



## Dissolved organic sulfur utilization by marine benthic microbial communities revealed by quantitative DNA stable isotope probing

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Microbial metabolisms are directly responsible for the production, degradation and recycling of dissolved organic matter (DOM) in the ocean. Many compounds within the DOM contain sulfur (dissolved organic sulfur, DOS) and in sum they represent the largest reservoir of organic sulfur in the ocean. Recent studies indicated an abundant and diverse suite of marine bacteria with the genetic capacity for DOS transformation. However, there is currently very little experimental data regarding the marine sediment microbial communities that are actively using DOS substrates as a source of carbon. Here, we use quantitative <sup>13</sup>C DNA stable isotope probing (qSIP) to provide the first quantitative measurements of DOS (taurine and methionine) utilization by specific operational taxonomic units in seafloor sediments from continental shelf of Puerto Rico (493 meter below sea surface). Immediately after sampling, seafloor sediments were amended with 500 µg / g <sup>13</sup>C-labeled taurine or methionine as well as natural-abundant (<sup>12</sup>C) substrates as a control and were incubated in gas-tight glass flasks with no headspace in the dark over two different timepoints (30 hours and 10 days) to unravel the active microbial communities. Our preliminary results by gas-chromatography mass spectrometry showed that there was 6 – 10% of <sup>13</sup>CO<sub>2</sub>-remineralization compared to control samples. This indicates that taurine and methionine are important DOS substrates supporting the activity of benthic microbial populations. Notably, the rate of taurine remineralization was five-fold higher than glucose and 50-fold higher than methionine over the first 30-hours of incubation, suggesting that taurine is an underappreciated, yet important DOS substrate for microbial activity at the seafloor. Oxygen was rapidly consumed to anoxic levels over the first 12 hours in all incubations, indicating that the taurine was utilized via anaerobic microbial metabolism. This was reflected by changes in the initial microbial community that was dominated by Thaumarchaeota (29%), Gammaproteobacteria (15%) and Planctomycetes (13%), which changed to being enriched by Firmicutes (8%-43%), Deltaproteobacteria (10%-26%), and Gammaproteobacteria (10%-29%) in the presence of taurine and methionine. Further quantitative DNA isotope probing study (in progress) will reveal the specific anaerobic microbial taxa that are responsible for driving the biogeochemical cycling of these important, yet overlooked DOS substrates at the seafloor.