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PG-7 Picophytoplankton in coastal waters of the Ryukyu Islands

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Picophytoplankton is the fraction of photosynthetic plankton composed by cells between 0.2 and 2 μm . They are found throughout the marine photic zone worldwide and are very important roles in oceanic primary productions and microbial loops. Recent studies suggest that picoplanktons are a major source of nitrogen for coral reef communities and tremendous molecular phylogenetic diversities have been indicated based mainly on size-fractionated 18S rRNA gene clone libraries. Hence information of picophytoplankton diversity is needed for the coasts of Ryukyu Islands.

The samples had been collected 23 coasts from Okinawajima, Okinoerabu, Ishigaki, Miyako, Ikema, Kurima and Yoron Islands. Samples were initially filtered by 2 μm followed by 0.1 μm pore sized filters. Picophytoplankton enumeration was conducted by a fluorescence microscopy. Cells were isolated by dilution method using IMK medium. The cultures were serially transferred for every ten days. Strains were observed by light microscopy and whole cell mount of *Micromonas* strains were observed by TEM. Also 18S rDNA sequences of the strains were determined.

Picophytoplankton numbers were ranged 10^2 and 10^4 cells ml^{-1} . The lowest count were about 270 cells ml^{-1} from a coast of Okinoerabu whereas the highest count were 20480 cells ml^{-1} from Motobu port, Okinawajima. The cell numbers of picophytoplankton were slightly lower than previous data from East China Sea and South China Sea. These discrepancies could be caused by differences between direct cell count and flow cytometry. The former method easily overlooked weak fluorescence signal, hence the latter was more accurate.

Twenty strains of picophytoplankton were cultured but only picoeukaryotes could be isolated. Among them, 10 strains of 18S rDNA sequences were determined including five *Micromonas* strains, one each strain of *Pelagomonas*, *Pinguiochrysis*, *Pyconococcus*, *Ostreococcus* and *Nanochlorum*. The medium and / or culture conditions used in this study were not suitable for *Synechococcus* and *Prochlorococcus*. Because these prokaryotic algae are known to dominate the picophytoplankton throughout the world and likely to exist in the samples.

Determined 18S rDNA sequences were closely related to at least one data set in DDBJ. Phylogenetic analyses of *Micromonas* strains revealed that three strains belonged to the Western Pacific clade and each of the other two strains were harbored in distant clades. From the results of 18S rDNA sequence diversity, free-living picoeukaryotes are cosmopolitan and diverse in the coasts of Ryukyu Islands as well as other areas. Further studies are needed to determine the diversity and importance of picophytoplankton in the coasts of Ryukyu Islands.