Depth-related metabolic diversity in the marine bacterial clade SAR324

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Abstract

Oceanic microbiomes are critical to the global carbon cycle and to oceanic carbon and energy cycling, and the Deltaproteobacteria clade SAR324 is one of the few microbial groups inhabiting all oceanic depth zones. Although the metabolic potential of dark-zone SAR324 has been investigated, the ecology and metabolic traits of euphotic- and twilight-zone SAR324 remain unclear. To learn more, a recent study collected SAR324 from various depths of the North Pacific Subtropical Gyre. A pangenomic analysis including published genomic data revealed considerable intra-clade diversity, as indicated by the average nucleotide identity (ANI). The bacteria clustered into four ecotypes with different spatiotemporal distributions, and bacteria at different depths had different metabolic characteristics. The deep- and twilight-zone bacteria exhibited genomic and metabolic traits consistent with sulfur-based chemolithoautotrophy. In contrast, the bacteria nearer the surface appeared to be photoheterotrophic, as supported by the presence and patterns of certain opsin proteins. Although the metabolic traits predicted by the genomic data still need to be linked to ecological functions, the findings reveal striking differences among members of the same bacterial clade living in different zones of the ocean and emphasize the importance of including functional analyses alongside phylogenetic analyses in studies on microbial communities.