Tracking the genomic signatures and metabolic interactions within single methane-oxidizing archaeal-bacterial consortia

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Microbially-mediated anaerobic oxidation of methane (AOM) coupled to sulfate reduction is the dominant methane sink in the oceans. At deep sea sites associated with methane hydrates and methane seepage, this process has been shown to be catalyzed through symbiotic interactions between multiple lineages of methanotrophic ANME archaea and deltaproteobacteria (SRB). These energy-limited organisms, like most environmental microbes, have been challenging to culture and many of the fundamental details of their metabolism and interactions between the syntrophic partners remain poorly constrained. Targeted metagenomic sequencing of diverse ANME-SRB consortia combined with FISH microscopy and single cell stable isotope probing experiments has led to new hypotheses regarding the interactions between these organisms and their metabolic potential. Sequencing of individual ANME-SRB consortia from methane seep sediments was accomplished through the application of a click-chemistry based technique called BONCAT (BioOrthognal Noncanonical Amino acid Tagging; Hatzenpichler et al., 2014 [1]), which enabled the separation of individual, translationally-active AOM consortia by fluorescence-activated cell sorting. Data collected from individual ANME-SRB consortia provided information about the specificity of archaeal-bacterial partnerships and when used in combination with complementary stable isotope probing and FISH-nanoSIMS experiments, offers insight into the potential physiology of distinct consortia types that co-exist within methane seep sediments.

[1] Hatzenpichler, R., Scheller, S., Tavormina, P. L., Babin, B. M., Tirrell, D. A., & Orphan, V. J. (2014). In situ visualization of newly synthesized proteins in environmental microbes using amino acid tagging and click chemistry. *Environmental Microbiology*, **16**(**8**), 2568-2590.