5216 – O+P

GENETIC ANALYSIS AND DIVERSITY OF PRIMARY BIOGENIC AEROSOL PARTICLES.

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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. Samples of fine particulate matter (PM2.5) and total suspended particulates (TSP) have been collected on different types of filter materials at German sampling locations.
From filter aliquots loaded with about one milligram of air particulate matter, DNA could be extracted and genetic sequences could be determined for bacteria, fungi, plants and animals. Molecular techniques (e.g., DNA sequencing, T-RFLP) were used to determine the identity of biological organisms, and to estimate diversities and relative abundances of microorganisms. 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.
Mass fractions of DNA in 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 ~105 haploid human genomes).
Most of the bacterial sequences found in PM2.5 were from Proteobacteria and some from Actinobacteria and Firmicutes. The fungal sequences were characteristic for Ascomycota and Basidiomycotas, which are known to actively discharge spores into the atmosphere. The plant sequences could be attributed to green plants and moss spores, while animal DNA was found only for one unicellular eukaryote (protist).
Over 80% of the 53 bacterial sequences could be matched with about 40% of the 19 T-RF peaks (58 to 494 base pair length) found in the investigated PM2.5 samples. The results demonstrate that the T-RFLP analysis covered more of the bacterial diversity than the sequence analysis.
Shannon-Weaver indices calculated from both sequence and T-RFLP data indicate that the bacterial diversity differs among sampling locations.