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Tracking down sulphate-reducing microorganisms by molecular and isotope-labelling techniques

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Sulphate-reducing microorganisms (SRM) are of great ecological importance for carbon compound degradation and sulphur cycling in many anoxic ecosystems, including marine sediments, peatlands, and oil reservoirs. However, the activity of SRM can result in oil souring and pipeline corrosion and thus is also an economic burden for the oil industry. Molecular diversity surveys based on rRNA genes and dsrAB, genes that encode major subunits of the dissimilatory sulfite reductase, indicate that our view of the natural diversity of SRM (as we know it from cultivation) is far from being complete. This enormous phylogenetic diversity complicates unbiased identification and quantification of SRM by molecular methods such as fluorescence in situ hybridization, real-time PCR or DNA microarrays. Combining these 16S rRNA and dsrAB-based molecular methods with substrate-mediated isotope labelling techniques is a potential solution for identification and functional characterization of yet uncultivated SRM. Using SRM in peatlands as an example, the problems and opportunities of these techniques for diagnosing and monitoring SRM in the environment will be discussed in this talk.