New *Thiomonas* and *Bordetella* strains involved in iron oxidation at a slightly acidic, heavy metal contaminated creek

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Legacy uranium mining in the area of Ronneburg, Germany, resulted in heavy metal contamination of small creeks. Iron rich creek sediments cover a wide pH range from extremely acidic (pH 2.7) over moderately acidic (pH 4.4) to slightly acidic (pH 6.3). In this study, we i) characterized the biogeochemistry of creek sites with different pHs, ii) studied bacterial communities in creek sediments and iii) isolated iron oxidizing bacteria (FeOB) at slightly acidic pH. Sediments were highly contaminated with up to 403 μ g g⁻¹ (dry wt) Zn, 201 μ g g⁻¹ (dry wt) Cu, and 165 μ g g⁻¹ (dry wt) Ni, and with smaller concentrations of up to 4.4 μ g g⁻¹ (dry wt) Cd. Oxic and anoxic in vitro sediment incubations revealed iron oxidation and reduction rates of same magnitude, indicating active iron cycling for all creek sediments regardless of pH. Members of the Betaproteobacteria dominated microbial communities in sediments as shown by 16S rRNA gene cloning and sequencing. High fractions of clones showed ≥97% sequence similarity to reported FeOB or iron reducers (FeRB), e.g., Gallionella ferruginea and Ferritrophicum radicicola (FeOB) or Rhodoferax ferrireducens and Geobacter argillaceus (FeRB), especially in a RNA-derived clone library from slightly acidic creek sediment (pH 6.3). Three novel FeOB strains, Thiomonas sp. strain FB-6 and FB-Cd and Bordetella petrii strain FB-8, were isolated from this sediment under lithoautotrophic, microoxic, pH 5.5 conditions. Due to its high similarity to one RNA-derived clone from this study, FB-6 is likely involved in active iron oxidation in creek sediment. Preliminary work indicated heavy metal tolerance and metabolic versatility for the 3 isolates. Future studies will investigate the mechanisms of metal attenuation by these novel FeOB under slightly acidic pH.

Source apportionment of atmospheric organic aerosol by nuclear magnetic resonance (NMR) spectroscopy: Results from EUCAARI project

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Submicron aerosol samples were collected in nine EUCAARI IOPs site and analysed by means of proton-Nuclear Magnetic Resonance (¹H-NMR) spectroscopy with aim of organic aerosol characterization and source apportionment.. Analogously to more established methodologies employing mass spectrometric techniques, we exploit factor analysis of spectra for the identification of a small number of recurrent chemical classes.

Factor analysis of NMR spectral datasets is already widely used for the analysis of complex organic matrices in several scientific fields, from pharmaceutics to food and medical chemistry. Deconvolution of main spectral profiles within each time series of ¹H-NMR spectra of submicron aerosol samples was conducted using non-negative factor analysis techniques, such as PMF, NMF and MCR.

Some recurrent profiles were identified in different IOPs of EUCAARI project and their contribution to the total mass of OA were quantified. The results of this statistical analysis were compared to those of existing methodologies of factor analysis applied to atmospheric aerosol spectroscopic datasets (AMS) collected in the same period for each measurement campaign.

Our findings indicate that factor analysis applied to NMR atmospheric datasets can efficiently complement AMS in lumping the complex oxidized organic mixtures into chemical classes characterized by specific sources or ageing states. More specifically, NMR spectroscopy provides a better discrimination between aromatic and aliphatic structures, which is critical for the quantification of biomass burning products, and for the discrimination between biogenic and anthropogenic SOA.

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