

**[C2-2]**

**The Changes in the Bacterial Community Composition Based on  
*amoA/pmoA* and *nirK/nirS* in Lakes and the Baltic Sea**

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In the present study the changes in the composition of the microbial gene pool in the lakes Plußsee and Schöhsee, and the Baltic Sea was studied using functional bacterial genes. Clone libraries were prepared for the monooxygenase genes *amoA/pmoA* (obligatory genes for survival) and nitrite reductase genes *nirK/nirS* (non-obligatory genes for survival). In the evolutionarily related genes for ammonia monooxygenase (AMO) and particulate methane monooxygenase (pMMO), a higher frequency of *pmoA* sequences, mainly belonging to the gammaproteobacterial methane oxidizing bacteria ( $\gamma$ -MOB), was detected. Dominant *amoA* sequences were related to the betaproteobacterial ammonia oxidizing bacteria ( $\beta$ -AOB), no sequences related to *amoA* of the  $\gamma$ -AOB were detected. The deduced amino acid sequences of some clones from lake sediments were distantly related to PmoA from *Crenothrix polyspora*, a filamentous methane oxidizer with an “unusual” methane monooxygenase. In the clone libraries of *nirK* and *nirS*, the dominant sequences of *nirK* from all clone libraries belonged to two distinct phylogenetic clusters, while *nirS* sequences from both lakes were scattered over several clusters throughout the complete phylogenetic tree, and only few sequences from Baltic Sea overlapped with those from freshwater. Comparing the nucleotide sequences and deduced amino acid sequences, the *nirK* and *nirS* sequences of the deduced amino acid were less conserved than those of *amoA* and *pmoA*, which might be an indication of a differential selection pressure over these genes.