Correlating bioaerosol load with PM2.5 and PM10cf concentrations: a comparison between natural desert and urban fringe aerosols

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Abstract

Seasonal allergic and respiratory health complaints are correlated with elevated particulate matter concentrations. Many of these allergic and asthmatic responses may be enhanced when chemical and biological constituents of particulate matter are combined together. Because of these associations and also the regulatory and health related impacts of monitoring PM2.5 and PM10 concentrations, it is crucial to investigate spatial and temporal differences in the urban fringe to understand the impacts on the Phoenix, Arizona metropolitan area during winter, spring, and summer seasons. Elemental carbon and organic ions were measured to determine the relative importance of anthropogenic sources, such as traffic, fuel at the sampling sites. Total particulate concentrations were used as a surrogate measure of total particulate concentration within the PM2.5 and PM10 (or larger sizes) size ranges. In all seasons, coarse particle concentrations at the urban fringe were consistently higher than concentrations at the natural desert. When high anthropogenic particulate matter was not present from the data set, a positive significant correlation (p < 0.05) was found between the total mass load and particulate organic and nodule matter in the fine fraction. As an additional study, we developed a new method to identify the type and density of airborne biogenic material (concentration) to identify particulate matter. Both sites contained allergenic organisms. Some groups of organisms were exclusive to only one of the sites. The natural desert contained more species of Fusarium and Penicillium fungi and the urban fringe contained more species of green plants (many of aphidophytes origin), suggesting that the biological loading at each site was different due to local influences.

Introduction/Methods

We compared the biological fraction of particulate matter between aerosols collected at a natural desert site and aerosols collected at the urban fringe of the Phoenix Metro Area (Figure 1). It was hypothesized that the urban fringe would have higher biological concentration than the natural desert, that the biological concentration would increase with particulate matter concentration, and that there would be differences in the types of bioaerosols at the two locations. In this study, PM2.5 and PM10 (or larger) were collected at a natural desert site and an urban fringe site for a year. We compared the biological and abiotic loading of fine and coarse particulate matter for different seasons of the year. The samples were analyzed for the composition of the bioaerosol and the nodule content of the bioaerosol. The results showed a significant correlation (p < 0.05) between the fine fraction of anthropogenic species and the total particulate matter concentration of the urban fringe.

Results

To explore the biological composition of the desert, a correlation analysis was performed between the coarse fraction of anthropogenic species and organic matter concentration (Figure 2). Correlation analysis revealed a significant correlation (p < 0.05) between the fine fraction of anthropogenic species and organic matter concentration at the fine fraction.

Table 1: Expanded list of the biogenic species detected by the 16S rDNA sequencing, that were closely related to the species isolated from a PM10 aerosol sample at both sites, segregated into four of the major groups of fungi (Hyphoe included in the phyllophaga flock).

Figure 3: Chlorophyceae: Chlorophaeae (Chlorophyta), forming a major part of the total bioaerosol load, most closely related to the species isolated from a PM10 aerosol sample at both sites, segregated into four of the major groups of fungi (Hyphoe included in the phyllophaga flock).

Figure 4: Molecular change in the 16S rDNA sequence of the bioaerosol species detected by the 16S rDNA sequencing, that were closely related to the species isolated from a PM10 aerosol sample at both sites, segregated into four of the major groups of fungi (Hyphoe included in the phyllophaga flock).

REFERENCES


Figure 5: Phylogenetic tree of 16S rDNA sequences obtained from a known PM10 aerosol sample at the natural desert (ND) and the urban fringe (UF). The scale corresponds to 0.1 substitutions per nucleotide position.