

Abdel Hameed, A.A., M.I. Khoder, Y.H. Ibrahim, Y. Saeed, M.E. Osman, S. Ghanem, 2011. Study on some factors affecting survivability of airborne fungi. *Science of the Total Environment* 414 (2012) 696–700.

The aim of the present study was to investigate the effect of some air pollutants and meteorological parameters on the survivability of airborne fungi. Fungi were collected by using a slit impactor sampler calibrated to draw 20 L/min, for 3 min. Nitrogen dioxide (NO<sub>2</sub>), sulfur dioxide (SO<sub>2</sub>), particulate matter (PM), relative humidity (RH %), temperature (T°C) and wind speed (WS) were also measured. Air samples were taken during the period from March 2006 to February 2007. Fungal concentrations ranged between 45 and 451 CFU/m<sup>3</sup> with an annual mean concentration of 216 CFU/m<sup>3</sup>. The lowest fungal concentration was found in the summer, however the highest one was found in the autumn. NO<sub>2</sub>, SO<sub>2</sub> and PM averaged 83.66 µg/m<sup>3</sup>, 67.01 µg/m<sup>3</sup>, and 237.69 µg/m<sup>3</sup>, respectively. T°C was positively and negatively correlated with *Aspergillus* (P=0.000) and *Penicillium* (P=0.007), respectively. RH% was positively correlated with total fungi (P=0.001), *Aspergillus* (P =0.002) and *Cladosporium* (P =0.047). Multiple regression analysis showed that T°C and RH% were the most predicted variants. Non-significant correlations were found between fungal concentrations and air pollutants. Meteorological parameters were the critical factors affecting fungal survivability.

Abe, Keiko, 1993. A Method for Numerical Characterization of Indoor Climates by a Biosensor using a Xerophilic Fungus. *Indoor Air* 1993, 3: 344-348.

A 'fungal index' is proposed as a new climate parameter for the characterization of the indoor environment. The index quantifies the environmental conditions in relation to the ability of fungi to grow by means of the response of a xerophilic fungus *Eurotium herbariorum*. The growth response of this fungus was found to be climate-dependent. The indoor environment in a residential building in Japan (1991-1992) was quantitatively assessed by this approach. In the assessment, the variation in microclimate, which differs greatly within and between rooms, could be demonstrated

Abe, K, 2010. Assessment of the environmental conditions in a museum storehouse by use of a fungal index. *International Biodeterioration & Biodegradation* 64 (2010) 32–40.

Fungal contamination (foxing) was detected on a painting stored in an art museum. The internal environments were assessed using a fungal index. The index is a biological climate-parameter, which represents the environmental capacity to allow fungal growth. To determine the index, fungal detectors encapsulating the spores of sensor fungi were placed at the site being examined. The growth response, germination of the spores and hyphal extension, of xerophilic sensor fungi was observed in the storehouse. The values of fungal index predicted propagation of fungi, although dehumidifiers were already in use. Next year, the number of dehumidifiers installed in the storehouse was increased from 3 to 8. After the number of dehumidifiers was increased, the indices were below the detectable limit in the storehouse indicating no fungal contamination will occur. The sensor fungi used in those assessments were five xerophilic and two non-xerophilic strains. In the assessment before countermeasures were taken, *Aspergillus penicillioides* showed the highest growth response among the sensor fungi in the fungal detector exposed in the room where the contaminated painting was stored. *Eurotium herbariorum* showed the highest growth response in other rooms. These two strains were selected as the sensor fungi for assessments of museum environments.

Abe, K, 2011. Assessment of home environments with a fungal index using hydrophilic and xerophilic fungi as biologic sensors. *Indoor Air* 2012; 22: 173–185

Previously, the author proposed a fungal index that quantifies the capacity for fungal growth in a test environment where a device (fungal detector) encapsulating spores of a xerophilic sensor fungus *Eurotium herbariorum* was placed. It was also found that an extremely xerophilic fungus, *Aspergillus penicillioides*, was suitable as a sensor fungus at sites with lower relative humidity (RH). In this report, the hydrophilic fungus *Alternaria alternata* was added to sensor fungi for the determination of the index in extremely humid environments. Measurements of the index and observations of the formation of spores by the sensor fungi were made in stable climates in moisture chambers, under natural conditions in homes, and in bathrooms prepared in an artificial climate chamber. Higher index values and earlier sporulation were obtained at higher RH in stable climates. The hydrophilic *Alt. alternata* showed the greatest response at 100% and 97.3% RH, the moderately xerophilic *Eur. herbariorum*, at 94%, 84%, and 75% RH, and the extremely xerophilic *Asp. penicillioides*, at 71% RH. In homes, the hydrophilic fungus was most active in water-usage areas, and the xerophilic fungi were most active in non-water-usage areas. Sporulation was observed on sensor fungi in fungal

detectors placed in rooms where the index exceeded 18 ru/week after one-month exposure. Sites where the index exceeded 18 ru/week were referred to as damp, where fungal contamination seems to be unavoidable. Evaluations of ventilation systems in bathrooms with extremely humid climates showed typical examples of a countermeasure to fungal contamination.

Abraham, Michael H., Rachel Kumarsingh J. Enrique Cometto-Muniz á William S. Cain, 1998. Microbiology of the Built Environment Literature Database Curation Process. *Arch Toxicol* (1998) 72: 227-232.

Nasal pungency thresholds (NPT) in man have been determined by Cometto-Muniz and Cain for 44 varied compounds, including esters, aldehydes, ketones, alcohols, carboxylic acids, aromatic hydrocarbons and pyridine. With the exclusion of acetic acid, 43 of these NPT values are well correlated through the general linear free energy equation of Abraham, leading to the algorithm, (please see hardcopy) where the independent variables are solute descriptors:  $\pi$  is the dipolarity/polarizability,  $RaH$  and  $RbH$  are the overall or effective hydrogen-bond acidity and basicity, and  $L16$  is the solute Ostwald solubility coefficient on hexadecane at 25 °C. Surprisingly, the aliphatic aldehydes and carboxylic acids fit the correlation and with respect to nasal pungency thresholds in man for brief (1± 3 s) presentations must be regarded as 'nonreactive' compounds. It is suggested mere transport of the compound from the air stream to the receptor area largely determines the potency to produce pungency. Various chemical properties of the receptor area are deduced from the coefficients in Eq. i.

Abraham JH, Gold DR, Dockery DW, Ryan L, Park J-H, Milton DK 2005. Within-Home versus Between-Home Variability of House Dust Endotoxin in a Birth Cohort. *Environ Health Perspect* 113:1516-1521

Endotoxin exposure has been proposed as an environmental determinant of allergen responses in children. To better understand the implications of using a single measurement of house dust endotoxin to characterize exposure in the first year of life, we evaluated room-specific within-home and between-home variability in dust endotoxin obtained from 470 households in Boston, Massachusetts. Homes were sampled up to two times over 5-11 months. We analyzed 1,287 dust samples from the kitchen, family room, and baby's bedroom for endotoxin. We fit a mixed-effects model to estimate mean levels and the variation of endotoxin between homes, between rooms, and between sampling times. Endotoxin ranged from 2 to 1,945 units per milligram of dust. Levels were highest during summer and lowest in the winter. Mean endotoxin levels varied significantly from room to room. Cross-sectionally, endotoxin was moderately correlated between family room and bedroom floor ( $r = 0.30$ ), between family room and kitchen ( $r = 0.32$ ), and between kitchen and bedroom ( $r = 0.42$ ). Adjusting for season, the correlation of endotoxin levels within homes over time was 0.65 for both the bedroom and kitchen and 0.54 for the family room. The temporal within-home variance of endotoxin was lowest for bedroom floor samples and highest for kitchen samples. Between-home variance was lowest in the family room and highest for kitchen samples. Adjusting for season, within-home variation was less than between-home variation for all three rooms. These results suggest that room-to-room and home-to-home differences in endotoxin influence the total variability more than factors affecting endotoxin levels within a room over time.

Adams, Rachel I, Marzia Miletto, John W Taylor and Thomas D Bruns, 2013. Dispersal in microbes: fungi in indoor air are dominated by outdoor air and show dispersal limitation at short distances. *The ISME Journal* (2013), 1–12.

The indoor microbiome is a complex system that is thought to depend on dispersal from the outdoor biome and the occupants' microbiome combined with selective pressures imposed by the occupants' behaviors and the building itself. We set out to determine the pattern of fungal diversity and composition in indoor air on a local scale and to identify processes behind that pattern. We surveyed airborne fungal assemblages within 1-month time periods at two seasons, with high replication, indoors and outdoors, within and across standardized residences at a university housing facility. Fungal assemblages indoors were diverse and strongly determined by dispersal from outdoors, and no fungal taxa were found as indicators of indoor air. There was a seasonal effect on the fungi found in both indoor and outdoor air, and quantitatively more fungal biomass was detected outdoors than indoors. A strong signal of isolation by distance existed in both outdoor and indoor airborne fungal assemblages, despite the small geographic scale in which this study was undertaken (500 m). Moreover, room and occupant behavior had no detectable effect on the fungi found in indoor air. These results show that at the local level, outdoor air fungi dominate the patterning of indoor air. More broadly,

they provide additional support for the growing evidence that dispersal limitation, even on small geographic scales, is a key process in structuring the often-observed distance–decay biogeographic pattern in microbial communities.

Adams RI, Miletto M, Lindow SE, Taylor JW, Bruns TD (2014) Airborne Bacterial Communities in Residences: Similarities and Differences with Fungi. *PLoS ONE* 9(3): e91283. doi:10.1371/journal.pone.0091283

Genetic analysis of indoor air has uncovered a rich microbial presence, but rarely have both the bacterial and fungal components been examined in the same samples. Here we present a study that examined the bacterial component of passively settled microbes from both indoor and outdoor air over a discrete time period and for which the fungal component has already been reported. Dust was allowed to passively settle in five common locations around a home 2 living room, bedroom, bathroom, kitchen, and balcony 2 at different dwellings within a university-housing complex for a one-month period at two time points, once in summer and again in winter. We amplified the bacterial 16S rRNA gene in these samples and analyzed them with high-throughput sequencing. Like fungal OTU-richness, bacterial OTU-richness was higher outdoors than indoors and was invariant across different indoor room types. While fungal composition was structured largely by season and residential unit, bacterial composition varied by residential unit and room type. Bacteria from putative outdoor sources, such as *Sphingomonas* and *Deinococcus*, comprised a large percentage of the balcony samples, while human-associated taxa comprised a large percentage of the indoor samples. Abundant outdoor bacterial taxa were also observed indoors, but the reverse was not true; this is unlike fungi, in which the taxa abundant indoors were also well-represented outdoors. Moreover, there was a partial association of bacterial composition and geographic distance, such that samples separated by even a few hundred meters tended to have greater compositional differences than samples closer together in space, a pattern also observed for fungi. These data show that while the outdoor source for indoor bacteria and fungi varies in both space and time, humans provide a strong and homogenizing effect on indoor bacterial bioaerosols, a pattern not observed in fungi.

Agrawal, Anurodh S. , Mehuli Sarkar, Sekhar Chakrabarti, K. Rajendran, Harpreet Kaur, Akhilesh C. Mishra, Mrinal K. Chatterjee, Trailokya N. Naik, Mandeep S. Chadha and Mamta Chawla-Sarkar, 2009. Comparative evaluation of real-time PCR and conventional RT-PCR during a 2 year surveillance for influenza and respiratory syncytial virus among children with acute respiratory infections in Kolkata, India, reveals a distinct seasonality of infection. *Journal of Medical Microbiology* (2009), 58, 1616-1622.

Acute respiratory tract infections (ARTIs) are one of the most common causes of morbidity and mortality in young children worldwide. Influenza virus and respiratory syncytial virus (RSV) are the predominant aetiological agents during seasonal epidemics, and thus rapid and sensitive molecular tests for screening for such agents and timely identification of epidemics are required. This study compared real-time quantitative PCR (qPCR) with conventional RT-PCR for parallel identification of influenza A virus (IAV) or influenza B virus (IBV) and RSV. A total of 1091 respiratory samples was examined from children with suspected ARTIs between January 2007 and December 2008. Of these, 275 (25.21 %) were positive for either influenza or RSV by PCR compared with 262 (24.01%) positive by RT-PCR. Overall, IAV, IBV and RSV were detected in 121 (11.09 %), 59 (5.41 %) and 95 (8.71 %) samples, respectively. In spite of overlapping clinical symptoms, RSV and influenza virus showed distinct seasonal peaks. IAV correlated positively and RSV negatively with rainfall and temperature. No distinct seasonality was observed in IBV infections. This is, to the best of our knowledge, the first report of a systemic surveillance of respiratory viruses with seasonal correlation and prevalence rates from eastern India. This 2 year comparative analysis also confirmed the feasibility of using qPCR in developing countries, which will not only improve the scope for prevention of epidemics, but will also provide crucial epidemiological data from tropical regions.

Aliabai, Amir A., Steven N. Rogak, Karen H. Bartlett, and Sheldon I. Green, 2011. Preventing Airborne Disease Transmission: Review of Methods for Ventilation Design in Health Care Facilities. *SAGE-Hindawi Access to Research*, Volume 2011, Article ID 124064, 21 pages doi:10.4061/2011/124064

Health care facility ventilation design greatly affects disease transmission by aerosols. The desire to control infection in hospitals and at the same time to reduce their carbon footprint motivates the use of unconventional solutions for building design and associated control measures. This paper considers indoor sources and types of infectious aerosols, and pathogen viability and infectivity behaviors in response to environmental conditions. Aerosol dispersion, heat and mass transfer, deposition in the respiratory tract, and infection mechanisms are discussed, with an

emphasis on experimental and modeling approaches. Key building design parameters are described that include types of ventilation systems (mixing, displacement, natural and hybrid), air exchange rate, temperature and relative humidity, air flow distribution structure, occupancy, engineered disinfection of air (filtration and UV radiation), and architectural programming (source and activity management) for health care facilities. The paper describes major findings and suggests future research needs in methods for ventilation design of health care facilities to prevent airborne infection risk.

