# Exploring Suruga Bay's Microbial Dynamics: Insights from Metagenomics and Single-Cell Genomics

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## Abstract

Suruga Bay is located in the middle of Japan. Recently, it has gained attention as a potential model for marine environments due to its depth range from shallow waters to deep zones (2,500m), its connection to human activities, productive fishery fields, and seasonal changes. These features provide an excellent opportunity to explore the blue economy in the future as well as marine sciences including microbial diversity and genetic adaptations. However, the comprehensive characterization of organisms in Suruga Bay remains limited. To establish a baseline for Suruga Bay research and activities, we have conducted metagenomic and single-cell genomic research since 2020, sampling at multiple locations in Suruga Bay and at different seasons to microbial community dynamics across varying depths and seasons. We have denoted this project as BISHOP (Blue Innovation of Shizuoka Open Data Platform). Our research clearly demonstrated seasonal and depth-dependent microbial community dynamics. Additionally, functional divergence of these ecosystems was revealed, highlighting metabolic adaptations to environmental conditions. We also focused on SAR11 clade microorganisms, widely distributed across global oceans. We identified a novel SAR11 subclade, likely to represent an ecological adaptation in the deep-sea environment. Our findings deepen the understanding of microbial diversity in Suruga Bay and offer insights into deep-sea ecosystems. In this presentation, we will provide an overview of our metagenomic and single-cell genomic analyses under BISHOP, focusing on microbial dynamics, SAR11 diversity, and deep-sea functional adaptations.

**Keywords:** metagenome, single, cell genome, SAR11, microbial community, microbial divergence

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