

Executive Summary

Background.

Recently, using a high-density 16S rRNA phylogenetic microarray it has been demonstrated that urban aerosols in two cities in Texas harbored highly diverse communities of bacterial taxa. These populations were so complex that they approximated the richness of bacterial diversity detected in some soil microbial populations (approximately 1,800 bacterial phylotypes [1]). More recently, we have demonstrated that polymicrobial communities composed of multiple pathogens exist in the airways of patients with a variety of respiratory disorders including ventilator-associated pneumonia [2], cystic fibrosis (CF; Cox *et al*, In review, PLoS One;[1]), chronic obstructive pulmonary disease (COPD;[2]) and asthma (In review; AJCCRM). We hypothesize that inhaled aerosolized microbial diversity seeds the airways of patients predisposed to colonization (e.g. asthmatics, CF patients) with organisms which may contribute to incidence and severity of pulmonary pathogenesis in these vulnerable patient populations.

In a survey conducted in 2006 by the CDC (<http://www.cdc.gov/nchs/data/ad/ad381.pdf>), Massachusetts had the highest prevalence of asthma amongst children aged 0-17 years old (12.1%), Pennsylvania and Michigan also had relatively high rates of 9.9 and 9.4% respectively. However, the rate of asthma prevalence in this age group was only 7.1% in California. The factors that underlie these rates and the increasing prevalence of asthma in the developed world are undoubtedly multi-faceted. However, we hypothesize that in addition to host genetic factors, environmental aspects such as the microbial composition of the air may also contribute to differential rates of asthma prevalence at geographically distinct sites.

Methods.

Bacterial community composition of aerosol (collected in 2003 – 2004 through a Homeland security bioterrorism program) and asthmatic airway respiratory samples (collected in an NIH-supported multi-center trial) was determined using a recently designed novel high-density 16S rRNA microarray, the PhyloChip [3, 4]. This tool uses amplified 16S rRNA genes from a mixed bacterial population, which is assayed in parallel by the microarray

that contains 500,000 probes and can detect approximately 8,500 bacterial taxa (defined as clusters of bacterial 16S rRNA signature sequences sharing at least 99% sequence identity). This tool can detect low abundance species (0.01% of the community) even when the community is dominated by a small number of highly abundant organisms.

Results

The objective of the proposed study was to compare seasonal aerosol samples collected during Spring, Summer, Fall and Winter from 3 US cities with high prevalence of asthma, Boston, Philadelphia and Detroit, to determine the effect of seasonal variation on bacterial urban aerosol composition. Bacterial community composition varied across sites but appeared to be more associated with specific geographic location than by seasonality. The primary phyla detected in these samples represented a vast diversity of bacteria and included a number of phyla, members of which are common inhabitants of human niches, including the respiratory tract of patients predisposed to airway colonization. A comparison of bacterial communities from these cities (collected in the Spring) to those detected in the same season in San Francisco revealed a core of bacteria common to all samples. Nonetheless, geographic-based differences in aerosol community composition were detected between San Franciscan and East Coast samples, suggesting that habitation at a specific site may result in exposure to a distinct community of bacteria and, potentially contribute to geographic-specific differences in airway disease prevalence. Comparative analysis of communities detected in urban aerosols and those found in the airways of asthmatics demonstrated a large overlap in these communities, supporting the notion that bacterial species present in environmental aerosols may serve as an inoculum for human respiratory surfaces.

Conclusions.

The diversity of bacteria detected in urban aerosols appears to be location-dependent rather than season, potentially acting as a source of geographic-specific microbial exposures. The large overlap in aerosol and airway bacterial communities, suggest that bacteria in inhaled air may serve as a reservoir for human inoculation, particularly for individuals predisposed to airway colonization due to underlying disease.