# Long-distance electron transport by cable bacteria in marine sediment: Insights from a combined geochemical and metagenomic analysis

JEANINE S. GEELHOED[1*], SEBASTIAAN VAN DE VELDE[2], SILVIA HIDALGO-MARTINEZ[1] AND FILIP J. R. MEYSMAN[12]

[1]NIOZ Royal Netherlands Institute for Sea Research, Yerseke, The Netherlands (*correspondence: jeanine.geelhoed@nioz.nl)

[2]Department of Analytical, Environmental and Geo-Chemistry, Vrije Universiteit Brussel, Brussels, Belgium

Sulfur-oxidizing cable bacteria induce electrical currents in marine sediments and strongly impact sediment geochemistry. Cable bacteria are long, filamentous, multi-cellular bacteria, which span sediment horizons of up to several centimeters from the oxic surface into deeper sulfidic sediment layers. They employ a radically novel microbial metabolism, in which electrons released from the oxidation of sulfide are transferred from cell to cell over the length of the filament to the sediment surface, where they react with oxygen. Due to the spatial separation of electron donor and electron acceptor reactions, a strong acidification of the pore water is induced in deeper sediment layers, which has a marked impact on the overall biogeochemical cycling in marine sediments.

In this study we examined a field site in the southern North Sea that showed cable bacteria activity using geochemical and metagenomic analyses. Pore water profiles of sulfate and sulfide indicated highly active cryptic sulfur cycling, whereas strongly increased concentrations of divalent cations ($Ca^{2+}$, $Mg^{2+}$, $Mn^{2+}$, $Fe^{2+}$) in the suboxic zone indicated strong mineral dissolution.

Cable bacteria density was assessed using fluorescent in situ hybridisation and quantitative PCR. Genomic DNA for shotgun sequencing was extracted from different sediment depths: the oxic sediment surface, the suboxic zone where neither oxygen nor sulfide was present and deeper sulfidic sediment where cable bacteria were not abundant. Using metagenomics analyses near-complete genomes of cable bacteria were recovered, while other genome bins could be assigned to members of Flavobacteraceae and Alpha, Gamma and Deltaproteobacteria. Analysis of these genome bins provides a first insight into the metabolic interactions of the microbial community in electro-active sediments under field conditions.