[BIOINFO 2025]

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

Amanzhanova Amina[1] *and Kang Yang Jae*[1,2,3]

[1] *Division of Bio & Medical Bigdata Department (BK4 Program), Gyeongsang National University, Republic of Korea*

[2]*Research Institute of Molecular Alchemy, Gyeongsang National University, Republic of Korea*
[3] *Division of Life Science Department, Gyeongsang National University, Republic of Korea*
**Corresponding author: kangyangjae@gnu.ac.kr*

Marine microbial communities drive key biogeochemical cycles and respond dynamically to seasonal environmental change. While shotgun metagenomics provides community-level profiles, genome-resolved approaches are required to resolve population dynamics and metabolic potential. Using a publicly available monthly surface-water dataset from the East Sea (South Korea; 10 m depth; 2009) published by Lim et al. (2023; doi:10.1038/s41597-023-02556-7), we reconstructed 305 metagenome-assembled genomes (MAGs) (271 Bacteria, 34 Archaea; ≥70% completeness, ≤10% contamination). About 40 MAGs could not be assigned to any named GTDB species because their ANI to the closest reference was below the species threshold; however, phylogenomic placement grouped them within recognized GTDB genera, indicating they likely represent previously uncharacterized (candidate) species within those lineages. We used DRAM to annotate metabolic functions—including pathways relevant to carbon fixation and nitrogen and sulfur cycling—to contextualize seasonal functional potential. Antibiotic resistance genes (ARGs) were profiled with RGI/CARD, with glycopeptide resistance gene clusters emerging as the most common category. Collectively, these genome-resolved data highlight the value of MAG-based approaches for studying seasonal microbial dynamics in the East Sea. The recovered MAGs—particularly the candidate novel lineages—provide a foundation for elucidating microbial functional potential and advancing our understanding of marine biogeochemical cycling.