Amend, Anthony S. Keith A. Seifert, Robert Samson, Thomas D. Bruns Indoor fungal composition is geographically patterned and more diverse in temperate zones than in the tropics. *Proceedings of the National Academy of Sciences*, Vol. 107, No. 31. (3 August 2010), pp. 13748-13753

Fungi are ubiquitous components of indoor human environments, where most contact between humans and microbes occurs. The majority of these organisms apparently play a neutral role, but some are detrimental to human lifestyles and health. Recent studies that used culture-independent sampling methods demonstrated a high diversity of indoor fungi distinct from that of outdoor environments. Others have shown temporal fluctuations of fungal assemblages in human environments and modest correlations with human activity, but global-scale patterns have not been examined, despite the manifest significance of biogeography in other microbial systems. Here we present a global survey of fungi from indoor environments ( $n = 72$ ), using both taxonomic and phylogeny-informative molecular markers to determine whether global or local indoor factors determine indoor fungal composition. Contrary to common ecological patterns, we show that fungal diversity is significantly higher in temperate zones than in the tropics, with distance from the equator being the best predictor of phylogenetic community similarity. Fungal composition is significantly auto-correlated at the national and hemispheric spatial scales. Remarkably, building function has no significant effect on indoor fungal composition, despite stark contrasts between architecture and materials of some buildings in close proximity. Distribution of individual taxa is significantly range- and latitude-limited compared with a null model of randomized distribution. Our results suggest that factors driving fungal composition are primarily global rather than mediated by building design or function.

Andersen, Birgitte, Jens C. Frisvad, Ib Søndergaard, Ib S. Rasmussen, and Lisbeth S. Larsen, 2011. Associations between Fungal Species and Water-Damaged Building Materials. *Applied and Environmental Microbiology*, June 2011, p. 4180-4188 Vol. 77, No. 12,

Fungal growth in damp or water-damaged buildings worldwide is an increasing problem, which has adverse effects on both the occupants and the buildings. Air sampling alone in moldy buildings does not reveal the full diversity of fungal species growing on building materials. One aim of this study was to estimate the qualitative and quantitative diversity of fungi growing on damp or water-damaged building materials. Another was to determine if associations exist between the most commonly found fungal species and different types of materials. More than 5,300 surface samples were taken by means of V8 contact plates from materials with visible fungal growth. Fungal identifications and information on building material components were analyzed using multivariate statistic methods to determine associations between fungi and material components. The results confirmed that *Penicillium chrysogenum* and *Aspergillus versicolor* are the most common fungal species in water-damaged buildings. The results also showed *Chaetomium* spp., *Acremonium* spp., and *Ulocladium* spp. to be very common on damp building materials. Analyses show that associated mycobiotas exist on different building materials. Associations were found between (i) *Acremonium* spp., *Penicillium chrysogenum*, *Stachybotrys* spp., *Ulocladium* spp., and gypsum and wallpaper, (ii) *Arthrinium phaeospermum*, *Aureobasidium pullulans*, *Cladosporium herbarum*, *Trichoderma* spp., yeasts, and different types of wood and plywood, and (iii) *Aspergillus fumigatus*, *Aspergillus melleus*, *Aspergillus niger*, *Aspergillus ochraceus*, *Chaetomium* spp., *Mucor racemosus*, *Mucor spinosus*, and concrete and other floor-related materials. These results can be used to develop new and resistant building materials and relevant allergen extracts and to help focus research on relevant mycotoxins, microbial volatile organic compounds (MVOCs), and microparticles released into the indoor environment.

Anderson, Glenn Anderson and Enzo A. Palombo, 2009. Microbial contamination of computer keyboards in a university setting. *Am J Infect Control* 2009;37:507-9

The keyboards of multiple-user (student) and single-user (staff) computers located on a university campus were sampled to assess microbial contamination. The average number of microorganisms present on multiple-user computer keyboards was significantly greater than on single-user keyboards, and the number of keyboards harboring potential pathogens was also greater for multiple-user computers. It is recommended that regular cleaning and disinfection of computers be used to reduce the microbial load, especially for multiple-user workstations.

Angenent, Lergus T., Scott T. Kelley, Allison St. Amand, Norman R. Pace, and Mark T. Hernandez, 2005. Molecular identification of potential pathogens in water and air of a hospital therapy pool. *PNAS* 102:13, pp. 4860-4865.

Indoor warm-water therapy pool workers in a Midwestern regional hospital were diagnosed with non-tuberculosis pulmonary hypersensitive pneumonitis and *Mycobacterium avium* infections. In response, we conducted a multiseason survey of microorganisms present in this therapy pool water, in biofilms associated with the pool containment walls, and in air immediately above the pool. The survey used culture, microscopy, and culture-independent molecular phylogenetic analyses. Although outfitted with a state-of-the-art UV-peroxide disinfection system, the numbers of bacteria in the therapy pool water were relatively high compared with the potable water used to fill the pool. Regardless of the source, direct microscopic counts of microbes were routinely ~1,000 times greater than conventional plate counts. Analysis of clone libraries of small subunit rRNA genes from environmental DNA provided phylogenetic diversity estimates of the microorganisms collected in and above the pool. A survey of >1,300 rRNA genes yielded a total of 628 unique sequences, the most common of which was nearly identical to that of *M. avium* strains. The high proportion of clones with different *Mycobacterium* spp. rRNA genes suggested that such organisms comprised a significant fraction of microbes in the pool water (to >30%) and preferentially partition into aerosols (to >80%) relative to other waterborne bacteria present. The results of the study strongly validate aerosol partitioning as a mechanism for disease transfer in these environments. The results also show that culture protocols currently used by public health facilities and agencies are seriously inadequate for the detection and enumeration of potential pathogens.

Araki, Atsuko, Toshio Kawai, Yoko Eitaki, Ayako Kanazawa, Kanehisa Morimoto, Kunio Nakayama, Eiji Shibata, Masatoshi Tanaka, Tomoko Takigawa, Takesumi Yoshimura, Hisao Chikara, Yasuaki Saijo, Reiko Kishi, 2010. Relationship between selected indoor volatile organic compounds, so-called microbial VOC, and the prevalence of mucous membrane symptoms in single family homes. *Science of the Total Environment* 408 (2010) 2208–2215

Microorganisms are known to produce a range of volatile organic compounds, so-called microbial VOC (MVOC). Chamber studies where humans were exposed to MVOC addressed the acute effects of objective and/or subjective signs of mucosal irritation. However, the effect of MVOC on inhabitants due to household exposure is still unclear. The purpose of this epidemiological study was to measure indoor MVOC levels in single family homes and to evaluate the relationship between exposure to them and sick building syndrome (SBS). All inhabitants of the dwellings were given a self-administered questionnaire with standardized questions to assess their symptoms. Air samples were collected and the concentrations of eight selected compounds in indoor air were analyzed by gas chromatography/mass spectrometry — selective ion monitoring mode (GC/MS-SIM). The most frequently detected MVOC was 1-pentanol at a detection rate of 78.6% and geometric mean of 0.60 µg/m<sup>3</sup>. Among 620 participants, 120 (19.4%) reported one or more mucous symptoms; irritation of the eyes, nose, airway, or coughing every week (weekly symptoms), and 30 (4.8%) reported that the symptoms were home-related (home-related symptoms). Weekly symptoms were not associated with any of MVOC, whereas significant associations between home-related mucous symptoms and 1-octen-3-ol (per log<sub>10</sub>-unit: odds ratio (OR) 5.6, 95% confidence interval (CI): 2.1 to 14.8) and 2-pentanol (per log<sub>10</sub>-unit: OR 2.3, 95% CI: 1.0 to 4.9) were obtained after adjustment for gender, age, and smoking. Associations between home-related symptoms and 1-octen-3-ol remained after mutual adjustment. However, concentrations of the selected compounds in indoors were lower than the estimated safety level in animal studies. Thus, the statistically significant association between 1-octen-3-ol may be due to a direct effect of the compounds or the associations may be being associated with other offending compounds. Additional studies are needed to evaluate these possibilities.

Arena, Lois, Pallavi Mantha and Achilles N. Karagiozis 2010. Monitoring of Internal Moisture Loads in Residential Buildings. HUD, December 2010.

An insufficient amount of measured data is available on actual indoor humidity levels in U.S. households, making it difficult to design durable homes. This research project has collected 1 full year of indoor temperature and humidity data for a sample of 60 homes across three different climate regions—the hot and humid Southeast (Zone 2), the cold Northeast (Zone 5), and the marine Northwest (Zone 4). This research was in direct support of the American Society of Heating, Refrigerating and Air- Conditioning Engineers (ASHRAE), Inc. Standard 160, Criteria for Moisture-Control Design Analysis in Buildings. A research methodology was developed with assistance from Oak Ridge National Laboratory (ORNL), a subcontractor and member of Standing Standards Project Committee 160 that acted in an advisory role. The monitoring protocol involved three site visits to each home to perform tasks such as collecting basic house and equipment characteristics, installing data loggers, performing testing to quantify envelope leakage and duct leakage, and collecting data recorded by the loggers. Data compiled in the field tests were analyzed to identify the potential relationships between certain household characteristics and the measured internal humidity levels.

Arens, E., and A. Baughman, 1996. Indoor humidity and human health - part II: buildings and their systems. ASHRAE Transactions Vol. 102, Pt. 1, pp. 212-221.

This paper continues a review of the humidity effects on health as addressed in indoor ventilation and environmental standards. Part I identified a number of health-related agents that are affected by indoor humidity; common sites of contamination within buildings, and common remediation measures. Part II discusses the physical causes of moisture-related health problems in buildings, subdividing them by climate and mechanical system type. It examines studies done on moisture problems in these different environments, showing that in most, if not all, cases the causes of the problem are only indirectly related to indoor humidity in the space. To do a better job of controlling such problems, the building- and system specific causes of the problems should be studied. A number of specific research needs are identified.

Atkinson, Michael P. and Lawrence M. Wein, 2008. Quantifying the Routes of Transmission for Pandemic Influenza. *Bulletin of Mathematical Biology* (2008) 70: 820-867

Motivated by the desire to assess nonpharmaceutical interventions for pandemic influenza, we seek in this study to quantify the routes of transmission for this disease. We construct a mathematical model of aerosol (i.e., droplet-nuclei) and contact transmission of influenza within a household containing one infected. An analysis of this model in conjunction with influenza and rhinovirus data suggests that aerosol transmission is far more dominant than contact transmission for influenza. We also consider a separate model of a close expiratory event, and find that a close cough is unlikely (~1% probability) to generate traditional droplet transmission (i.e., direct deposition on the mucous membranes), although a close, unprotected and horizontally-directed sneeze is potent enough to cause droplet transmission. There are insufficient data on the frequency of close expiratory events to assess the relative importance of aerosol transmission and droplet transmission, and it is prudent to leave open the possibility that droplet transmission is important until proven otherwise. However, the rarity of close, unprotected and horizontally-directed sneezes-coupled with the evidence of significant aerosol and contact transmission for rhinovirus and our comparison of hazard rates for rhinovirus and influenza—leads us to suspect that aerosol transmission is the dominant mode of transmission for influenza.

Aydogdu H, Asan A, Otkun M, Ture M. 2005. Monitoring of fungi and bacteria in the indoor air of primary schools in Edirne city, Turkey. *Indoor and Built Environment* 14(5):411-25.

We monitored levels of bacteria and fungi in the indoor air at selected sites of several public primary schools in the city of Edirne, Turkey. Sampling was by the Petri plate method onto both a Rose-Bengal streptomycin agar medium and a 5% sheep-blood agar medium exposed to the air for 10-minute periods. Samples were collected monthly over a period of 6 months between August 2001 and January 2002. A total of 941 microfungi and 2066 bacterial colonies were counted on 90 Petri plates. During this 6-month period, 19 bacterial genera, 15 fungal genera and 48 species of fungi were isolated from the air in the schools. Some bacteria, such as coagulase-negative *Staphylococcus*, *Corynebacterium* and *Bacillus*, were predominant (42.7%, 20.4% and 6.9% of the total, respectively). *Penicillium*, *Cladosporium* and *Alternaria* were the most common fungal genera (42.8%, 19.3% and 10.1% of the total, respectively). *Staphylococcus*, *Acinetobacter*, *Corynebacterium*, *Propionibacterium* and *Pseudomonas* genera were found in every month. Statistical analysis of the data showed a positive correlation between the concentrations of bacteria and air humidity ( $p = 0.002$ ,

R<sup>2</sup> = 0.726) and between bacterial concentrations and age of the schools ( $p = 0.045$ , R<sup>2</sup> = 0.787). Also, that there was seasonal variation since the concentrations of fungi and bacteria varied according to the months ( $p = 0.001$ ).

Azad, Meghan B, Theodore Konya, Heather Maughan, David S Guttman, Catherine J Field, Malcolm R Sears, Allan B Becker, James A Scott, Anita L Kozyrskyj and CHILd Study Investigators, 2013. Infant gut microbiota and the hygiene hypothesis of allergic disease: impact of household pets and siblings on microbiota composition and diversity. *Allergy, Asthma & Clinical Immunology* 2013, 9:15

Background: Multiple studies have demonstrated that early-life exposure to pets or siblings affords protection against allergic disease; these associations are commonly attributed to the “hygiene hypothesis”. Recently, low diversity of the infant gut microbiota has also been linked to allergic disease. In this study, we characterize the infant gut microbiota in relation to pets and siblings. Methods: The study population comprised a small sub-sample of 24 healthy, full term infants from the Canadian Healthy Infant Longitudinal Development (CHILd) birth cohort. Mothers reported on household pets and siblings. Fecal samples were collected at 4 months of age, and microbiota composition was characterized by high-throughput signature gene sequencing. Results: Microbiota richness and diversity tended to be increased in infants living with pets, whereas these measures were decreased in infants with older siblings. Infants living with pets exhibited under-representation of Bifidobacteriaceae and over-representation of Peptostreptococcaceae; infants with older siblings exhibited under-representation of Peptostreptococcaceae. Conclusions: This study provides new evidence that exposure to pets and siblings may influence the early development of the gut microbiota, with potential implications for allergic disease. These two traditionally protective “hygiene hypothesis” factors appear to differentially impact gut microbiota composition and diversity, calling into question the clinical significance of these measures. Further research is required to confirm and expand these findings.

Bargellini, Annalisa, Isabella Marchesi, Elena Righi, Angela Ferrari, Stefano Cencetti, Paola Borella, Sergio Rovesti, 2011. Parameters predictive of Legionella contamination in hot water systems: Association with trace elements and heterotrophic plate counts. *Water Research*, 45:2315-2321.

