



## **Role of the ubiquitous bacterial family Woeseiaceae for N<sub>2</sub>O production in marine sediments**

Isabella Hinger, Claus Pelikan, and Marc Mußmann

Department of Microbiology and Ecosystem Science, Division of Microbial Ecology, Research Network “Chemistry meets Microbiology”, University of Vienna, Althanstrasse 14, Vienna, A-1090, Austria.

The global warming potential of laughing gas, nitrous oxide (N<sub>2</sub>O) is almost 300 times higher than that of CO<sub>2</sub>. Coastal marine ecosystems receive large amounts of natural and anthropogenic nitrogen such as nitrate through riverine and estuarine input. Biogeochemical cycling of benthic marine nitrogen is driven to a large part by microbial denitrification and nitrification that can lead to substantial releases of N<sub>2</sub>O from marine shelf sediments. However, despite their potentially high impact on benthic N<sub>2</sub>O emissions, the major microbial players are still largely unknown. Recently, the gammaproteobacterial family Woeseiaceae has been identified as abundant core member of microbial communities in global marine sediments. As a common feature published (meta)genomes encode an incomplete denitrification pathway, which includes the subunits for nitrite reduction (*nirS*) and NO reduction (*norB*) to the ozone-depleting greenhouse gas N<sub>2</sub>O. Given their high abundances and widespread occurrence we hypothesize that these bacteria could have significant implications for N<sub>2</sub>O emissions from sediments. However, the production of N<sub>2</sub>O, or rather the anaerobic growth of Woeseiaceae with nitrite has not been shown so far. Using gas chromatography and microrespirometry measurements of N<sub>2</sub>O in pure cultures, we demonstrate whether the currently only available strain of this family, *Woeseia oceani*, produces N<sub>2</sub>O. Further, we use anaerobic growth experiments with *W. oceani* on nitrite and nitric oxide to understand the ecophysiology and role of Woeseiaceae in marine sediments. In addition, based on the metagenomic findings we designed growth media to enrich and isolate new members of the Woeseiaceae from tidal sediment in Normandy/France, where high relative abundances of the target family have been found in earlier studies. Combined with findings from 16S amplicon, metagenomic and metatranscriptomic analyses from various global sediment samples, our study will help to understand the N<sub>2</sub>O production potential and the interaction of Woeseiaceae with other N-cycling microorganisms. These findings are crucial to elucidate the sources and dynamics of marine sediment N<sub>2</sub>O flux to the atmosphere.