

Weekly monitoring of eukaryote biodiversity using massively parallel sequencing (MPS)-based technology in Okhotsk Sea in Japan

Satoshi Nagai, Shingo

National Research Institute of Fisheries Science, Japan

Abstract

We have conducted a monitoring of eukaryote biodiversity by using massively parallel sequencing (MPS)-based technology one a week for nearly four years in Mombetsu city, Hokkaido, Japan (44°20.22'N, 143°22.85'E). Water temperature, salinity and chlorophyll-fluorescence were 1.6–22.4 °C, 18.3–33.7 PSU, <0.0–9.8 µg L⁻¹ during the survey periods of 2012–2014, respectively. In this study, we analyzed the biodiversity of seawater samples (n = 112) and succeeded in detecting over twenty hundreds of operational taxonomic units (OTUs) from 500 mL seawaters. In the NMDS analysis, samples taken at the same month but in different dates were more closely plotted and also the samples of closest months were located in the closest positions, showing the consecutive transition of species composition and the clear seasonal pattern of eukaryote species in Okhotsk Sea. In the relative abundance of identified OTUs at the supergroup levels,

Alveolata, Opisthokonta, Stramenopiles were 27.3, 22.5 and 21.5%, respectively and followed by Rhizaria (12.9%) and Viridiplantae (12.9%), indicating the typical pattern in Japanese coastal waters. Interestingly, the heatmap and cluster dendrogram indicated the samples (n = 116) were divided into two large different nodes, i.e. samples obtained in Jun–Nov and remaining samples obtained in Dec–May, showing the strong influence by ocean current systems of Tsushima warm current (= Soya warm current) in summer and East Sakhalin current in winter season. The MPS-based technology also enabled to detect conspicuous diatom spring blooms and sudden blooms, which occurred irregularly, caused by dinoflagellate, ciliate or metazoa species, strongly suggesting the effectiveness of the monitoring by the MPS-based technology.

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