The contamination of hot water samples with Legionella spp. was studied in relation to temperature, total hardness, trace element concentrations (iron, zinc, manganese, and copper) and heterotrophic plate counts (HPC) at both 22 and 37 °C. Factor analysis and receiver operating characteristic (ROC) curves were used to establish the cut-off of water parameters as predictors for Legionella contamination. Legionella spp. was isolated in 194 out of 408 samples (47.5%), with Legionella pneumophila being the most common (92.8%). After multiple logistic regression analysis, the risk for legionellae colonisation was positively associated with Mn levels >6 µg l<sup>-1</sup>, HPC at 22 °C >27 CFU l<sup>-1</sup>, and negatively with temperature >55 °C and Cu levels >50 µg l<sup>-1</sup>. Multiple regression analysis revealed that Legionella spp. counts were positively associated with Mn, HPC at 37 °C and Zn and negatively associated with temperature. Only 1 out of the 97 samples (1%) having a Mn concentration, an HPC at 22 °C and an HPC at 37 °C below the respective median values exhibited a Legionella spp. concentration exceeding 104 CFU l<sup>-1</sup> vs. 41 out of the 89 samples (46.1%) with the three parameters above the medians. Our results show a qualitative and quantitative relationship between Legionella spp., the Mn concentration and heterotrophic plate counts in hot water samples from different buildings, suggesting that these parameters should be included in a water safety plan. The role of manganese in biofilm formation and its possible involvement in the mechanisms favouring Legionella survival and growth in water niches should be investigated further

Bartlett, Karen H., Susan M. Kennedy, Michael Brauer, Chris van Netten & Barbara Dill (2004): Evaluation and Determinants of Airborne Bacterial Concentrations in School Classrooms, *Journal of Occupational and Environmental Hygiene*, 1:10, 639-647

A survey of 39 elementary schools was undertaken to determine indoor air concentrations of bioaerosols within a coastal, temperate climatic zone in British Columbia, Canada. This article reports the results for airborne bacteria. Determinants of exposure were grouped into environmental (outdoor temperature, relative humidity, season, weather), ventilation and comfort parameter (indoor relative humidity, temperature, indoor CO<sub>2</sub> concentration, indoor fungal concentration), and occupancy (number of occupants, activity levels, occupancy patterns) variables. Regression modeling was used to evaluate the association between these factors and measured concentrations of indoor mesophilic bacteria. Naturally ventilated rooms (47% of the total rooms surveyed) had higher bacterial counts than

mechanically ventilated rooms (geometric mean 325 vs. 166 CFU/m<sup>3</sup>, respectively,  $p < 0.001$ ). In univariate analyses, bacterial counts were negatively correlated with supply and exhaust flow rates, air exchange rates, and the percentage of the day that occupants spent quietly sitting at their desks. Analysis of bacterial groups indicated various sources of the bacterial aerosol, with micrococci and staphylococci closely associated with occupancy variables, *Bacillus* with site and occupancy, and coryneform bacteria with site variables only. Approximately 60% of the variance in the outcome measurement of total bacteria was accounted for by indoor CO<sub>2</sub>, lower air exchange rate, the age of the building, signs of current or old moisture stains, room volume, indoor relative humidity, and occupant activity level in a multiple linear regression model, with ventilation factors accounting for 40% of the variance.

Baughman, A.V. and E.A. Arens, 1996. Indoor Humidity and Human Health - Part I: Literature Review of Health Effects of Humidity-Influenced Indoor Pollutants. ASHRAE Transactions, Vol. 102, Part 1, 3951.

Standards for indoor thermal conditions and ventilation include upper limits for relative humidity (RH) that typically are in the range of 60% to 80% RH. Although the reasons for the limits are often not explicitly stated, it is generally known that they were set out of concern for the health effects that might occur should the humidity become too high. The primary health effects of high humidity are caused by the growth and spread of biotic agents, although humidity interactions with nonbiotic pollutants, such as formaldehyde, may also cause adverse effects. This literature review identifies the most important health issues associated with high humidities and presents humidity requirements, typical contamination sites within buildings, and remediation measures for each pollutant. Part two of the paper addresses the physical causes of moisture-related problems in buildings

Bean B., B. M. Moore, B. Sterner, L. R. Peterson, D. N. Gerding and H. H. Balfour Jr., 1982. Survival of Influenza Viruses on Environmental Surfaces. The Journal of Infectious Diseases, Vol. 146, No. 1 (Jul., 1982), pp. 47-51

To investigate the transmission of influenza viruses via hands and environmental surfaces, the survival of laboratory-grown influenza A and influenza B viruses on various surfaces was studied. Both influenza A and B viruses survived for 24-48 hr on hard, nonporous surfaces such as stainless steel and plastic but survived for <8-12 hr on cloth, paper, and tissues. Measurable quantities of influenza A virus were transferred from stainless steel surfaces to hands for 24 hr and from tissues to hands for up to 15 min. Virus survived on hands for up to 5 min after transfer from the environmental surfaces. These observations suggest that the transmission of virus from donors who are shedding large amounts could occur for 2-8 hr via stainless steel surfaces and for a few minutes via paper tissues. Thus, under conditions of heavy environmental contamination, the transmission of influenza virus via fomites may be possible.

Beggs, Clive B., Simon J Shepherd and Kevin G Kerr, 2008. Increasing the frequency of hand washing by healthcare workers does not lead to commensurate reductions in staphylococcal infection in a hospital ward. BMC Infectious Diseases, 2008, 8:114 doi:10.1186/1471-2334-8-114.

Background: Hand hygiene is generally considered to be the most important measure that can be applied to prevent the spread of healthcare-associated infection (HAI). Continuous emphasis on this intervention has led to the widespread opinion that HAI rates can be greatly reduced by increased hand hygiene compliance alone. However, this assumes that the effectiveness of hand hygiene is not constrained by other factors and that improved compliance in excess of a given level, in itself, will result in a commensurate reduction in the incidence of HAI. However, several researchers have found the law of diminishing returns to apply to hand hygiene, with the greatest benefits occurring in the first 20% or so of compliance, and others have demonstrated that poor cohorting of nursing staff profoundly influences the effectiveness of hand hygiene measures. Collectively, these findings raise intriguing questions about the extent to which increasing compliance alone can further reduce rates of HAI. Methods: In order to investigate these issues further, we constructed a deterministic Ross-Macdonald model and applied it to a hypothetical general medical ward. In this model the transmission of staphylococcal infection was assumed to occur after contact with the transiently colonized hands of HCWs, who, in turn, acquire contamination only by touching colonized patients. The aim of the study was to evaluate the impact of imperfect hand cleansing on the transmission of staphylococcal infection and to identify, whether there is a limit, above which further hand hygiene compliance is unlikely to be of benefit. Results: The model demonstrated that if transmission is solely via the hands of HCWs, it should, under most circumstances, be possible to prevent outbreaks of staphylococcal infection from occurring at a hand cleansing frequencies < 50%, even with imperfect hand hygiene. The analysis also indicated that the relationship between hand cleansing efficacy and frequency



is not linear - as efficacy decreases, so the hand cleansing frequency required to ensure  $R_0 < 1$  increases disproportionately. Conclusion: Although our study confirmed hand hygiene to be an effective control measure, it demonstrated that the law of diminishing returns applies, with the greatest benefit derived from the first 20% or so of compliance. Indeed, our analysis suggests that there is little benefit to be accrued from very high levels of hand cleansing and that in most situations compliance > 40% should be enough to prevent outbreaks of staphylococcal infection occurring, if transmission is solely via the hands of HCWs. Furthermore we identified a non-linear relationship between hand cleansing efficacy and frequency, suggesting that it is important to maximise the efficacy of the hand cleansing process.

Berg, Gabriele, Alexander Mahnert and Christine Moissl-Eichinger, 2014. Beneficial effects of plant-associated microbes on indoor microbiomes and human health? *Frontiers in Microbiology*, January 2014 Volume 5 Article 15

Just like humans, plants have recently been recognized as meta-organisms, possessing a distinct microbiome and revealing close symbiotic relationships with their associated microorganisms (Berg et al., 2013; Mendes et al., 2013). Each plant harbor specific species to a certain degree but also cosmopolitan and ubiquitous microbial strains; the majority of them fulfill important host as well as ecosystem functions (rev. in Berg and Smalla, 2009).

Blaser, Martin, 2011. Stop the Killing of Beneficial Bacteria. *Nature*, 476: 25 Aug, pp. 393-394.

The average child in the United States and other developed countries has received 10–20 courses of antibiotics by the time he or she is 18 years old. In many respects, this is a life-saving development. The average US citizen born in 1940 was expected to live to the age of 63; a baby born today should reach 78, in part because of antibiotics. But the assumption that antibiotics are generally safe has fostered overuse and led to an increase in bacterial resistance to treatments.

Bloom, Erica, Eva Nyman, Aime Must, Christina Pehrson & Lennart Larsson (2009): Molds and Mycotoxins in Indoor Environments - A Survey in Water-Damaged Buildings, *Journal of Occupational and Environmental Hygiene*, 6:11, 671-678.

Mycotoxins are toxic, secondary metabolites frequently produced by molds in water-damaged indoor environments. We studied the prevalence of selected, potent mycotoxins and levels of fungal biomass in samples collected from water-damaged indoor environments in Sweden during a 1- year period. One hundred samples of building materials, 18 samples of settled dust, and 37 samples of cultured dust were analyzed for: (a) mycoflora by microscopy and culture; (b) fungal chemical marker ergosterol and hydrolysis products of macrocyclic trichothecenes and trichodermin (verrucarol and trichodermol) by gas chromatography-tandem mass spectrometry; and (c) sterigmatocystin, gliotoxin, aflatoxin B1, and satratoxin G and H by high performance liquid chromatography-tandem mass spectrometry. Sixty-six percent of the analyzed building materials samples, 11% of the settled dust samples, and 51% of the cultured dust samples were positive for at least one of the studied mycotoxins. In addition, except in the case of gliotoxin, mycotoxin-positive building material samples contained 2-6 times more ergosterol than mycotoxin-negative samples. We show that (a) molds growing on a range of different materials indoors in water-damaged buildings generally produce mycotoxins, and (b) mycotoxin-containing particles in mold-contaminated environments may settle on surfaces above floor level. The mass spectrometry methods used in this study are valuable tools in further research to survey mycotoxin exposure and investigate potential links with health effects.

Bogaert D, Keijsers B, Huse S, Rossen J, Veenhoven R, van Gils E, Bruin J, Montijn R, Bonten M, Sanders E. 2011. Variability and diversity of nasopharyngeal microbiota in children: A metagenomic analysis. *PLoS One* 6(2):e17035.

The nasopharynx is the ecological niche for many commensal bacteria and for potential respiratory or invasive pathogens like *Streptococcus pneumoniae*, *Haemophilus influenzae*, and *Neisseria meningitidis*. Disturbance of a balanced nasopharyngeal (NP) microbiome might be involved in the onset of symptomatic infections with these pathogens, which occurs primarily in fall and winter. It is unknown whether seasonal infection patterns are associated with concomitant changes in NP microbiota. As young children are generally prone to respiratory and invasive infections, we characterized the NP microbiota of 96 healthy children by barcoded pyrosequencing of the V5-V6 hypervariable

region of the 16S-rRNA gene, and compared microbiota composition between children sampled in winter/fall with children sampled in spring. The approximately 1000000 sequences generated represented 13 taxonomic phyla and approximately 250 species-level phyla types (OTUs). The 5 most predominant phyla were Proteobacteria (64%), Firmicutes (21%), Bacteroidetes (11%), Actinobacteria (3%) and Fusobacteria (1,4%) with *Moraxella*, *Haemophilus*, *Streptococcus*, *Flavobacteria*, *Dolosigranulum*, *Corynebacterium* and *Neisseria* as predominant genera. The inter-individual variability was that high that on OTU level a core microbiome could not be defined. Microbiota profiles varied strongly with season, with in fall/winter a predominance of Proteobacteria (relative abundance (% of all sequences): 75% versus 51% in spring) and Fusobacteria (absolute abundance (% of children): 14% versus 2% in spring), and in spring a predominance of Bacteroidetes (relative abundance: 19% versus 3% in fall/winter, absolute abundance: 91% versus 54% in fall/winter), and Firmicutes. The latter increase is mainly due to (*Brevi*)*bacillus* and *Lactobacillus* species (absolute abundance: 96% versus 10% in fall/winter) which are like Bacteroidetes species generally related to healthy ecosystems. The observed seasonal effects could not be attributed to recent antibiotics or viral co-infection. The NP microbiota of young children is highly diverse and appears different between seasons. These differences seem independent of antibiotic use or viral co-infection.

Bohannan, Brendan JM and Jennifer Hughes, 2003. New approaches to analyzing microbial biodiversity data. *Current Opinion in Microbiology* 2003, 6:282-287

Modern molecular techniques have revealed an extraordinary diversity of microorganisms, most of which are as yet uncharacterized. This poses a major challenge to microbial ecologists: how can one compare the microbial diversity of different environments when the vast majority of microbial taxa are usually unknown? Three statistical approaches developed by ecologists and evolutionary biologists - parametric estimation, nonparametric estimation and community phylogenetics - are proving to be promising tools to meet this challenge. The combination of these tools with molecular biology techniques allow the rigorous estimation and comparison of microbial diversity in different environments.

Bok, Gunilla, Nils Hallenberg, Olle Åberg, 2009. Mass occurrence of *Penicillium corylophilum* in crawl spaces, south Sweden. *Building and Environment* 44 (2009) 2413-2417.

Buildings with crawl space foundations are looked upon as high-risk constructions with respect to mould growth, especially on the blind floor. This mould growth can be extensive and cover several square meters of the blind floor with potential health risks as a consequence. Mould occurrence and mould species diversity were investigated in a large small-house area in the south of Sweden, comprising 212 buildings. The crawl spaces were inspected and samples from the blind floor were taken. The relative humidity was measured and reached 80-100% for several consecutive months. Subsets of the samples were cultured and the fungi isolated were further analyzed by sequencing of the Internal Transcribed Spacer (ITS) region of nuclear ribosomal Deoxyribo Nucleic Acid (DNA). The results were compared with results from other, relevant studies and confirm that *Penicillium corylophilum* is the completely dominating mould species in crawl spaces. The occurrences could not be explained as accidental since the extensive occurrence in many dwellings had developed over several years.

Bolashikov, Z.D. and A.K. Melikov, 2009. Methods for air cleaning and protection of building occupants from airborne pathogens. *Building and Environment*, Volume 44, Issue 7, July 2009, Pages 1378-1385.

This article aims to draw the attention of the scientific community towards the elevated risks of airborne transmission of diseases and the associated risks of epidemics or pandemics. The complexity of the problem and the need for multidisciplinary research is highlighted. The airborne route of transmission, i.e. the generation of pathogen laden droplets originating in the respiratory tract of an infected individual, the survivability of the pathogens, their dispersal indoors and their transfer to a healthy person are reviewed. The advantages and the drawbacks of air dilution, filtration, ultraviolet germicidal irradiation (UVGI), photocatalytic oxidation (PCO), plasmacluster ions and other technologies for air disinfection and purification from pathogens are analyzed with respect to currently used air distribution principles. The importance of indoor air characteristics, such as temperature, relative humidity and velocity for the efficiency of each method is analyzed, taking into consideration the nature of the pathogens themselves. The applicability of the cleaning methods to the different types of total volume air distribution used at present indoors, i.e. mixing, displacement and underfloor ventilation, as well as advanced air distribution techniques (such as personalized ventilation) is discussed.

