

BIOLOGICAL CHARACTERIZATION OF ATMOSPHERIC AEROSOL PARTICLES.

Nowoisky, Janine
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Despres Viviane
Biogeochemistry Department, MPI for Chemistry, P.O. Box 3060, D-55020 Mainz Germany

Cimbal Julia
Biogeochemistry Department, MPI for Chemistry, P.O. Box 3060, D-55020 Mainz Germany

Klose Melanie
Biogeochemistry Department, MPI for Terrestrial Microbiology, Karl-von-Frisch-Strae, D-35043, Marburg Germany

Conrad Ralf
Biogeochemistry Department, MPI for Terrestrial Microbiology, Karl-von-Frisch-Strae, D-35043, Marburg Germany

Andreae Meinrat O.
Biogeochemistry Department, MPI for Chemistry, P.O. Box 3060, D-55020 Mainz Germany

Puschl Ulrich
Biogeochemistry Department, MPI for Chemistry, P.O. Box 3060, D-55020 Mainz Germany

Aerosol particles are of central importance for atmospheric chemistry and physics, climate and public health. A significant fraction of the atmospheric particles are of biological origin, e.g. bacteria, bacterial and fungal spores, pollen, plant and animal fragments, etc. So far, however, the abundance, diversity, sources, properties and effects of biological particles in the atmosphere have not been well characterized. The use of molecular genetic methods resolves many limitations of traditional detection methods for the analysis of biological aerosol particles.

In this study, air filter samples were collected with a High Volume Sampler separating fine and coarse particles (aerodynamic cut-off diameter 2.5µm) over a period of one year 2006/2007 in Mainz, Germany. The samples were analyzed for the presence of fungal, plant, bacterial and archaeal DNA. All PCR products were cloned and several clones sequenced. The sequences were blasted in the National Center for Biotechnology Information databank to find the closest match and determine the taxonomy of the organisms from which the DNA had originated.

Fungal DNA was detected on coarse and fine particle filters. Preliminary results show high taxonomic diversity for the 161 fungal sequences obtained from coarse particle samples. The sequences were characteristic for different groups of Ascomycota and Basidiomycota, which are known to actively discharge spores into the atmosphere. Ten genera within the phylum Basidiomycota were found. Eight of them belong to the class Homobasidiomycetes and some of them include species which can act as plant pathogens or human allergens (e.g. *Stereum*). Few sequences belong to the genus *Itersonilia* within in the class of the Heterobasidiomycetes. Among them are typical plant pathogens. Further the allergenic genus *Sporobolomyces* was detected from the Basidiomycota class Urediniomycetes. The sequences within the Ascomycota belong to the genera *Cladosporium* (an important allergen) and *Epicoccum* (a soil and litter fungus and allergen) as well as to some other genera which include plant pathogen species (e.g. *Stemphylium*).

The plant sequences could be attributed to green plants, within the families Betulaceae (e.g. birch), Poaceae (e.g. barley), Plantagiaceae (e.g. plantain), Urticaceae (e.g. nettle), Taxaceae (e.g. yew), Cupressaceae (e.g. fir) and moss spores within the Bryophyta moss superclasses.

Bacterial sequences could be attributed to Proteobacteria, Actinobacteria and Bacteroidetes, which are known to be widespread in the atmosphere.

Archaeal DNA could also be detected on the coarse particle filters and the first sequence analysis points to high similarity with Archaea and Crenarchaeota environmental sample sequences. 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 different kinds of soil, ocean water and sediments.