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

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Abstract

Seasonal allergies and microbial mediated respiratory diseases can coincide 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 interests of monitoring PM2.5, separately from total PM10, the biological loading between the fine (dp<2.5?m) and coarse (2.5?m<dp<10?m) size ranges of particulate matter was studied. To investigate spatial and seasonal differences, 24-hour fine and coarse particulate matter fractions were collected at a natural desert area and an urban fringe site located in the expanding Phoenix, Arizona metropolitan area during winter, spring, and summer seasons. Elemental carbon and inorganic ions were measured to determine the relative influence that anthropogenic sources, such as traffic, had at the sampling sites. Total protein concentration was used as a surrogate measure of total biological concentration within the PM2.5 and PM10cf (coarse fraction) size ranges. In all seasons, coarse protein concentrations at the urban fringe was consistently higher than concentrations at the natural desert. When high anthropogenic particulate matter events were separated from the data set, a positive significant correlation ($p<0.05$) was found between protein and total mass and protein and organic matter in the course fraction, but not in the fine fraction. An 18S rDNA clone library was developed from PM10 aerosol samples to characterize the type and diversity of airborne biological material (nonbacterial) existing in ambient 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 Basidiomycota fungi and the urban fringe contained more species of green plants (many of agricultural 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 a higher biological concentration than the natural desert, that the biological concentration would increase with particulate matter concentrations, and that there would be differences in the types of bioaerosols at the two locations. In this study, PM2.5 and PM10cf samples were collected at a natural desert area and an urban fringe location around the expanding Phoenix metropolitan area to characterize the biological and abiotic loading of fine and coarse particulate matter for different seasons of the year. During the summer season, an 18S rDNA clone library was developed from PM10 aerosol samples to compare the eukaryotic (nonbacterial), bioaerosol diversity and identify potential allergens within ambient particulate matter at the urban fringe and natural desert. The clone library is a bio-molecular method recently developed in other fields of environmental engineering (soil, water, and wastewater medias) and provides a broader means of identification than culture-based studies.

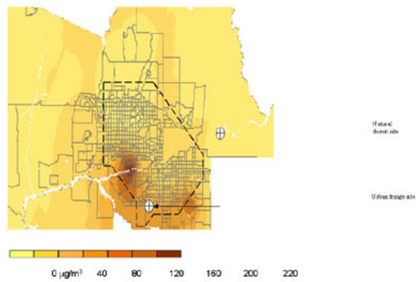


Figure 1: Maximum 24-average PM10 concentrations (2001) in Phoenix Metro area (GIS map based on data from ADEQ, 2002; MCESD, 2002). Average population density within the encompassed area of the dashed line is greater than 800 people/km².

Results

To separate the anthropogenic generated components, which have no biological content, from the total particulate matter and focus on the natural source of particulate matter fraction that can have a biological component and possibly a significant correlation with protein concentrations, the particulate matter collected was divided into anthropogenic species, organic matter, and residual (Figure 2). Anthropogenic species and organic matter concentrations were both higher ($p<0.05$) in the fine fraction than in the coarse fraction both on a basis of mass concentration and percentage of total particulate matter at the natural desert. In contrast, there was no significant difference ($p<0.05$) between the two size ranges of anthropogenic species and organic matter concentrations at the urban fringe.

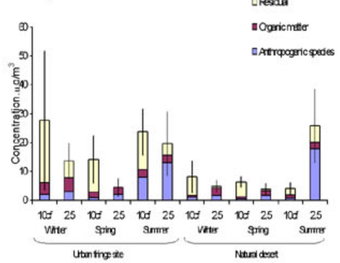
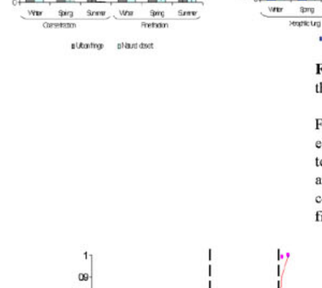
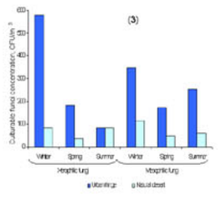
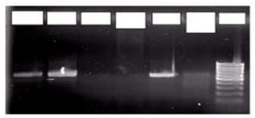


Figure 2: Average particulate matter concentrations, consisting of three major groups: anthropogenic species (SO_4^-, Cl^-, NO_3^-, NH_4^+, and elemental carbon), organic matter, and residual. The standard deviation of total particulate matter concentrations for the five different sampling days during each season are shown.