Bonetta, Sa., Si. Bonetta · S. Mosso · S. Sampò · E. Carraro 2010, Assessment of microbiological indoor air quality in an Italian office building equipped with an HVAC system, *Environ Monit Assess* (2010) 161:473-483

The purpose of this study was to evaluate the level and composition of bacteria and fungi in the indoor air of an Italian office building equipped with a heating, ventilation and air conditioning (HVAC) system. Airborne bacteria and fungi were collected in three open-space offices during different seasons. The microbial levels in the outdoor air, supply air diffusers, fan coil air flow and air treatment unit humidification water tank were used to evaluate the influence of the HVAC system on indoor air quality (IAQ). A medium-low level of bacterial contamination (50- 500 CFU/m<sup>3</sup>) was found in indoor air. *Staphylococcus* and *Micrococcus* were the most commonly found genera, probably due to human presence. A high fungal concentration was measured due to a flood that occurred during the winter. The indoor seasonal distribution of fungal genera was related to the fungal outdoor distribution. Significant seasonal and daily variation in airborne microorganisms was found, underlining a relationship with the frequency of HVAC system switching on/off. The results of this monitoring highlight the role of the HVAC system on IAQ and could be useful to better characterise bacterial and fungal population in the indoor air of office buildings.

Boone SA and Gerba CP. 2010. The prevalence of human parainfluenza virus 1 on indoor office fomites. *Food and Environmental Virology* 2(1):41-6

The objective of this study was to evaluate the potential role of fomites in human parainfluenza virus 1 (HPIV1) transmission by assessing the occurrence of HPIV1 on surfaces in an adult setting (office). In 2004, a total of 328 fomites from 12 different office buildings in five different cities were evaluated for HPIV1 viral RNA. HPIV1 was isolated using reverse transcriptase-polymerase chain reaction (RT-PCR) and detected on 37% of all office fomites. HPIV1 RNA was frequently isolated on desk tops (47%), and infrequently isolated on light switches (19%). Data revealed a statistically significant difference between the percentage of HPIV1 positive fomites in office cubicles and conference rooms (Chisquare  $P < 0.011$ , Fisher's Exact  $P = 0.054$ ). A statistically significant difference was also found among positive fomites in different buildings (Chi-square  $P < 0.011$ ). HPIV1 was consistently isolated on various indoor fomites in the 12 office buildings assessed during 2004, a low HPIV incident year.

Bornehag, C. G. J. Sundell, S. Bonini, A. Custovic, P. Malmberg, S. Skerfving, T. Sigsgaard, A. Verhoeff, 2004a. Dampness in buildings as a risk factor for health effects, EUROEXPO: a multidisciplinary review of the literature (1998-2000) on dampness and mite exposure in buildings and health effects.

The scientific literature on health effects from dampness in buildings, including mite exposure over the period 1998-2000 has been reviewed by a European group (EUROEXPO) of eight scientists in experience from medicine, epidemiology, toxicology and engineering. Forty studies deemed relevant have been the foundation for the conclusions. Dampness in buildings is a risk factor for health effects among atopics and non-atopics both in domestic and in public environments. However, the literature is not conclusive in respect of causative agents, e.g. mites, microbiological agents and organic chemicals from degraded building materials. There is a strong need for more multidisciplinary studies including expertise from all relevant areas. A general conclusion from the work was that there is a strong need for multidisciplinary reviews in scientific journals of articles dealing with associations between indoor environmental factors and health effects.

Brankston, Gabrielle, Leah Gitterman, Zahir Hirji, Camille Lemieux, Michael Gardam, 2007. Transmission of influenza A in human beings. *Lancet Infect Dis* 2007; 7:257-65.

Planning for the next influenza pandemic is occurring at many levels throughout the world, spurred on by the recent spread of H5N1 avian influenza in Asia, Europe, and Africa. Central to these planning efforts in the health-care sector are strategies to minimise the transmission of influenza to health-care workers and patients. The infection control precautions necessary to prevent airborne, droplet, and contact transmission are quite different and will need to be decided on and planned before a pandemic occurs. Despite vast clinical experience in human beings, there continues to be much debate about how influenza is transmitted. We have done a systematic review of the English language experimental and epidemiological literature on this subject to better inform infection control planning efforts. We have found that the existing data are limited with respect to the identification of specific modes of transmission in the natural setting. However, we are able to conclude that transmission occurs at close range rather than over long

distances, suggesting that airborne transmission, as traditionally defined, is unlikely to be of significance in most clinical settings. Further research is required to better define conditions under which the influenza virus may transmit via the airborne route.

Brar T, Nagaraj S, Mohapatra S. 2012. Microbes and asthma: The missing cellular and molecular links. *Curr Opin Pulm Med* 18(1):14-22.

Asthma is a complex chronic disease of the lung whose incidence is growing at all ages despite the progress that has been made in the areas of diagnosis and treatment of asthma. The complexity is partly due to the environmental insults such as allergens and microbial infections that play differential roles in the pathogenesis of childhood vis-a-vis elderly asthma. Microbes may play important roles in the exacerbation of asthma and hence in the comorbidities due to asthma, and also in the causation of asthma

Bright KR, Boone SA, Gerba CP. 2010. Occurrence of bacteria and viruses on elementary classroom surfaces and the potential role of classroom hygiene in the spread of infectious diseases. *Journal of School Nursing* 26(1):33-41

The presence of microorganisms on common classroom contact surfaces (fomites) was determined to identify the areas most likely to become contaminated. Six elementary classrooms were divided into control and intervention groups (cleaned daily with a quaternary ammonium wipe) and tested for heterotrophic bacteria. Three classrooms were also tested for norovirus and influenza A virus. Frequently used fomites were the most contaminated; water fountain toggles, pencil sharpeners, keyboards, and faucet handles were the most bacterially contaminated; desktops, faucet handles, and paper towel dispensers were the most contaminated with viruses. Influenza A virus was detected on up to 50% and norovirus on up to 22% of surfaces throughout the day. Children in the control classrooms were 2.32 times more likely to report absenteeism due to illness than children in the intervention classrooms and were absent longer (on average). Improved classroom hygiene may reduce the incidence of infection and thus student absenteeism.

BRITAIN-LONG, ROBIN, LARS-MAGNUS ANDERSSON, SIGVARD OLOFSSON, MAGNUS LINDH & JOHAN WESTIN, 2011. Seasonal variations of 15 respiratory agents illustrated by the application of a multiplex polymerase chain reaction assay. *Scandinavian Journal of Infectious Diseases*, 2011; Early Online, 1-9

Background: Nucleic acid amplification tests are increasingly being used to diagnose viral and bacterial respiratory tract infections. The high sensitivity of these tests affects our understanding of the epidemiology of respiratory tract infections. We have assessed the detection rate of a multiplex real-time polymerase chain reaction (PCR) test, with emphasis on epidemiology and seasonal distribution of the most common respiratory tract infections. Methods: Seven thousand eight hundred and fifty-three nasopharyngeal samples from 7220 patients (age range 0 - 98 y, median 22 y) obtained during 36 consecutive months (November 2006 - October 2009), were analyzed with a multiplex PCR panel including influenza A (IfA) and B (IfB) virus, parainfluenza virus (PIV) 1 - 3, respiratory syncytial virus (RSV), human rhinovirus (HRV), human coronavirus (CoV) OC43, NL63, and 229E, human metapneumovirus (HMPV), adenovirus (AdV), enterovirus (EV), and 2 bacteria - *Mycoplasma pneumoniae* and *Chlamydia pneumoniae*. Results: Of the total samples, 44.5% (n = 3496) were positive for at least 1 agent, with HRV being the most common (n = 1482, 38.0%), followed by RSV (n = 526, 13.5%) and IfA (n = 403, 10.3%). The diagnostic yield was significantly higher during the winter and early spring compared to the summer (n = 2439 of 4458 samples, 54.7% and n = 1057 of 3395 samples, 31.1%, respectively; p < 0.001). Conclusions: The diagnostic yield was highly dependent on the month of sampling and the age of the patient. However, the overall detection rate per month was above 30%, apart for August and September. Our findings support the use of similar tests in routine clinical care all year round. HRV was the most common finding in the respiratory tract, independent of season.

Cabral, João P.S., 2010. Can we use indoor fungi as bioindicators of indoor air quality? Historical perspectives and open questions. *Science of the Total Environment* 408 (2010) 4285-4295.

Microbiological analysis of atmospheres witnessed substantial technical improvements in the 1940s to 1960s. May's cascade impactor and Hirst's spore trap allowed the counting of total cells but had limited capacity for identification of the spores. Bourdillon's sampler enabled the counting of cultivable fungi and their identification. A great step forward was given with the Andersen's six-stage impactor, which allowed discrimination of particles by size,

counting of cultivable cells, and species identification. This period also witnessed the development of impingers, namely, the AGI-30 described by Malligo and Idoine, and the three-stage model designed by K. R. May. The 1990s to 2000s witnessed innovative discoveries on the biology of indoor fungi. Work carried out in several laboratories showed that indoor fungi can release groups of spores, individual spores and fungal fragments, and produce volatile organic compounds and mycotoxins. Integrating all findings a holistic interpretation emerged for the sick building syndrome. Healthy houses and buildings, with low indoor humidity, display no appreciable indoor fungal growth, and outdoor *Cladosporium* dominates. On the contrary, in sick houses and buildings, high indoor humidity allows fungal growth (mainly of *Penicillium* and *Aspergillus*), with concomitant release of conidia and fragments into the atmosphere. The intoxication probably results from a chronic exposure to volatile organic compounds and mycotoxins produced by *Penicillium*, *Aspergillus*, and *Stachybotrys*.

Cai G-, Broms K, Malarstig B, Zhao Z-, Kim JL, Svardsudd K, Janson C, Norback D. 2009. Quantitative PCR analysis of fungal DNA in Swedish day care centers and comparison with building characteristics and allergen levels. *Indoor Air* 19(5):392-400.

Sweden has had allergen-avoidance day care centers (AADCs) since 1979. The aim of this study was to measure fungal DNA by quantitative polymerase chain reaction (qPCR), a new method, in AADCs and ordinary day care centers (ODCs) and examine associations between allergen levels and building characteristics. Dust samples were collected by swabbing doorframes, vacuum-cleaning, and using Petri dishes. In total, 11 AADCs and 11 ODCs were studied (70 rooms). Total fungal DNA, measured by qPCR in the swab dust, was detected in 89%, *Aspergillus* or *Penicillium* (Asp/Pen) DNA in 34%, and *Stachybotrys chartarum* DNA in 6% of the rooms. Total fungal DNA was significantly higher in rooms with linoleum floor ( $P = 0.02$ ), textile carpets ( $P = 0.03$ ), reported dampness/molds ( $P = 0.02$ ) and reported odor ( $P < 0.001$ ) in the buildings, and significantly lower in wooden facade buildings ( $P = 0.003$ ). Reported odor was related to the amount of sieved fine dust, reported dampness/molds and type of building construction. Total fungal DNA was related to cat, dog, horse and total allergen levels ( $P = 0.003$ ) in the day care centers. In conclusion, total fungal DNA is related to reported dampness/molds, reported odor, and type of wall construction. The association between fungal and allergen contamination indicated a general 'hygiene factor' related to biological contaminants.

Cai G, Malarstig B, Kumlin A, Johansson I, Janson C, Norback D. 2011. Fungal DNA and pet allergen levels in Swedish day care centers and associations with building characteristics. *Journal of Environmental Monitoring* 13(7):2018-24

Pet allergens and mold growth related to damp are common phenomena in day care centers in Sweden but exposure measurements of these factors are lacking. The aim of this study was to investigate the relationship between building construction and indoor environment quality in Swedish day care centers and the potential for exposure to fungi (analyzed by quantitative PCR) and animal allergens (analyzed by ELISA). Measurements were performed in 21 day care centers (103 rooms) from one municipality in Sweden, which were identified as constructions at risk of dampness (85% of the buildings) and with visible damage and mold growth (54% of the buildings). Dust samples were collected using cotton swab and Petri dishes. Total fungal DNA was detected in 99% and 100%, *Aspergillus*/*Penicillium* DNA in 54% and 68%, and *Stachybotrys chartarum* DNA in 4% and 9% of the investigated rooms in cotton swab and Petri dish samples, respectively. The total fungal DNA levels (Geometric Mean, GM) were  $4.2 \times 10^6$  cell equivalents per  $m^2$  and  $2.9 \times 10^5$  cell equivalents per  $m^2$  per day in the swab and Petri dish samples, respectively. The concentrations (GM) of cat (Fel d1), dog (Can f1), and horse (Equ cx) allergens were 9.4, 7.2  $ng\ m^{-2}\ day^{-1}$ , and 5.0 unit per  $m^2$  per day, respectively. Total fungal DNA levels were higher in risk construction buildings ( $p = 0.01$ ), in rooms with linoleum flooring material ( $p \leq 0.003$ ), and in buildings with rotating heat exchangers ( $p \leq 0.02$ ). There were associations between total fungal DNA levels and cat ( $p = 0.02$ ), dog ( $p < 0.001$ ), and horse ( $p = 0.001$ ) allergens. In conclusion, risk constructions, damp constructions, mould growth, fungal DNA, and animal allergens were common exposure factors in Swedish day care centers. Building constructions that represent a high risk for internal dampness should be avoided in the future, and measures to reduce allergen levels should be considered to protect pet-allergic children from asthmatic problems.

Cappitelli, Francesca, Paola Fermo, Roberta Vecchi, Andrea Piazzalunga, Gianluigi Valli, Elisabetta Zanardini, Claudia Sorlini, 2009. Chemical-physical and Microbiological Measurements for Indoor Air Quality Assessment at the Ca' Granda Historical Archive, Milan (Italy). *Water Air Soil Pollut* (2009) 201:109-120.

