MICROBIAL COMMUNITY AND GENOMIC INSIGHT TO PREDOMINANT CANDIDATUS ATRIBACTERIA JS1 LINEAGE IN MARINE SEIMENTS OF THE ROSS SEA, ANTARCTICA

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ABSTRACT

The microbial biomass of the subseafloor with majority of uncultivated candidate phyla plays an important role in global biogeochemical cycles. Candidate phylum *Atribacteria* JS1 is among the predominant members in anoxic subseafloor environments, especially in methane-rich sediments. However, the metabolic potential and biogeochemical role of this phylum have remained elusive due to the lack of axenic culture representatives. Here, weinvestigated the microbial communities of marine sediments of the Ross Sea, Antarctica and genomic features of candidate phylum *Atribacteria* JS1. Candidate phyla accounted for 21.4–56.2% of bacterial communities, with *Atribacteria* JS1 as the most abundant candidate phylum (9.0–39.6%). Genomic analysis revealed that 18 single-cell amplified genomes (SAGs) of *Atribacteria* JS1were from a single species with a high 16S

rRNA gene similarity (> 99.3%) and average nucleotide identity value (>96.8%). The composite genome constructed by co-assembly showed the highest genome coverage among *Atribacteria* JS1 genomes. *Atribacteria* JS1 was predicted to be a homoacetogenic bacterium capable of growing on H_2/CO_2 or CO_2, with a heterotrophic lifestyle. The presence of the Wood-Ljungdahl pathway suggested that *Atribacteria* JS1 may be a syntrophic acetate-oxidizer explaining the high abundance of this group in anoxic methane-rich sediments. These data expand our knowledge of *Atribacteria* JS1 and the ecological function of this uncultivated group in carbon cycling.