Estimating fish fauna in the central Bering Sea by using environmental

DNA

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1. Introduction

Recently, environmental DNA (eDNA) metabarcoding method has been developing as a new biological survey method. However, information on the sensitivity of this method in the wild is limited, and there are few eDNA applications to marine ecosystems. In this study, I conducted an eDNA metabarcoding for investigating fish fauna in the central Bering Sea, verifying whether eDNA can be detected in the open ocean. In addition, by comparing the results of the surface trawl conducted at the sampling site at the same day, I evaluated the effectiveness of eDNA metabarcoding method.

2. Method

As a part of the 2017 Central Bering Sea survey operated by the Hokkaido National Fisheries Research Institute (HNF), I conducted the eDNA sampling on site followed by the metabarcoding analysis in the lab. Between July 24 and August 2, 2017, sea surface water was sampled from nine sites in the central Bering Sea (52° 33' N- 58° 32' N, 175^{\circ} 01' E-174° 53' W). Using a bleached bucket, one litter of sea surface water was sampled per site and filtered using a GF/F filter on the research vessel under the cooperation of HNF. I used MiFish, which are fish universal primers, for DNA amplification and metabarcoding on a Next-Generation sequencer (MiSeq, Illumina).

3. Result

eDNA from fish species was detected in all the samples. In total, six genera were detected: *Oncorhynchus, Salvelinus, Pleurogrammus, Sebastes, Stenobrachius,* and *Leuroglossus. Oncorhynchus* was detected in all sites. On the other hand, six genera were caught by sea surface trawl: *Oncorhynchus, Salvelinus, Pleurogrammus, Theragra, Zaprola,* and *Anoplopoma.* Regarding genera confirmed commonly in trawl and eDNA, coincidence rate of the results of detection of eDNA and surface trawl were;

Oncorhynchus 100%, Pleurogrammus 62.5%, Salvelinus 75%.

4. Conclusion

Robust detection of eDNA was confirmed in the central Bering Sea. The coincidence rates of the results of eDNA detection and surface trawl were high in many genera, suggesting a high sensitivity of eDNA metabarcoding method even at the open sea.