In a few cases, atmospheric particulate matter characterization was taken into account together with aerobiological monitoring but never in an archive. The aim of this study was to estimate the air quality, by means of both chemical-physical and microbiological studies, at the Ca' Granda Historical Archive (Milan, Italy) that houses an important collection of documents from the 12th century. Temperature and relative humidity were measured in the rooms. Particulate matter (PM<sub>2.5</sub>) concentrations were quantified and the chemical composition, in terms of ionic components, elements, and carbonaceous fraction (total, organic, and elemental carbon) determined. The gaseous pollutants NO<sub>2</sub>, SO<sub>2</sub>, and O<sub>3</sub> and indoor acidity were also measured. Aerobiological monitoring (aerobic heterotrophic bacteria and fungi) was performed as volumes stored in the Archive were composed of organic materials, a potential energy and carbon source. In this paper, we present our findings and propose some guidelines for a better preservation of the documents.

Casanova, Lisa M., Soyounng Jeon, William A. Rutala, David J. Weber, and Mark D. Sobsey, 2010. Effects of Air Temperature and Relative Humidity on Coronavirus Survival on Surfaces. *APPLIED AND ENVIRONMENTAL MICROBIOLOGY*, May 2010, p. 2712-2717

Assessment of the risks posed by severe acute respiratory syndrome (SARS) coronavirus (SARS-CoV) on surfaces requires data on survival of this virus on environmental surfaces and on how survival is affected by environmental variables, such as air temperature (AT) and relative humidity (RH). The use of surrogate viruses has the potential to overcome the challenges of working with SARS-CoV and to increase the available data on coronavirus survival on surfaces. Two potential surrogates were evaluated in this study; transmissible gastroenteritis virus (TGEV) and mouse hepatitis virus (MHV) were used to determine effects of AT and RH on the survival of coronaviruses on stainless steel. At 4°C, infectious virus persisted for as long as 28 days, and the lowest level of inactivation occurred at 20% RH. Inactivation was more rapid at 20°C than at 4°C at all humidity levels; the viruses persisted for 5 to 28 days, and the slowest inactivation occurred at low RH. Both viruses were inactivated more rapidly at 40°C than at 20°C. The relationship between inactivation and RH was not monotonic, and there was greater survival or a greater protective effect at low RH (20%) and high RH (80%) than at moderate RH (50%). There was also evidence of an interaction between AT and RH. The results show that when high numbers of viruses are deposited, TGEV and MHV may survive for days on surfaces at ATs and RHs typical of indoor environments. TGEV and MHV could serve as conservative surrogates for modeling exposure, the risk of transmission, and control measures for pathogenic enveloped viruses, such as SARS-CoV and influenza virus, on health care surfaces.

Cermak R and Melikov AK. 2007. Protection of occupants from exhaled infectious agents and floor material emissions in rooms with personalized and underfloor ventilation. *Hvac&R Research* 13(1):23-38.

The performance of two personalized ventilation systems supplying air at the breathing zone was tested in conjunction with underfloor ventilation generating two different airflow patterns in a full-scale test room. Two breathing thermal manikins were used to simulate occupants. The distribution of pollutants associated with exhaled air and floor material emissions was evaluated at various combinations of personalized and underfloor airflow rates. Compared to underfloor ventilation alone, personalized and underfloor ventilation provided excellent protection of seated occupants from any pollution, while the concentration of exhaled air pollution increased in the room. The two types of personalized ventilation performed differently. Subsequent analyses of airborne infection transmission risk indicated that personalized ventilation could become a supplement to traditional methods of infection control.

Cerolini, S., M. D'Orazio, C. Di Perna, A. Stazi, 2009 Moisture buffering capacity of highly absorbing materials. *Energy and Buildings* 41 (2009) 164-168

This research investigates the possibility to use highly absorbing materials to dampen indoor RH% variations. The practical MBV of sodium polyacrylate, cellulose-based material, perlite and gypsum is evaluated for a daily cyclic exposure that alternates high (75%) and low (33%) RH% levels for 8 h and 16 h, respectively. The adjustment velocity to RH% variations and the presence of hysteretic phenomena are also presented. The cellulose-based material proves to be the most suitable for moisture buffering applications. Starting from this material's properties, the effect of thickness, vapour resistance factor ( $\mu$ ) and mass surface exchange coefficient ( $Z_v$ ) on sorption capacity is evaluated by the use of a numerical model

Ceylan E, Ozkutuk A, Ergor G, Yucesoy M, Itil O, Caymaz S, Cimrin A. 2006. Fungi and indoor conditions in asthma patients. *J Asthma* 43(10):789-94.

This study was carried out with 127 asthmatic patients and 127 controls, which aimed to compare and evaluate the environmental conditions in the homes of asthmatic patients and the control group. Air samples were obtained by using an air sampler and the mean mould colony counts were established. *Aspergillus* and *Penicillium* were the most common isolated species. No significant difference was observed with regard to various house conditions and the mean mould colony counts between the houses of patients and controls. The mould colony counts were found to be lower in houses with wooden parquet flooring. The odds ratio for stone floors vs. wood floors was 2.3 (95% CI 1.08-4.98) for mould growth.

Chaibenjawong, Plykaeow, Simon J. Foster, 2011. Desiccation tolerance in *Staphylococcus aureus*. *Arch Microbiol* (2011) 193:125-135

*Staphylococcus aureus* is a multidrug-resistant pathogen that not only causes a diverse array of human diseases, but also is able to survive in potentially dry and stressful environments, such as the human nose, on skin and on inanimate surfaces such as clothing and surfaces. This study investigated parameters governing desiccation tolerance of *S. aureus* and identified several components involved in the process. Initially, the role of environmental parameters such as temperature, growth phase, cell density, desiccation time and protectants in desiccation tolerance were determined. This established a robust model of desiccation tolerance in which *S. aureus* has the ability to survive on dry plastic surfaces for more than 1,097 days. Using a combination of a random screen and defined mutants, *clpX*, *sigB* and *yjbH* were identified as being required for desiccation tolerance. *ClpX* is a part of the ATP-dependent *ClpXP* protease, important for protein turnover, and *YjbH* has a proposed linked function. *SigB* is an accessory sigma factor with a role in generalized stress resistance. Understanding the molecular mechanisms that govern desiccation tolerance may determine the break points to be exploited to prevent the spread of this dangerous pathogen in hospitals and communities

Chan DWT, Leung PHM, Tam CSY, Jones AP. 2008. Survey of airborne bacterial genus at a university campus. *Indoor Built Environ* 17(5):460-6.

Indoor airborne bacterial concentrations were measured at different locations in a university campus in Hong Kong where there was a Mechanical Ventilation and Air-conditioning (MVAC) system. Total bacterial counts were enumerated for both indoor and outdoor areas at specific time intervals. Information on temperature, relative humidity, number of occupants, and carbon dioxide levels were recorded simultaneously. Those parameters were correlated with total bacterial counts and each identifiable genus. Although, the number of genera for Gram-negative bacteria was higher than Gram-positive bacteria, the most abundant airborne genera found were Gram-positive bacteria especially *Micrococcus* and *Staphylococcus*. The indoor-to-outdoor ratios for the two predominant Gram-positive genera were greater than one, indicating that the source of the bacteria was indoors. There was a correlation between total bacterial counts with temperature, but the correlation was not significant. *Pseudomonas* had a correlation with relative humidity, but the correlation was not significant. The study also found that the total bacterial counts and a few genera including *Staphylococcus* and *Pseudomonas*, had a strong correlation with ventilation.

Chang, C-W and F-C Chou, 2010. Methodologies for quantifying culturable, viable, and total *Legionella pneumophila* in indoor air. *Indoor Air* 21:4, 291-299.

*Legionella pneumophila*, aerosolized from numerous indoor facilities (e.g., shower heads, hot tubs, spas), may cause Pontiac fever (PF) and lethal pneumonia named Legionnaires disease (LD) in humans. Reliable methods on quantitative exposure assessment of this bioaerosol are essential for the prevention of PF and LD. Coupled with culture, ethidium monoazide with qPCR, and qPCR assays, the collection efficiency for culturable, viable, and total *L. pneumophila* was assessed by means of filtration sampling (IOM with gelatin filter and cassette with polycarbonate filter) and liquid-based sampling methods (BioSampler, AGI-30, MAS-100 sampler with Tween mixture and deionized water (DW)). Results show IOM/gelatin filter was comparable to cassette/ polycarbonate filter ( $P = 0.33$ ) and performed greater than all of tested liquidbased methods for total cell collection. On the other hand, IOM/gelatin filter obtained greater efficiencies than cassette/polycarbonate filter by a factor of 3.8- 8.6 for viable cells ( $P = 0.0006$ ) and two orders of magnitude for culturable cells ( $P = 0.00002$ ). Further comparison between liquid impingement and filtration methods

indicates the sampling by IOM/gelatin filter, AGI-30, and BioSampler with DW were the most appropriate for viable cells, while culturable cells were collected most efficiently by BioSampler/DW with periodical replenishment during the sampling.

Chang, C.-W, S.-Y. Li, S.-H. Huang, C.-K. Huang, Y.-Y. Chen, C.-C. Chen, 2012. Effects of ultraviolet germicidal irradiation and swirling motion on airborne *Staphylococcus aureus*, *Pseudomonas aeruginosa* and *Legionella pneumophila* under various relative humidities. *Indoor Air* 2012; 23: 74-84

*Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Legionella pneumophila* have been detected in indoor air and linked to human infection. It is essential to adopt control methods to inactivate airborne pathogens. By passing bioaerosols horizontally into a UV device at two flow rates ( $Q_s$ ) and moving cells around a central UVC lamp at relative humidity (RH) of 12.7-16.7%, 58.7-59.6%, and 87.3-90%, the effects of swirling motion and 254-nm ultraviolet germicidal irradiation (UVGI) against bioaerosols were assessed under UVoff and UV-on settings, respectively. An inverse relationship between RH and UVGI effectiveness was observed for every test bioaerosol ( $r = 0.74 \sim 0.81$ ,  $P < 0.0001$ ). Increased UV resistance with RH is likely associated with the hygroscopicity of bioaerosols, evident by increased aerodynamic diameters at high RH ( $P < 0.05$ ). UVGI effectiveness was significantly increased with decreasing  $Q$  ( $P < 0.0001$ ). Moreover, *P. aeruginosa* was the most susceptible to UVGI, while the greatest UV resistance occurred in *L. pneumophila* at low RH and *S. aureus* at medium and high RH ( $P < 0.05$ ). Results of UV off show *P. aeruginosa* and *L. pneumophila* were more sensitive to air-swirling motion than *S. aureus* ( $P < 0.05$ ). Overall, test bioaerosols were reduced by 1.7-4.9 and 0.2-1.7 log units because of the UVGI and swirling movement, respectively.

Charlson, Emily S., Kyle Bittinger, Andrew R. Haas, Ayannah S. Fitzgerald, Ian Frank, Anjana Yadav, Frederic D. Bushman, and Ronald G. Collman, 2011. Topographical Continuity of Bacterial Populations in the Healthy Human Respiratory Tract *Am. J. Respir. Crit. Care Med.* 2011; 184: 957-963

Rationale: Defining the biogeography of bacterial populations in human body habitats is a high priority for understanding microbial- host relationships in health and disease. The healthy lung was traditionally considered sterile, but this notion has been challenged by emerging molecular approaches that enable comprehensive examination of microbial communities. However, studies of the lung are challenging due to difficulties in working with low biomass samples. Objectives: Our goal was to use molecular methods to define the bacterial microbiota present in the lungs of healthy individuals and assess its relationship to upper airway populations. Methods: We sampled respiratory flora intensively at multiple sites in six healthy individuals. The upper tract was sampled by oral wash and oro-/nasopharyngeal swabs. Two bronchoscopes were used to collect samples up to the glottis, followed by serial bronchoalveolar lavage and lower airway protected brush. Bacterial abundance and composition were analyzed by 16S rDNA Q-PCR and deep sequencing. Measurements and Main Results: Bacterial communities from the lung displayed composition indistinguishable from the upper airways, but were 2 to 4 logs lower in biomass. Lung-specific sequences were rare and not shared among individuals. There was no unique lung microbiome. Conclusions: In contrast to other organ systems, the respiratory tract harbors a homogenous microbiota that decreases in biomass from upper to lower tract. The healthy lung does not contain a consistent distinct microbiome, but instead contains low levels of bacterial sequences largely indistinguishable from upper respiratory flora. These findings establish baseline data for healthy subjects and sampling approaches for sequence-based analysis of diseases.

Chen, Qing and Lynn Hildemann, 2009. The Effects of Human Activities on Exposure to Particulate Matter and Bioaerosols in Residential Homes. *Environ. Sci. Technol.* 2009, 43, 4641-4646

Indoor and outdoor airborne particle mass, protein, endotoxin and (1 $\rightarrow$ 3)- $\beta$ -D-glucan in three size fractions (PM<sub>2.5</sub>, PM<sub>10</sub>, and TSP) were measured in ten single-family homes, along with quantifying household activities in the sampling room. Correlations between human activity levels and elevations in the indoor concentrations of particles and biomarkers were evaluated using four approaches for distinguishing activity levels: diurnal differences, the number of occupants, self-estimated occupancy, and activity strength. The concentrations of particles, protein, endotoxin and (1 $\rightarrow$ 3)- $\beta$ -D-glucan in all three size fractions (PM < 2.5  $\mu$ m, PM<sub>10-2.5</sub>, and PM > 10  $\mu$ m) were found, in most cases, to be significantly elevated during the day, and with higher activity levels in the room. The coarser fractions of particle mass and bioaerosols were more strongly correlated with human activity levels. Activity strength was the most statistically robust measure for relating human activities to indoor bioaerosol levels. While self-estimated activity and analysis of



diurnal differences both offer reasonable (but not perfect) alternatives to activity strength, the number of occupants appears to be a weaker indicator for homes.

Chen Q and Hildemann LM. 2009. Size-resolved concentrations of particulate matter and bioaerosols inside versus outside of homes. *Aerosol Science and Technology* 43(7):699-713

Size-resolved airborne particulate matter samples (PM<sub>2.5</sub>, PM<sub>10</sub>, and TSP collected inside ten northern California homes over four days and one night (9-12 h/sample, spanning a 3.5 week period) were analyzed for protein, endotoxin, and (1→3)-β-D-glucan concentrations. Some simultaneous size-resolved outdoor samples were also collected. The associations of residential characteristics and occupant behavior with the indoor airborne levels were investigated. In addition, the relation between these chemical biomarkers and the more traditional culturing approaches was studied. Most of the indoor mass concentration of airborne particles and protein was in the fine fraction (PM<sub>2.5</sub>), while the mass of airborne endotoxin and (1→3)-β-D-glucan was mainly in the coarser fractions (PM<sub>10-2.5</sub> and PMTSP-10). No strong correlations were seen between short-term (3-6 min) culturable bacteria and fungi counts and the corresponding longer-term (9-12 h) biomarker levels. Daytime indoor levels of the biomarkers tended to be higher than outdoors, especially for the PM<sub>10-2.5</sub> fraction, but only in a few cases were the indoor/outdoor relationships statistically significant. Indoor pets were associated with elevated airborne PM and bioaerosols inside homes. Two other factors, wall-to-wall carpet and older houses, also appear to be associated with some elevations in indoor levels.

