Exploration of Rates and Controls of Anaerobic Methane Oxidation in the Anoxic Basin of Golfo Dulce

HERDÍS STEINSDÓTTIR[1], EDDY GÓMEZ RAMÍREZ[2], SNEHIT MHATRE[1], BO THAMDRUP[1], LAURA A BRISTOW[1]

[1] Nordcee, Department of Biology, University of Southern Denmark, Odense, Denmark
[2] CIMAR, Universidad de Costa Rica, San Pedro de Montes de Oca, Costa Rica

The ocean represents a net source of methane to the atmosphere, with oxygen minimum zones (OMZs) being hot-spots for marine methane emission. Such systems have been studied extensively for their active role in nitrogen cycling, but their relevance to the methane cycle is much less explored. The extent of methane cycling that occurs within OMZs as a result of anaerobic methane oxidation (AOM) is virtually unknown but might play a significant role in attenuating the flux of methane through the OMZ, especially since, at these active nitrogen cycling sites, AOM can be driven by the reduction of nitrite or nitrate.

To identify and quantify pathways of AOM, sampling was undertaken in the anoxic basin of Golfo Dulce, Costa Rica, which shares biogeochemical features with oceanic OMZs. Methane oxidation rates in the water column were measured in batch incubations with ^{3}H-labelled methane carried out at oxygen concentrations less than 0.1 µM. Methane oxidation rates increased below the oxic-anoxic interface, coinciding with increasing nitrite and methane concentrations. In oxygen addition experiments (0 to 10 µM), oxygen appeared to inhibit methane oxidation at depths below the interface, while at and above the interface, rates increased or remained constant and low in response to oxygen. This suggests that the activity observed below the interface is not driven by oxygen respiration, but more likely by the reduction of nitrite and/or nitrate, i.e., that methane oxidation is indeed AOM. The results thus indicate that AOM is an active process in the water column of Golfo Dulce, attenuating the flux of methane from the sediment. On-going biomolecular analyses aim to identify the microbes and pathways involved.