Molecular genetics and diversity of Bacteria and Archaea in urban, rural and high alpine air

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This study explores the applicability of molecular genetic methods for the characterization of primary biogenic aerosol (PBA) particles in the atmosphere, focusing on Bacteria and Archaea. Samples of fine (<2.5 µm), coarse (>2.5 µm), and total suspended particles were collected at four different German sampling locations: Mt. Zugspitze (high alpine, 2962 m a.s.l.), Hohenpeissenberg (rural, 990 m a.s.l.), Munich and Mainz (urban, 550 m and 150 m a.s.l.).

Investigations of blank and background samples showed that filter materials have to be decontaminated prior to use, and that the sampling and handling procedures have to be carefully controlled to avoid artifacts in the genetic analyses.

From filter aliquots loaded with about one milligram of air particulate matter, DNA could be extracted and genetic sequences could be determined for Bacteria and Archaea in Mainz, and only for Bacteria in the three other locations. Molecular techniques (e.g., DNA sequencing, T-RFLP) were used to determine the identity of the microorganisms, and to estimate their diversity and relative abundances.

Mass fractions of DNA in fine particulate matter (PM2.5) were found to be around ~0.05% in all sampled locations. The average concentration of DNA determined for urban air was on the order of ~7 ng m⁻³, indicating that human adults may inhale about one microgram of DNA per day (corresponding to ~10⁷ haploid human genomes).

There was no obvious difference in the composition of Bacteria present in fine and coarse particulate matter. Most of the bacterial sequences belong to the phyla of Proteobacteria, Actinobacteria, Bacteroidetes and Firmicutes. Among the Proteobacteria all four classes (Alpha-, Beta-, Gamma-, and Deltaproteobacteria) were present in varying amounts (Figure 1).

T-RFLP analysis on bacteria was performed for all locations. Over 80% of the bacterial PM2.5 sequences of Munich, Hohenpeissenberg and Mt. Zugspitze could be matched with about 40% of the T-RF peaks (ranging from 58 to 494 base pairs in length). These results demonstrate that the T-RFLP analysis covered more of the bacterial diversity than the sequence analysis. For the coarse particle samples from Mainz, preliminary results indicate a more diverse bacterial composition than for the other locations.

Archaeal DNA was detected on the coarse particle samples from Mainz but could not yet be retrieved from other samples. First sequence analyses point to high similarities with Archaea and Crenarchaeota environmental sample sequences in the databank of the National Center for Biotechnology Information (NCBI). Besides Pro- and Eukaryotes, Archaea represent the third domain of life and are potentially the most abundant organism group on Earth. They are bacteria-like microorganisms which are mostly found under extreme environmental conditions and have the capability of living in almost all kinds of environments, including ocean water and sediments.

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References