Chen S. C., C. P. Chio, L. J. Jou, C. M. Liao, 2009. Viral kinetics and exhaled droplet size affect indoor transmission dynamics of influenza infection. *Indoor Air* 2009; 19: 401-413.

The purpose of this paper was to investigate the effects of viral kinetics and exhaled droplet size on indoor transmission dynamics of influenza infection. The target cell-limited model with delayed virus production was adopted to strengthen the inner mechanisms of virus infection on human epithelial cell. The particle number and volume involved in the viral kinetics were linked with Wells- Riley mathematical equation to quantify the infection risk. We investigated population dynamics in a specific elementary school by using the seasonal susceptible - exposed - infected - recovery (SEIR) model. We found that exhaled pulmonary bioaerosol of sneeze (particle diameter <10 μm) have 102-fold estimate higher than that of cough. Sneeze and cough caused risk probabilities range from 0.075 to 0.30 and 0.076, respectively; whereas basic reproduction numbers (R<sub>0</sub>) estimates range from 4 to 17 for sneeze and nearly 4 for cough, indicating sneeze-posed higher infection risk. The viral kinetics and exhaled droplet size for sneeze affect indoor transmission dynamics of influenza infection since date post-infection 1-7. This study provides direct mechanistic support that indoor influenza virus transmission can be characterized by viral kinetics in human upper respiratory tracts that are modulated by exhaled droplet size.

Chew, G. L., C. Rogers, H. A. Burge, M. L. Muilenberg, D. R. Gold, 2003. Dustborne and airborne fungal propagules represent a different spectrum of fungi with differing relations to home characteristics. *Allergy* 2003; 58: 13-20.

Background: Exposure to fungi is often assessed by culturing floor dust or air samples. Our objective was to evaluate the relationships between dustborne and airborne fungi and to identify factors that modify these relationships. Methods: From November 1994 to September 1996 sequential duplicate 45-l air samples were collected in bedrooms of 496 homes in the Boston area, using a Burkard culture plate sampler. After air sampling, bedroom floors were sampled with a vacuum cleaner that was modified to collect dust in a cellulose extraction thimble. Dust was sieved, and the fine dust was dilution-plated onto DG-18 media. Results: Concentrations of total culturable fungi per gram of bedroom-floor dust were correlated weakly, but significantly, with those of indoor air ( $r = 0.13$ ,  $P < 0.05$ ). Concentrations of some individual taxa in the dust and indoor air were also weakly associated. Adjusting for the concentrations of fungi in outdoor air, dustborne fungal concentrations were positively associated with those in indoor air for the taxa *Cladosporium* and *Penicillium*, but not for total fungi. The indoor air fungal levels were often predicted by different covariates to those predicting fungal levels in dust. The type of housing (house or apartment) and the presence of carpeting were often predictive factors for dust fungi. In contrast, outdoor fungal levels were often predictive of the indoor air fungal levels. Conclusions: Because our data do not indicate a strong overall relationship between culturable fungi in dust and indoor air, the results from these two methods (dust and air sampling) likely represent different types of potential fungal exposures to residents. It may be essential to collect both air and dust samples, as well as information on housing characteristics, as indicators for fungal exposure.

Cho, Sook Ja, Ju-Hyeong Park, Kathleen Kreiss and Jean M. Cox-Ganser, 2010. Levels of microbial: agents in floor dust during remediation of a water-damaged office building. *Indoor Air*. Accepted manuscript online

We examined the effects of remediation on loads of culturable fungi in floor dust collected from a large water-damaged office building during 4 cross-sectional surveys (2002, 2004, 2005, and 2007, respectively). We created a binary remediation variable for each year for each sampled workstation using information on remediation associated with water damage obtained from building management and used generalized linear mixed-effects models. We found significantly lower levels of culturable total and hydrophilic fungi at remediated workstations than at nonremediated workstations in 2004 and 2005 after completion of major remediation. The remediation effect, however, disappeared in 2007. The fraction of hydrophilic to total fungal concentrations was lowest in 2004, increased in 2005 and was highest in 2007. Our results indicate that the 2003 remediation lowered dust indices of dampness temporarily, but remediation was incomplete, consistent with a building assessment report of water infiltration. This study demonstrates the utility of longitudinal evaluation of microbial indices during remediation of water damage in this building, in which elimination of sources of moisture was not fully addressed. Our findings indicate that the fraction of hydrophilic fungi derived from concentrations of fungal species may be a useful index for assessing the long-term effectiveness of remediation.

Choi, H. S. Byrn, L. S. Larsen, T. Sigsgaard, P. S. Thorne, L. Larsson, A. Sebastian, C.-G. Bornehag, 2014. Residential culturable fungi, (1-3, 1-6)-  $\beta$ -D-glucan, and ergosterol concentrations in dust are not associated with asthma, rhinitis, or eczema diagnoses in children. *Indoor Air* 2014; 24: 158–170.

Qualitative reporting of home indoor moisture problems predicts respiratory diseases. However, causal agents underlying such qualitative markers remain unknown. In the homes of 198 multiple allergic case children and 202 controls in Sweden, we cultivated culturable fungi by directly plating dust, and quantified (1-3, 1-6)-  $\beta$ -D-glucan and ergosterol in dust samples from the child's bedroom. We examined the relationship between these fungal agents and degree of parent or inspector-reported home indoor dampness, and microbiological laboratory's mold index. We also compared the concentrations of these agents between multiple allergic cases and healthy controls, as well as IgE-sensitization among cases. The concentrations of culturable fungal agents were comparable between houses with parent and inspector-reported mold issues and those without. There were no differences in concentrations of the individual or the total summed culturable fungi, (1-3, 1-6)-  $\beta$ -D-glucan, and ergosterol between the controls and the multiple allergic case children, or individual diagnosis of asthma, rhinitis, or eczema. Culturable fungi, (1-3, 1-6)-  $\beta$ -D-glucan, and ergosterol in dust were not associated with qualitative markers of indoor dampness or mold or indoor humidity. Furthermore, these agents in dust samples were not associated with any health outcomes in the children.

Ciencewicky, Jonathan and Illona Jaspers 2007. Air Pollution and Respiratory Viral Infection. *Inhalation Toxicology*, 19:1135-1146, 2007

Despite current regulations, which limit the levels of certain air pollutants, there are still a number of adverse health effects that result from exposure to these agents. Numerous epidemiological studies have noted an association between the levels of air pollution and hospital admissions for a variety of different health reasons, including a number of respiratory diseases, as well as increased morbidity and mortality associated with various respiratory conditions and diseases. Because of the large impact respiratory virus infections have on morbidity and even mortality, it is important to understand whether and how exposure to common air pollutants could exacerbate the susceptibility to and severity of respiratory virus infections. This review focuses on current epidemiological and experimental studies, which have examined the association between and effect of air pollutants and respiratory viral infections, as well as potential mechanisms associated with these effects. Examined in this review are U.S. Environmental Protection Agency (EPA) "criteria" pollutants nitrogen dioxide (NO<sub>2</sub>), ozone (O<sub>3</sub>), and particulate matter (PM), as well as indoor pollutants such as environmental tobacco smoke (ETS) and combustion products of biomass fuels. Although a number of studies indicate associations between exposure to air pollutants and increased risk for respiratory virus infections, potential mechanisms mediating these effects are largely unexplored. Therefore, additional studies, both epidemiologic and mechanistic, are necessary to increase our understanding of how exposure to air pollutants could affect respiratory virus infections, especially in populations already at risk of developing significant morbidity/mortality after infections with respiratory viruses.

Cimolai, N., 2008. MRSA and the environment: implications for comprehensive control measures. *European Journal of Clinical Microbiology & Infectious Diseases*, 2008, Volume 27, Number 7, Pages 481-493

Environmental contamination with methicillin-resistant *Staphylococcus aureus* (MRSA) is established soon after colonized or infected patients become resident. There are many studies that detail the mechanisms of spread and environmental survival of methicillin-susceptible *Staphylococcus aureus* (MSSA); this knowledge translates directly into the same findings for MRSA. The potential ubiquity of MRSA in a health-care setting poses challenges for decontamination. Whereas patients and medical staff are important sources for MRSA spread, the environmental burden may contribute significantly in various contexts. Effective control measures must therefore include consideration for MRSA in the environment.

Claeson A-, Sandstrom M, Sunesson A-. 2007. Volatile organic compounds (VOCs) emitted from materials collected from buildings affected by microorganisms. *Journal of Environmental Monitoring* 9(3):240-5

In this study mould damaged materials, including carpet, concrete, gypsum board, insulation, plastic, sand and wood, from 20 different buildings with moisture problems were collected. To study emissions from these materials both conventional methods for sampling, such as collection on Tenax TA, were used as well as complementary methods for sampling a wider spectrum of compounds, such as more volatile VOCs, amines and aldehydes. Analysis was carried out using gas chromatography and high-performance liquid chromatography. Mass spectrometry was used for identification of compounds. Alcohols and ketones were almost exclusively emitted from the materials after they had been wet for a week. Acids were also emitted in large quantities from wet gypsum board and plastic. No primary or secondary amines could be identified, but two tertiary amines, trimethylamine and triethylamine, were emitted from sand contaminated by *Bacillus*. The most common moulds found were *Penicillium* and *Aspergillus*. A multivariate method (partial least squares, PLS) was used to investigate the emission patterns from the materials. Materials with bacterial growth had a different VOC profile to those with only mould growth.

Clark, Raymond P. and Mervyn L. de Calcina-Goff, 2009. Some aspects of the airborne transmission of infection. *J. R. Soc. Interface* (2009) 6, S767-S782

The relationship between the human body and the dissemination of potentially pathogenic particles and droplets is described. Airborne transmission of infection in operating theatres and a burns unit and the part played by the human microclimate and its interaction with ventilating air flows is discussed. The mechanisms by which different garment assemblies used for surgery can enhance particle dispersion are illustrated and the way that floor cleaning can increase the concentration of airborne organisms is described. The development of the successful use of ultra-clean air systems in orthopaedic implant surgery is reviewed. Relationships between contact and airborne transmission of disease are explored and ways by which containment strategies and metrics used in pharmaceutical and electronics manufacturing can be applied to the design and monitoring of healthcare areas is discussed. It is suggested that currently available techniques involving architectural, ventilation and operational aspects of healthcare provision, when properly applied, can markedly improve treatment outcomes that may otherwise be compromised by hospital-acquired infections involving both bacteria and viruses.

Clausen, G., A. Høst, J. Toftum, G. Beko, C. Weschler, M. Callesen, S. Buhl, M. B. Ladegaard, S. Langer, B. Andersen, J. Sundell, C.-G. Bornehag, T. Sigsgaard, 2012. Children's health and its association with indoor environments in Danish homes and daycare centres – methods. *Indoor Air* 2012; 22: 467–475

The principle objective of the Danish research program 'Indoor Environment and Children's Health' (IECH) was to explore associations between various exposures that children experience in their indoor environments (specifically their homes and daycare centers) and their well-being and health. The targeted health endpoints were allergy, asthma, and certain respiratory symptoms. The study was designed with two stages. In the first stage, a questionnaire survey was distributed to more than 17 000 families with children between the ages of 1 and 5. The questionnaire focused on the children's health and the environments within the homes they inhabited and daycare facilities they attended. More than 11 000 questionnaires were returned. In the second stage, a subsample of 500 children was selected for more detailed studies, including an extensive set of measurements in their homes and daycare centers and a clinical examination; all clinical examinations were carried out by the same physician. In this study, the methods used for data collection within

the IECH research program are presented and discussed. Furthermore, initial findings are presented regarding descriptors of the study population and selected characteristics of the children's dwellings and daycare centers.

Codina R, Fox RW, Lockey RF, DeMarco P, Bagg A. 2008. Typical levels of airborne fungal spores in houses without obvious moisture problems during a rainy season in Florida, USA. *Journal of Investigational Allergology and Clinical Immunology* 18(3):156-62.

**Objective:** The aim of this study was to determine types and levels of airborne fungal spores in air-conditioned homes built after 1980 without obvious moisture problems during the 2004 summer (rainy season) in central Florida, USA. **Methods:** Eighteen single-family homes were selected based on protocol questionnaire and cursory inspection, which revealed no obvious moisture or visible fungal growth. Non-cultured spores were collected with Air-O-Cell cassettes. Three indoor air samples and 2 outdoor air samples were collected from each home. One indoor and 2 outdoor samples were not interpretable. Fifty-three indoor and 34 outdoor air samples were analyzed by optical microscopy. **Results:** Several spore types were detected in the indoor samples, at levels generally lower than those detected in the outdoor samples. Spores from the *Penicillium/Aspergillus* group were the most prevalent types indoors, exceeding the absolute levels and relative percentages of these spores outdoors. Ascospores and basidiospores were the most prevalent spore types outdoors. The percentages of other spore types (*Cladosporium* and *Curvularia*) were similar in the indoor and outdoor samples. Moisture-indicator fungi (*Chaetomium*, *Stachybotrys*, and *Ulocladium* species) were nearly absent in both indoor and outdoor samples. **Conclusion:** Airborne fungal spores are present in average central Florida homes without obvious moisture problems during the summer, at levels that are lower than those found outdoors. Spores from the *Penicillium/Aspergillus* group are prevalent in these homes, and moisture-indicator fungi (*Chaetomium*, *Stachybotrys*, and *Ulocladium* species) are nearly absent. Despite climatic differences, airborne fungal spore types and levels in central Florida houses are similar to those found in other geographical locations.

Costello, Elizabeth K., Christian L. Lauber, Micah Hamady, Noah Fierer, Jeffrey I. Gordon, Rob Knight, 2009. Bacterial Community Variation in Human Body Habitats Across Space and Time. *Science* 326, 1694 (2009)

Elucidating the biogeography of bacterial communities on the human body is critical for establishing healthy baselines from which to detect differences associated with diseases. To obtain an integrated view of the spatial and temporal distribution of the human microbiota, we surveyed bacteria from up to 27 sites in seven to nine healthy adults on four occasions. We found that community composition was determined primarily by body habitat. Within habitats, interpersonal variability was high, whereas individuals exhibited minimal temporal variability. Several skin locations harbored more diverse communities than the gut and mouth, and skin locations differed in their community assembly patterns. These results indicate that our microbiota, although personalized, varies systematically across body habitats and time; such trends may ultimately reveal how microbiome changes cause or prevent disease.

