

Monthly-resolved marine metagenome-assembled genomes (MAGs) from the East Sea (South Korea): temporal dynamics and functional potential

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Marine microbial communities drive key biogeochemical cycles and respond dynamically to seasonal environmental changes. While shotgun metagenomic sequencing provides valuable community-level insights, genome-resolved approaches such as metagenome-assembled genomes (MAGs) are needed to uncover population-level dynamics and metabolic potential. In this study, we utilized a publicly available monthly metagenomic dataset collected in 2009 from surface seawater (10 m depth) off the east coast of South Korea (East Sea) and published by Lim et al. (2023; doi:10.1038/s41597-023-02556-7). Our objective was to restore microbial genomes on a month-by-month basis in order to perform comprehensive functional annotation, elucidate novel or previously uncultured lineages, and characterize marine antibiotic resistance genes (ARGs).

So far, we have reconstructed 252 MAGs ($\geq 70\%$ completeness, $\leq 10\%$ contamination), including several from previously uncultured lineages, with additional months still under analysis. Functional annotation with DRAM highlighted genes involved in carbon fixation pathways, nitrogen, and sulfur cycling, along with other central metabolic processes. Furthermore, antibiotic resistance genes (ARGs) were systematically identified using the RGI tool against the CARD database, providing initial insight into the resistome of marine microbial populations.

This analysis highlights the value of MAG-based approaches for studying seasonal microbial dynamics in the East Sea. The recovered MAGs are expected to illuminate microbial functional potential and advance our understanding of biogeochemical cycling in marine systems.