

Metaproteomic analysis of atmospheric aerosol samples

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Metaproteomic analysis of air particulate matter provides information about the abundance and properties of bioaerosols in the atmosphere and their influence on climate and public health.

In this study, we developed and applied bioanalytical methods for an efficient extraction and analysis of proteins from air filter samples. Total suspended, coarse, and fine particulate matter samples have been collected in Mainz, Germany. Figure 1 provides an overview of the developed method for the identification of proteins in ambient aerosol samples. Size exclusion chromatography was used to remove matrix components, and SDS-PAGE was applied for protein fractionation according to molecular size, followed by in-gel digestion and LC-MS/MS analysis of peptides using hybrid Quadrupole-Orbitrap MS. Maxquant software and the Swiss-Prot database were used for analysis of proteomic data.

Extraction solvents were substantially optimized to overcome the interaction between proteins and filter material and achieve high protein recoveries. An interference of soot in air filter sample extracts hampered the measurement of total protein content by BCA assay, which could be minimized by performing size-exclusion chromatography of air filter sample extracts.

Proteins in ambient air particulate matter were found to mainly originate from plants, microorganisms, and animals, which is in line with the major categories of primary biological aerosol particles (PBAP). Allergic pollen proteins, e.g., from perennial ryegrass, were found in fine particles, which can penetrate deep into the lower part of the respiratory tract. In addition, the molecular size dependent analysis of proteins extracted from the aerosol samples revealed the presence of fragmented proteins in atmospheric aerosols.

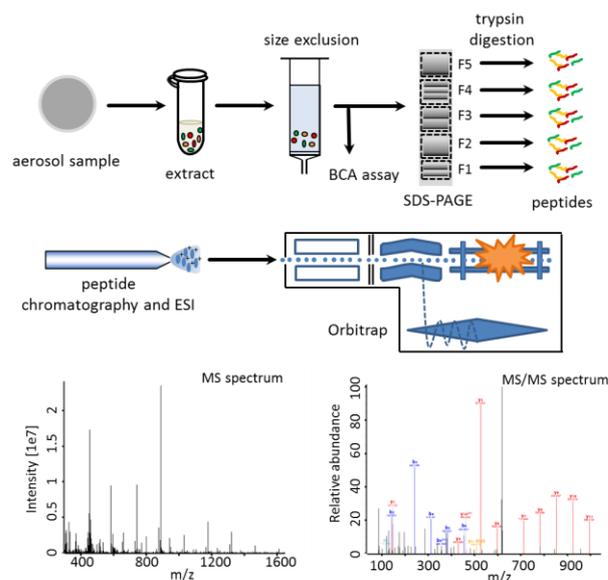


Figure 1. Schematic overview of the developed method for the metaproteomic analysis of atmospheric aerosol samples

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