Coughenour, C, Stevens, V and Stetzenbach, LD, 2011. An Evaluation of Methicillin-Resistant *Staphylococcus aureus* Survival on Five Environmental Surfaces. *MICROBIAL DRUG RESISTANCE*, Vol. 17 No. 3, pp. 457-461

This study evaluated methicillin-resistant *Staphylococcus aureus* (MRSA) survival on environmental surfaces: glass, wood, vinyl, plastic, and cloth. Effects of relative humidity (RH) and bovine serum albumin (BSA) were examined. Surfaces were inoculated with 107-108 colony forming units per milliliter (CFU/ml) of MRSA with and without 1% BSA and incubated at 35 °C at 45%-55% and 16% RH. Surfaces were sampled, and each collected sample was re-suspended in phosphate buffer, spread plated, and incubated at 35 °C for 24 hrs; resulting colonies were enumerated. Samples were collected immediately on drying, and at 3 hrs, 24 hrs, 2 days, 3 days, 4 days, and 5 days. Results demonstrated that MRSA survived the longest on plastic and vinyl and for the least amount of time on wood ( $p < 0.001$ ). BSA enabled MRSA to survive for significantly longer duration ( $p < 0.001$ ). The number of CFU/ml was significantly lesser on surfaces stored in 45%-55% RH versus 16% RH. This study demonstrates that viable MRSA bacteria can remain on surfaces for days, which may impact the public health of occupants in workplace and residential settings.

CROOK, Brian, Nancy C. BURTON, 2010. Indoor moulds, Sick Building Syndrome and building related illness. *fungal biology reviews* 24 (2010) 106 -113

Humans are constantly exposed to fungi, or moulds, usually without suffering harm to health. However, in some instances inhalation of sufficient numbers of mould spores can trigger symptoms of asthma, rhinitis or bronchitis. Respiratory ill health associated with the built environment is often referred to either as Sick Building Syndrome [SBS] (i.e. building related symptoms) or building related illness. For many, the difference between SBS and building related illness is unclear and the two overlap. This review examines the differences between the two and describes in more detail the role of moulds in building related illness. Using as examples the after-effects of flooding in the UK in 2007, and Hurricane Katrina in USA in 2005, methods used to investigate exposure to indoor mould contamination are described, together with strategies for remediating mould contaminated buildings.

Daisey, J. M. Daisey, W. J. Angell and M. G. Apte, 2003. Indoor air quality, ventilation and health symptoms in schools: an analysis of existing information. *Indoor Air* 2003; 13: 53-64

We reviewed the literature on Indoor Air Quality (IAQ), ventilation, and building-related health problems in schools and identified commonly reported building-related health symptoms involving schools until 1999. We collected existing data on ventilation rates, carbon dioxide (CO<sub>2</sub>) concentrations and symptom-relevant indoor air contaminants, and evaluated information on causal relationships between pollutant exposures and health symptoms. Reported ventilation and CO<sub>2</sub> data strongly indicate that ventilation is inadequate in many classrooms, possibly leading to health symptoms. Adequate ventilation should be a major focus of design or remediation efforts. Total volatile organic compounds, formaldehyde (HCHO) and microbiological contaminants are reported. Low HCHO concentrations were unlikely to cause acute irritant symptoms (<0.05 ppm), but possibly increased risks for allergen sensitivities, chronic irritation, and cancer. Reported microbiological contaminants included allergens in deposited dust, fungi, and bacteria. Levels of specific allergens were sufficient to cause symptoms in allergic occupants. Measurements of airborne bacteria and airborne and surface fungal spores were reported in schoolrooms. Asthma and 'sickbuilding syndrome' symptoms are commonly reported. The few studies investigating causal relationships between health symptoms and exposures to specific pollutants suggest that such symptoms in schools are related to exposures to volatile organic compounds (VOCs), molds and microbial VOCs, and allergens.

Dancer, Stephanie, 2008. Importance of the environment in meticillin-resistant *Staphylococcus aureus* acquisition: the case for hospital cleaning. *Lancet Infect Dis* 2008; 8: 101-13.

In the UK, we continue to debate the importance of hospital cleaning in relation to increasing numbers of patients acquiring meticillin-resistant *Staphylococcus aureus* (MRSA). However, there is little direct evidence for the effectiveness of cleaning because it has never been afforded scientific status. Hospital hygiene is usually assessed visually, but this does not necessarily correlate with microbiological risk. A more robust case for hospital cleaning can be presented by considering the evidence for all the stages of the staphylococcal transmission cycle between human beings and their environment. Cleaning has already been accepted as an important factor in the control of other hardy environmental pathogens, such as *Clostridium difficile*, vancomycin-resistant enterococci, norovirus, and *Acinetobacter* spp. This Review will show why the removal of dirt might have more impact on the control of MRSA than previously thought. Introduction of additional cleaning services is easier than improvements in hand-hygiene compliance.

Dancer, S.J., 2011. Hospital cleaning in the 21st century. *European Journal of Clinical Microbiology & Infectious Diseases* Volume 30, Number 12 (2011), 1473-1481, DOI: 10.1007/s10096-011-1250-x

More evidence is emerging on the importance of the clinical environment in encouraging hospital infection. This review considers the role of cleaning as an effective means to control infection. It describes the location of pathogen reservoirs and methods for evaluating hospitals' cleanliness. Novel biocides, antimicrobial coatings and equipment are available, many of which have not been assessed against patient outcome. Cleaning practices should be tailored to clinical risk, given the wide-ranging surfaces, equipment and building design. There is confusion between nursing and domestic personnel over the allocation of cleaning responsibilities and neither may receive sufficient training and/or time to complete their duties. Since less labourious practices for dirt removal are always attractive, there is a danger that traditional cleaning methods are forgotten or ignored. Few studies have examined detergent-based regimens or modelled these against infection risk for different patient categories. Fear of infection encourages the use of powerful disinfectants for the elimination of real or imagined pathogens in hospitals. Not only do these agents offer false assurance against contamination, their disinfection potential cannot be achieved without the prior removal of organic

soil. Detergent-based cleaning is cheaper than using disinfectants and much less toxic. Hospital cleaning in the 21st century deserves further investigation for routine and outbreak practices.

Dannemiller, K. C., M. J. Mendell, J. M. Macher, K. Kumagai, A. Bradman, N. Holland, K. Harley, B. Eskenazi, J. Peccia, 2013. Next-generation DNA sequencing reveals that low fungal diversity in house dust is associated with childhood asthma development. *Indoor Air* 2014; 24: 236–247.

Dampness and visible mold in homes are associated with asthma development, but causal mechanisms remain unclear. The goal of this research was to explore associations among measured dampness, fungal exposure, and childhood asthma development without the bias of culture-based microbial analysis. In the low-income, Latino CHAMACOS birth cohort, house dust was collected at age 12 months, and asthma status was determined at age 7 years. The current analysis included 13 asthma cases and 28 controls. Next-generation DNA sequencing methods quantified fungal taxa and diversity. Lower fungal diversity (number of fungal operational taxonomic units) was significantly associated with increased risk of asthma development: unadjusted odds ratio (OR) 4.80 (95% confidence interval (CI) 1.04–22.1). Control for potential confounders strengthened this relationship. Decreased diversity within the genus *Cryptococcus* was significantly associated with increased asthma risk (OR 21.0, 95% CI 2.16–204). No fungal taxon (species, genus, class) was significantly positively associated with asthma development, and one was significantly negatively associated. Elevated moisture was associated with increased fungal diversity, and moisture/mold indicators were associated with four fungal taxa. Next-generation DNA sequencing provided comprehensive estimates of fungal identity and diversity, demonstrating significant associations between low fungal diversity and childhood asthma development in this community.

Dassonville C, Demattei C, Detaint B, Barral S, Bex-Capelle V, Momas I. 2008. Assessment and predictors determination of indoor airborne fungal concentrations in paris newborn babies' homes. *Environ Res* 108(1):80-5.

Indoor mould growth can affect health, especially in early childhood. As part of a birth cohort follow-up, the purpose of this study was firstly to examine spectrum and levels of airborne fungi in 190 Paris newborns' dwellings, and secondly to identify predictors of these levels. Sequential duplicate air samples were collected twice a year in the newborn's bedroom and outside the building. A single-stage multi-holed impactor (Air Ideals) was used with chloramphenicol/MEA agar. Housing characteristics were assessed using a questionnaire administered by a trained interviewer. *Cladosporium* and *Penicillium* were isolated in, respectively, 77% and 93% of homes in the cold season, and in 95% and 83% of homes in the hot season. *Aspergillus* and *Alternaria* were recovered from indoor air in, respectively, 60% and less than 20% of homes. Geometric means (geometric standard deviation) of indoor total airborne fungal concentrations at two different visits were, respectively, 232.4 (3.2) and 186.7 (2.7) cfu/m<sup>3</sup>. In the GEE multivariate analysis, outdoor fungal concentrations were the best predictors for variability of indoor total fungal and *Cladosporium* concentrations (respectively, R<sup>2</sup> = 32% and 31%). Levels of total airborne fungal and *Cladosporium* concentrations were significantly higher during the hot season (respectively, p = 0.003 and p = 0.001) and were positively correlated with the duration of bedroom aeration (respectively, p = 0.004 and p = 0.001). Signs of dampness were associated with higher total airborne fungi (p = 0.031) and *Aspergillus* levels (p = 0.055). This study provides for the first time indoor airborne fungal spectrum and concentrations in Paris. Outdoor levels and season largely contributed to the variability of indoor total airborne fungal concentrations, which also depended on aeration and signs of dampness.

Davies, David G., Matthew R. Parsek, James P. Pearson, Barbara H. Iglewski, J. W. Costerton, E. P. Greenberg 1998. The Involvement of Cell-to-Cell Signals in the Development of a Bacterial Biofilm. *Science* 280: 295-298. 10 April 1998.

Bacteria in nature often exist as sessile communities called biofilms. These communities develop structures that are morphologically and physiologically differentiated from freeliving bacteria. A cell-to-cell signal is involved in the development of *Pseudomonas aeruginosa* biofilms. A specific signaling mutant, a *lasI* mutant, forms flat, undifferentiated biofilms that unlike wild-type biofilms are sensitive to the biocide sodium dodecyl sulfate. Mutant biofilms appeared normal when grown in the presence of a synthetic signal molecule. The involvement of an intercellular signal molecule in the development of *P. aeruginosa* biofilms suggests possible targets to control biofilm growth on catheters, in cystic fibrosis, and in other environments where *P. aeruginosa* biofilms are a persistent problem.

de Oliveira, Adriana Cristina and Quésia Souza Damasceno, 2010. Surfaces of the hospital environment as possible deposits of resistant bacteria: a review. *Rev Esc Enferm USP* 2010; 44(4):1112-7

The main objective of this study is to identify, in the literature, articles about the occurrence of contamination from inanimate surfaces and a possible dissemination of resistant bacteria in the hospital environment. A bibliographic survey was performed with articles published in the databases LILACS, MEDLINE, Science Direct, SCOPUS and ISI Web of Knowledge, between 2000 and 2008. Twenty-one articles were selected and analyzed. The analyzed studies highlighted the presence of bacteria on monitors, bed grids, tables, faucets, telephones, keyboards and other objects. There was a prevalence of *Staphylococcus aureus* resistant to methicillin, *Clostridium difficile*, *Acinetobacter baumannii* and *Enterococcus* resistant to vancomycin, being the predictive factor the previous occupation of patients colonized by these microorganisms. There was a similarity observed among the isolated strains of colonized and/or infected patients and the strains of the environment by molecular typification. These evidences reinforce the need for knowledge and control of the sources of pathogens in the hospital environment.

Dettenkofer, M., A. Ammon, P. Astagneau, S.J. Dancer, P. Gastmeier, S. Harbarth, H. Humphreys, W.V. Kern, O. Lyytikäinen, H. Sax, A. Voss, A.F. Widmer, 2010. Infection control e a European research perspective for the next decade. *Journal of Hospital Infection* 77 (2011) 7-10.

A symposium was held in June 2009 near Freiburg in Germany. Twenty-nine attendees from several European countries participated, most of whom are actively involved in research and hospital infection prevention and control. The following topics were presented and discussed: isolation and screening for control of multidrug-resistant organisms; impact of the environment on healthcare-associated infection (HAI); new technologies to control infection e state of evidence; surveillance of HAI; methodological challenges and research priorities for infection control and control of HAI: learning from each other in a united Europe. This Leader summarises the main issues for debate and the number of consensus points agreed amongst delegates.

Dillon, H. Kenneth, J. David Miller, W.G. Sorenson, Jeroen Douwes, and Robert R. Jacobs 1999 Review of Methods Applicable to the Assessment of Mold Exposure to Children. *Environ Health Perspect* 107(suppl 3):473-480 (1999).

This article presents discussion of the assessment of the exposure of children to fungi, substances derived from fungi, and the environmental conditions that may lead to exposure. The principles driving investigations of fungal contamination and subsequent exposure are presented as well as guidelines for conducting these investigations. A comprehensive description of available research sampling and analysis techniques is also presented

D'Orazio, Marco, Marco Palladini, Lucia Aquilanti, Francesca Clementi 2009. Experimental evaluation of the growth rate of mould on finishes for indoor housing environments: Effects of the 2002/91/EC directive. *Building and Environment* 44 (2009) 1668-1674.

We report the results of a study to evaluate the growth rate of three species of mould on plasters, finishes and paints typically used in structures with heavy weight building envelopes. The aim was to determine the influence of the chemical composition (in terms of organic fraction of the materials) on the growth rate of moulds. The study was carried out in the following steps: - characterization of materials; - inoculation of mould spores (3 species) on 7 types of material (2 plasters, 3 finishes, 2 paints); - growth in a climatic chamber (23 °C and 90% RH); - analysis of the mould growth rate using various experimental techniques (fluorescence microscopy analysis, thermogravimetric analysis, etc.). Results show a clear correlation between the organic substances contained in paints, plasters and finishes and the growth rate of the mould. This study is part of a more general research program which addresses the effects on indoor environment air quality based on the European directive 2002/91/EC. This directive specifically indicates that energy consumption in buildings should be limited and sets threshold values for the thermal resistance of the building walls and windows. As a consequence window manufacturers are improving the thermal property of windows by reducing the air permeability, which may increase the indoor and surface relative humidity percentage (RH%) and lead to the development of mould in the indoor environments.

