Onagawa Bay: A Model for Advanced Coastal Ecosystem Research Through Genomics and Data Integration

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The Advanced Institute for Marine Ecosystem Change (WPI-AIMEC) is on a mission to explore the response and adaptation mechanisms of marine ecosystems to changes in the Earth's system. In particular, the Coastal Ecosystem Services Research Unit in WPI-AIMEC, in collaboration with the Onagawa Field Center, aims to comprehensively elucidate the biological dynamics of Onagawa Bay through the analysis of physicochemical data and plankton genome analysis based on long-read sequencing. Furthermore, using Onagawa Bay as a model case, the unit strives to elucidate the marine dynamics of the Sanriku coast, ultimately contributing to environmental conservation on a global scale.

In Onagawa Bay, we have conducted regular sampling for physicochemical measurements and genome analysis. There are several challenges to be considered for a comprehensive, integrated understanding of the bay. (1) The data are quite heterogeneous: they include physical measurements such as sea flow dynamics; chemical measurements such as Chemical Oxygen Demand; and biological measurements such as plankton composition. (2) The physicochemical impact of biological species composition is largely unknown. (3) There are cost limitations to increasing the number of sampling sites and the frequency of sampling. (4) Different bays have different physicochemical and biological properties, making comparisons among bays challenging to achieve a higher understanding.

To overcome these challenges, our unit introduces two fundamental approaches. First, we actively harness the power of genomics. A genome sequence contains two fundamental types of information: species identity and function. Metabarcoding focuses on the former, where species composition can be determined using highly informative short fragments such as nucleic 18S rRNA, mitochondrial cox1, and chloroplast rbcL, among others. However, the reference sequence is not fully available to determine the species from observed barcode fragments, and thus understanding the compositional changes of marine plankton species is still a challenge. In addition to conducting metabarcoding, we will determine the genomes of major plankton in Onagawa Bay through long-read metagenomics. Based on the genome sequences, we will further estimate the physicochemical characteristics of species identified through functional genomics approaches. Second, an appropriate framework is essential for integrating heterogeneous data. In addition to high-dimensional statistical analyses, numerical simulations are a powerful approach to leverage the observed data. This enables us to estimate the dynamics of the measurements at any location and time, under various external oceanic conditions, including future warming trends. Furthermore, this approach is also useful for comparing bays with different properties across Japan.

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