

Using sediment fuel cells to detect contaminants in aquatic and shallow subsurface estuarine environments

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A variant of the microbial fuel cell (MFC), the sediment microbial fuel cell (SMFC) can be used to harvest energy from the natural redox conditions and bacteria in aquatic sediments. SMFC's have been applied as a simple and cheap way of powering sensors and data transmission [1]. The possibility to use SMFC's themselves as sensors remains relatively unexplored, though using SMFC's to determine the microbial activity *in situ* has already been studied [2]. Clauwaert *et al.* have suggested SMFC's can be used to measure nutrient or contaminant pulses [3]. Using the open cell voltage, SMFC's can be used to detect (potentially toxic) changes in either the sediment or overlying water.

Contaminant influence on the output of SMFC's was tested for sediments from estuarine salt marshes from the Western Scheldt and Eastern Scheldt in the Netherlands. Contaminants tested were; heavy metals (copper (II) chloride, sodium-molybdate), organic solvents (tetrachloroethylene, trichloroethylene), sunflower oil, a leaching agent (EDTA), macro-eutrophication (acetate), and CO₂ leakage from CCS.

After cell equilibration to reach V_{Max}, the contaminants were added. The open cell voltage was measured continuously to investigate the response to the contaminants. Other parameters measured include cathode and anode electrode potential and pH.

	5mM EDTA	100mL C ₂ HCl ₃	100mL sunflower oil	control
uncontaminated	748 mV	632 mV	682 mV	751 mV
contaminated	614 mV	485 mV	83 mV	718 mV

Table 1: Open cell voltage before and after the addition of contaminants (the period between the two readings is one week).

As can be seen in Table 1, the cells showed a clear response to the introduction of EDTA and sunflower oil, indicating that SMFCs can be used as contaminant.

[1] Shantaram *et al.* (2005) *Environ. Sci. Technol.* **39**, 5037–5042 [2] Tront *et al.* (2008) *Biosens. Bioelectron* **24**, 586–590 [3] Clauwaert, *et al.* (2008) *Appl. Microbiol. Biotechnol.* **79**, 1522–1524

Carbon fluxes in natural plankton communities under elevated CO₂ levels: A stable isotope labelling study

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The potential impact of rising CO₂ on carbon fluxes in natural plankton communities was investigated during the 2005 PeECEIII mesocosm study in Bergen, Norway. Triplicate mesocosms, in which a phytoplankton bloom was induced by nutrient addition, were incubated with 1x (~350 μatm), 2x (~700 μatm), and 3x present day CO₂ (~1050 μatm) levels for 3 weeks. ¹³C labeled bicarbonate was added to all mesocosms to follow the transfer of carbon from dissolved inorganic carbon (DIC) into phytoplankton and subsequently heterotrophic bacteria, zooplankton, and settling particles. Isotope ratios of polar lipid fatty acids (PLFA) were used to infer the biomass and production of phytoplankton and bacteria. Phytoplankton PLFA were enriched within one day after label addition, while it took another 3 days before bacteria showed substantial enrichment. Group-specific primary production measurements revealed that coccolithophores grew faster than green algae and diatoms. Elevated CO₂ had a significant positive effect on post-bloom biomass of green algae, diatoms, and bacteria. A simple model based on measured isotope ratios of phytoplankton and bacteria revealed that CO₂ had no significant effect on the carbon transfer efficiency from phytoplankton to bacteria. There was no indication of enhanced settling based on isotope mixing models during the phytoplankton bloom. Our results suggest that CO₂ effects are most pronounced in the post-bloom phase, under nutrient limitation.