (0.22-3.0 μm), were obtained by seawater filtration. After extracting DNA, V4 hyper variable region of 16S rRNA gene was amplified and sequenced using an archaea specific primer set. Obtained sequences were clustered with 3 % cutoff value and assigned using Greengenes database. As a result, about 98 % of total reads were assigned to MG-I, MG-II, MG-III and the rest of 2 % reads were assigned to *Parvarchaeota*, Marine Benthic Group, MG-IV. Sequence reads assigned to MG-I were reanalyzed using our own database to have their subgroup assignment. The MG-I sequences were assigned to 9 of 10 subgroups. MG-I-alpha, MG-I-beta, MG-I-gamma were major subgroups and dominated about 93 % of total MG-I reads. Community structure showed depth-dependent patterns of each phylogenetic group. MG-II dominated in a surface layer (0-200 m) and MG-I dominated in subsurface and deep layers (>200 m) in the Pacific Ocean. Also, MG-I-alpha was more abundant than other subgroups in the surface layer, whereas MG-I-gamma was abundant in the subsurface and deep layers. These depth-dependent patterns agreed well with previous knowledges. However, MG-I dominated in the surface layer at some Arctic locations and MG-I-beta was abundant in chlorophyll maximum depths at locations in the subtropical Pacific Ocean, which were previously unknown patterns and thus should be further investigated. In summary, we revealed seawater archaeal community structure in a wide climatic range of the ocean, from subtropical to the Arctic oceans. Our own database of MG-I archaea contains more detailed information of phylogenetic clustering than conventional 16S rRNA gene databases and thus enables subgroup assignments. Such subgroup assignment is important to understand archaeal contribution to biogeochemical cycles, because some of the MG-I subgroups such as MG-I-alpha, MG-I-beta, MG-I-gamma are known to be ammonia oxydizers and also ecotypes preferentially living in different habitats. Our MG-I database is useful for further analyses of archaeal community structure at the level of ecotypes and contributes to have more comprehensive view of their distribution in the ocean than before.

Keywords: Archaea, The western North Pacific Ocean, The Arctic Ocean

Phytoplankton group-specific size structure and primary production in the Kuroshio waters by satellite observation

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Phytoplankton group-specific chlorophyll abundance, quantum yield of photosynthesis, primary production and cell size were analyzed using earth observation satellite data. Monthly climatology over 1998-2007 of these variables suggested that haptophytes were relatively abundant than diatoms and cyanobacteria in Kuroshio and surrounding waters. According to our analysis, primary production of diatoms in the waters were more regulated by its abundance than its quantum yield of photosynthesis whereas the production of cyanobacteria varied with its quantum yield than its abundance. The production of haptophytes was influenced by the both factors, showing a seasonal dependence. When the group-specific cell size was compared with the group-specific production, the largest primary production of diatoms tended to occur at its model cell size, whereas the largest production of haptophytes and cyanobacteria did not.

Keywords: Kuroshio, Phytoplankton, Primary Production, Satellite, size