

Seasonal microbial community dynamics in the Ariake Sea responding to coastal hypoxia and algal blooms

*Fumiaki Mori^{1,2}, Akira Yamaguchi³, Takuya Iwanaga⁴, Tomoyuki Hori⁵, Tomo Aoyagi⁵, Yuki Morono¹, Tatsuhiko Hoshino^{2,6,7}

1. Marine Core Research Institute, Kochi University, 2. Kochi Institute for Core Sample Research, Japan Agency for Earth-Marine Science and Technology, 3. Fisheries Technology Institute, Japan Fisheries Research and Education Agency, 4. Saga Prefectural Ariake Fisheries Research and Development Center, 5. Environmental Management Research Institute, National Institute of Advanced Industrial Science and Technology (AIST), 6. Advanced Institute for Marine Ecosystem Change (WPI-AIMEC), Japan Agency for Earth-Marine Science and Technology, 7. WPI-AIMEC, Tohoku University

The Ariake Sea, characterized by Japan's largest tidal range, frequently suffers from severe algal blooms and seasonal bottom water hypoxia in summer. Eutrophication and tidal currents drive these dynamic environmental fluctuations that alter oxygen availability and organic matter supply, thereby influencing microbial community composition and biogeochemical cycling. However, the spatiotemporal dynamics of these microbial communities remain poorly understood. This study investigates the distribution and response of particle-associated ($>3 \mu\text{m}$) and free-living ($0.2\text{--}3 \mu\text{m}$) microbial communities in the water column to these environmental changes in the inner Ariake Sea. Monthly observations were conducted starting in August 2023 at two distinct stations: Stn. 5, located in the inner bay where bottom water hypoxia typically develops in summer, and Stn. 6, a reference site that remains normoxic throughout the year. We monitored environmental parameters and analyzed microbial community composition using 16S rRNA gene amplicon sequencing. Microbial cell abundance was also estimated to assess microbial biomass dynamics.

In surface waters, Cyanobacteria became the dominant group during summer regardless of the size fraction, reaching up to 49% relative abundance in the particle-associated fraction. Planctomycetes in the particle-associated fraction also increased during both summer and winter. Total microbial abundance showed a positive trend with chlorophyll-a concentration ($r = 0.36$). In bottom waters, a distinct spatial contrast was observed. At Stn. 5, the relative abundance of ammonia-oxidizing archaea (Nitrososphaeria) in the free-living fraction notably increased during hypoxic periods. In contrast, no such distinct shift was observed at the normoxic Stn. 6.

These findings highlight microbial responses to the eutrophic and hypoxic environment of the Ariake Sea. The dominance of Cyanobacteria indicates that microbial primary production makes a significant contribution to the carbon dynamics. Furthermore, the synchronization of particle-associated Planctomycetes with algal blooms suggests that these microbes probably play a pivotal role in the rapid degradation of bloom-derived particulate organic matter. In the bottom layer, oxygen depletion creates a distinct niche for chemolithoautotrophs, as evidenced by the proliferation of Nitrososphaeria. Collectively, this study elucidates how microbial communities spatially and temporally differentiate their ecological roles in response to algal blooms and hypoxia.

Keywords: Coastal hypoxia, Ariake Sea, Algal blooms, Microbial community