Opening a single-cell genomic window on the ecological distribution and metabolic potential of uncultivated Sulfiphilic Bacteroidetes

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The Bacteroidetes are a ubiquitous phylum of bacteria found in diverse environments spanning the human gastrointestinal tract to the deep subsurface. Marine Bacteroidetes are known to utilize complex carbohydrates and have a potentially important role in the global carbon cycle through processing these compounds, which are not digestible by many other microbes. Some members of the phylum are known to perform denitrification and are facultative anaerobes, but Bacteroidetes are not known to participate in sulfur redox cycling. Recently, it was shown that a clade of uncultured Bacteroidetes, including the VC2.1_Bac22 group, appears to be endemic to sulfidic environments, including hydrothermal vent sulfide chimneys, sediments and marine water column oxygen minimum zones (OMZs). To test the hypothesis that this clade, recently dubbed the "Sulphiphilic Bacteroidetes," plays a putative role in sulfur redox chemistry, we updated our meta-analysis using widespread 16s rRNA sequences from public databases and employed single-cell genomics to survey their metabolic potential along a defined redox gradient. A total of 19 single-cell amplified genomes (SAGs) were recovered from the stratified waters of Saanich Inlet, a seasonally anoxic fjord on the coast of Vancouver Island British Columbia Canada that serves as a model ecosystem for understanding microbial community responses to ocean deoxygenation. Initial analysis of these SAGs indicates the Sulphiphilic Bacteroidetes may perform sulfur redox reactions using a three gene psrABC operon encoding the polysulfide reductase enzyme complex with a thiosulfate sulfurtransferase (rhodanese), which putatively uses cyanide to convert thiosulfate to sulfite, just upstream. Interestingly, this is the same configuration as discovered recently in some Marine Group A bacteria. Further aspects of the Sulphiphilic Bacteroidetes' biogeography and metabolic potential will be evaluated with respect to coupled carbon, nitrogen and sulfur cycling processes and the role of lateral gene transfer in shaping these networks in reducing environments.