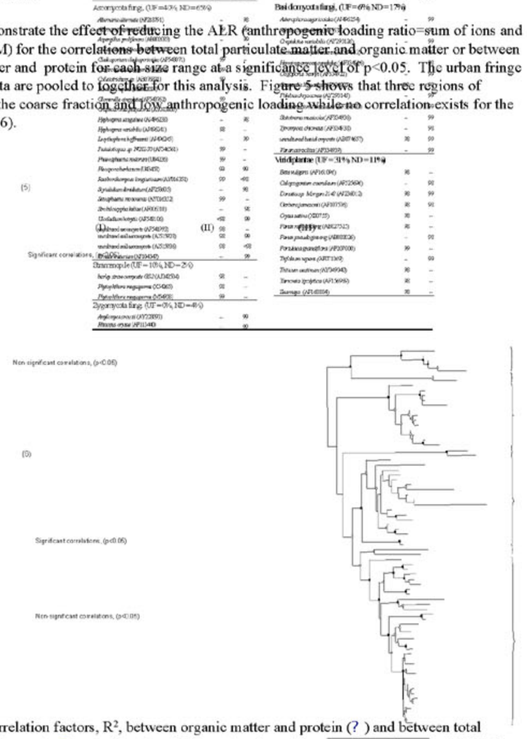
In addition to PM10 concentration, Protein concentration in PM10 samples (a surrogate measure of biomass) were consistently higher at the urban fringe than in the natural desert (Figure 3). Culturable mesophilic and xerophilic fungi concentrations were also higher at the urban fringe than the natural desert site (Figure 4).





Figures 3 and 4: Biological fraction ~~of PM10 is greater in aerosols located in Phoenix's urban~~ fringe than the natural desert aerosols.

Figures 5 and 6 demonstrate the effect of reducing the AER (anthropogenic loading ratio=sum of ions and elemental carbon/ PM) for the correlations between total particulate matter and organic matter or between total particulate matter and protein for each size range at a significance level of $p<0.05$. The urban fringe and natural desert data are pooled together for this analysis. Figure 5 shows that three regions of correlation exist for the coarse fraction and low anthropogenic loading while no correlation exists for the fine fraction (Figure 6).



Figures 5 and 6: Correlation factors, R^2, between organic matter and protein (?) and between total particulate matter and protein (?), as a function of decreasing the anthropogenic loading ratio (ALR) for coarse particulate matter (5) and fine particulate matter (6). Correlation with a significance level of $p<0.05$ is in the region above the line (—). Non-significant correlations are in the region below the line.

Results Cont: Bioaerosol Identification

PCR amplification (Figure 7) and cloning was performed on PM10 aerosol samples collected at the urban fringe and natural desert site. Seven different phyla of eukaryotic (excludes bacteria) organisms (including fragments of some organisms larger than 10μm) were identified including: (1) Stramenopile (water molds and algae), (2) Zygomycota fungi, (3) Viridiplantae (green plants), (4) Arthropoda (insects), (5) Basidiomycota fungi, (6) Glomeromycota fungi, and (7) Ascomycota fungi. Table 1 and Figure 8 presents the list species identified in the five of the seven phyla that contained species that most closely match (>98%) with the sequences isolated from a PM10 aerosol sample at both sites, defined by the 18s rDNA encoding gene.

Figure 7. Gel electrophoresis image representing PCR products of aerosol sample DNA from the urban fringe and natural desert sites. The bands and the pure fungi positive control are lined up at a 561 bp length.

Table 1. Expanded list of the eukaryotic species, defined by the 18s rDNA encoding gene, that most closely match (>98% similarity) with the sequences isolated from a PM10 aerosol sample at both sites, organized into five of seven of the major groups of phyla included in the phylogenetic tree.

The two sites contained distinct differences in biological species within PM10 samples: the urban fringe had more plant species (likely from an agricultural, municipal, or residential source) and fewer species of Basidiomycota fungi compared to the natural desert site, indicating that the biological loading at each site was locally influenced.

Figure 8. Phylogenetic tree of 18S rDNA sequences obtained from a three hour PM10 aerosol samples at the natural desert (ND) and the urban fringe (UF). The scale corresponds to 0.1 substitutions per nucleotide postion.

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