DOUWES, J, VANDERSLUIJ, B, DOEKES, G, VANLEUSDEN, F, WIJNANDS, L, VANSTRIEN, R, VERHOEFF, A & BRUNEKREEF, B, 1999, 'Fungal extracellular polysaccharides in house dust as a marker for exposure to fungi: Relations with culturable

fungi, reported home dampness, and respiratory symptoms', *Journal of Allergy and Clinical Immunology*, vol. 103, no. 3, pp. 494-500.

Epidemiologic studies have demonstrated an association between indoor fungal growth and respiratory symptoms. However, in only a few studies was fungal exposure actually measured. Objective: The purpose of this study was to evaluate the measurement by enzyme immunoassay of extracellular polysaccharides of *Aspergillus* and *Penicillium* species (EPS-Asp/Pen) in house dust as a marker for fungal exposure and to study the relations between EPS-Asp/Pen levels and home dampness and respiratory symptoms in children. Methods: Extracts of house dust samples from bedroom and living room floors and mattresses from homes of 31 children with chronic respiratory symptoms and 29 children with no chronic respiratory symptoms were analyzed for EPS-Asp/Pen. Results: EPS-Asp/Pen were readily detectable (40 to 46,513 nanogram equivalent/g dust) in 161 house dust extracts, with highest concentrations in living room floor dust. EPS-Asp/Pen levels were 2 to 3 times higher on carpeted floors than on smooth floors. EPS-Asp/Pen were significantly correlated with total culturable fungi ( $r = 0.3$  to  $0.5$ ) and with house dust mite allergens ( $r = 0.3$  to  $0.5$ ). EPS-Asp/Pen levels in living room floor dust were positively associated with occupant-reported home dampness. This was not observed for EPS-Asp/Pen in bedroom floor and mattress dust. EPS-Asp/Pen levels in living room floor dust were positively associated with respiratory symptoms. EPS-Asp/Pen in bedroom floor and mattress dust showed a reversed association with respiratory symptoms, possibly because of allergen-avoidance measures taken in the bedroom. Conclusion: The enzyme immunoassay for fungal EPS-Asp/Pen may be a useful method for exposure assessment of indoor fungi.

Douwes J., Thorne P., Pearce N., & Heederik D. (2003). Bioaerosol health effects and exposure assessment: Progress and prospects. *Annals of Occupational Hygiene*, 47(3), 187-200

Exposures to bioaerosols in the occupational environment are associated with a wide range of health effects with major public health impact, including infectious diseases, acute toxic effects, allergies and cancer. Respiratory symptoms and lung function impairment are the most widely studied and probably among the most important bioaerosol-associated health effects. In addition to these adverse health effects some protective effects of microbial exposure on atopy and atopic conditions has also been suggested. New industrial activities have emerged in recent years in which exposures to bioaerosols can be abundant, e.g. the waste recycling and composting industry, biotechnology industries producing highly purified enzymes and the detergent and food industries that make use of these enzymes. Dose-response relationships have not been established for most biological agents and knowledge about threshold values is sparse. Exposure limits are available for some contaminants, e.g. wood dust, subtilisins (bacterial enzymes) and flour dust. Exposure limits for bacterial endotoxin have been proposed. Risk assessment is seriously hampered by the lack of valid quantitative exposure assessment methods. Traditional culture methods to quantify microbial exposures have proven to be of limited use. Non-culture methods and assessment methods for microbial constituents [e.g. allergens, endotoxin,  $\beta(1\rightarrow3)$ -glucans, fungal extracellular polysaccharides] appear more successful; however, experience with these methods is generally limited. Therefore, more research is needed to establish better exposure assessment tools and validate newly developed methods. Other important areas that require further research include: potential protective effects of microbial exposures on atopy and atopic diseases, inter-individual susceptibility for biological exposures, interactions of bioaerosols with non-biological agents and other potential health effects such as skin and neurological conditions and birth effects.

Dowell S. 2001. Seasonal variation in host susceptibility and cycles of certain infectious diseases. *Emerg Infect Dis* 7(3):369-74.

Seasonal cycles of infectious diseases have been variously attributed to changes in atmospheric conditions, the prevalence or virulence of the pathogen, or the behavior of the host. Some observations about seasonality are difficult to reconcile with these explanations. These include the simultaneous appearance of outbreaks across widespread geographic regions of the same latitude; the detection of pathogens in the off-season without epidemic spread; and the consistency of seasonal changes, despite wide variations in weather and human behavior. In contrast, an increase in susceptibility of the host population, perhaps linked to the annual light/dark cycle and mediated by the pattern of melatonin secretion, might account for many heretofore unexplained features of infectious disease seasonality. Ample evidence indicates that photoperiod-driven physiologic changes are typical in mammalian species, including some in humans. If such physiologic changes underlie human resistance to infectious diseases for large portions of the year and the changes can be identified and modified, the therapeutic and preventive implications may be considerable.



Dowell S and Ho M. 2004. Seasonality of infectious diseases and severe acute respiratory syndrome - what we don't know can hurt us. *Lancet Infect Dis* 4(11):704-8.

The novel severe acute respiratory syndrome (SARS) coronavirus caused severe disease and heavy economic losses before apparently coming under complete control. Our understanding of the forces driving seasonal disappearance and recurrence of infectious diseases remains fragmentary, thus limiting any predictions about whether, or when, SARS will recur. It is true that most established respiratory pathogens of human beings recur in wintertime, but a new appreciation for the high burden of disease in tropical areas reinforces questions about explanations resting solely on cold air or low humidity. Seasonal variation in host physiology may also contribute. Newly emergent zoonotic diseases such as ebola or pandemic strains of influenza have recurred in unpredictable patterns. Most established coronaviruses exhibit winter seasonality, with a unique ability to establish persistent infections in a minority of infected animals. Because SARS coronavirus RNA can be detected in the stool of some individuals for at least 9 weeks, recurrence of SARS from persistently shedding human or animal reservoirs is biologically plausible.

Doyen, Virginie, Anne-Britt Johansson, Laurence Hanssens, Nathalie Dehennin, Duc Huy Phong Dinh, Georges Casimir, Olivier Michel, 2011. Relationship between the presence of newborn and the house dust endotoxin. *Science of the Total Environment* 409 (2011) 5313-5317

Exposure to house dust endotoxin induces of airways' inflammation. Endotoxin are produced by the Gram-negative bacteria, which are released into the stools and could contaminate domestic environment. Objective: The newborn could contaminate his mattress by endotoxin. Methods: The dusts of mattress and carpets of 97 newborn' dwellings were sampled at birth and after six months of life. Samplings were made in the bedroom from the baby and in the second place where the baby spent the longer time. The endotoxin concentration was measured by a quantitative Limulus assay and the bacterial contamination was evaluated using 3 selective agar media. Results: Endotoxin concentration at birth was positively associated with the presence of both sibling and the number of inhabitants ( $p < 0.01$ ). At 6 months of life, the endotoxin concentration raised significantly not only in the mattresses (from a median of 17.6 (ranges: 0.4-346.7) to 79.6 (3.8-518.8) EU/mg ( $p < 0.0001$ ), but also in the dust from the second place where the baby is sleeping (from 20.4 (0.8-226.3) to 101.8 (6.5- 634.3) EU/mg ( $p < 0.001$ ). Importantly, there was no change in endotoxin concentration from the carpets dust, and the environmental dwelling characteristics remained unchanged. The total bacterial contamination was also positively associated with endotoxin concentration in newborn mattress at birth ( $p < 0.01$ ) and showed a significant increase at 6 months of life of the newborn ( $p < 0.01$ ). Conclusion: The newborn is a significant source of house dust's endotoxin.

du Prel, Jean-Baptist, Wolfram Puppe, Britta Grondahl, Markus Knuf, Josef A. I. Weigl, Franziska Schaaff, and Heinz-Josef Schmitt, 2009. Are Meteorological Parameters Associated with Acute Respiratory Tract Infections? *Clinical Infectious Diseases* 2009; 49:861-8.

Background. Information on the onset of epidemics of acute respiratory tract infections (ARIs) is useful in timing preventive strategies (eg, the passive immunization of high-risk infants against respiratory syncytial virus [RSV]). Aiming at better predictions of the seasonal activity of ARI pathogens, we investigated the influence of climate on hospitalizations for ARIs. Methods. Samples obtained from 3044 children hospitalized with ARIs in Mainz, Germany, were tested for pathogens with a multiplex reverse-transcriptase polymerase chain reaction enzyme-linked immunosorbent assay from 2001 through 2006. Hospitalizations for ARIs were correlated with meteorological parameters recorded at the University of Mainz. The frequency of hospitalization for RSV infection was predicted on the basis of multiple time series analysis. Results. Influenza A, RSV, and adenovirus were correlated with temperature and rhinovirus to relative humidity. In a time series model that included seasonal and climatic conditions, RSV-associated hospitalizations were predictable. Conclusions. Seasonality of certain ARI pathogens can be explained by meteorological influences. The model presented herein is a first step toward predicting annual RSV epidemics using weather forecast data.

Dunn RR, Fierer N, Henley JB, Leff JW, Menninger HL (2013) Home Life: Factors Structuring the Bacterial Diversity Found within and between Homes. *PLoS ONE* 8(5): e64133. doi:10.1371/journal.pone.0064133

Most of our time is spent indoors where we are exposed to a wide array of different microorganisms living on surfaces and in the air of our homes. Despite their ubiquity and abundance, we have a limited understanding of the microbial diversity found within homes and how the composition and diversity of microbial communities change across different locations within the home. Here we examined the diversity of bacterial communities found in nine distinct locations within each of forty homes in the Raleigh-Durham area of North Carolina, USA, using high-throughput sequencing of the bacterial 16S rRNA gene. We found that each of the sampled locations harbored bacterial communities that were distinct from one another with surfaces that are regularly cleaned typically harboring lower levels of diversity than surfaces that are cleaned infrequently. These location-specific differences in bacterial communities could be directly related to usage patterns and differences in the likely sources of bacteria dispersed onto these locations. Finally, we examined whether the variability across homes in bacterial diversity could be attributed to outdoor environmental factors, indoor habitat structure, or the occupants of the home. We found that the presence of dogs had a significant effect on bacterial community composition in multiple locations within homes as the homes occupied by dogs harbored more diverse communities and higher relative abundances of dog-associated bacterial taxa. Furthermore, we found a significant correlation between the types of bacteria deposited on surfaces outside the home and those found inside the home, highlighting that microbes from outside the home can have a direct effect on the microbial communities living on surfaces within our homes. Together this work provides the first comprehensive analysis of the microbial communities found in the home and the factors that shape the structure of these communities both within and between homes.

Eboigbodin, Kevin, Allyson Seth and Catherine Biggs, 2008. A review of biofilms in domestic plumbing. *Journal AWWA*, 100:10, 131-137

Several factors have been shown to favor biofilm formation in water distribution systems, including the capability of bacteria to resist disinfectants, improper use of disinfectants, the nature and concentration of biodegradable substances, temperature, and plumbing materials. To date, most research relating to drinking water biofilms has focused on the materials that make up the distribution system before water enters the consumers' plumbing systems. However, drinking water should also meet the necessary quality requirements at the point of consumption even though domestic plumbing systems are usually not constructed from the same materials that are used to construct distribution systems. This article provides a review of the current literature related to the analysis of biofilms found or produced in domestic plumbing systems and highlights the microorganisms identified as well as causes and strategies for control.

Eckert, Debra M. and Michael S. Kay, 2010. Stalking Influenza. *PNAS*, vol. 107, no. 31, 13563-13564

Influenza A virus causes seasonal flu epidemics and periodic worldwide pandemics (e.g., the 1918 Spanish flu, which caused ~50 million deaths). The viral surface protein HA is the primary target of neutralizing Abs in natural infections (1). At any given time there are a limited number of viral strains circulating in humans, restricting widespread immunity to a small subset of potential viruses. Yearly seasonal epidemics arise from antigenic drift in the sequence of HA of currently circulating viruses, whereas pandemics are caused by the emergence of new, antigenically divergent viruses to which there is little to no immunity in the population (i.e., antigenic shift). The worldwide spread of a new H1N1 virus in 2009 caused the first recorded pandemic in more than 40 years. Current influenza vaccines are primarily produced from killed virus and mimic natural infection, inducing strain-specific, mainly HA-based, neutralization. Vaccine is produced from representative circulating strains grown in chicken eggs in a months-long process. Recent efforts aim to produce a broader influenza vaccine that focuses on common neutralization epitopes shared by multiple influenza strains. Such a vaccine should target a variety of influenza strains and better combat pandemics. A study published in *PNAS* describes an exciting strategy toward developing a broader influenza vaccine (2).

Eduard, Wijnand, 2009. Fungal spores: A critical review of the toxicological and epidemiological evidence as a basis for occupational exposure limit setting. *Critical Reviews in Toxicology*, 2009; 39(10): 799–864

Fungal spores are ubiquitous in the environment. However, exposure levels in workplaces where mouldy materials are handled are much higher than in common indoor and outdoor environments. Spores of all tested species induced inflammation in experimental studies. The response to mycotoxin-producing and pathogenic species was much stronger. In animal studies, nonallergic responses dominated after a single dose. Allergic responses also occurred,

especially to mycotoxin-producing and pathogenic species, and after repeated exposures. Inhalation of a single spore dose by subjects with sick building syndrome indicated no observed effect levels of  $4 \times 10^3$  *Trichoderma harzianum* spores/m<sup>3</sup> and  $8 \times 10^3$  *Penicillium chrysogenum* spores/m<sup>3</sup> for lung function, respiratory symptoms, and inflammatory cells in the blood. In asthmatic patients allergic to *Penicillium* sp. or *Alternaria alternata*, lowest observed effect levels (LOELs) for reduced airway conductance were  $1 \times 10^4$  and  $2 \times 10^4$  spores/ m<sup>3</sup>, respectively. In epidemiological studies of highly exposed working populations lung function decline, respiratory symptoms and airway inflammation began to appear at exposure levels of 105 spores/m<sup>3</sup>. Thus, human challenge and epidemiological studies support fairly consistent LOELs of approximately 105 spores/m<sup>3</sup> for diverse fungal species in nonsensitised populations. Mycotoxin-producing and pathogenic species have to be detected specifically, however, because of their higher toxicity

Edwards, Michael R, Nathan W. Bartlett, Tracy Hussell, Peter Openshaw and Sebastian L. Johnston, 2012. The microbiology of asthma. *Nature Reviews Microbiology*, Vol 10, pp. 459-471, doi:10.1038/nrmicro2801

Asthma remains an important human disease that is responsible for substantial worldwide morbidity and mortality. The causes of asthma are multifactorial and include a complex mix of environmental, immunological and host genetic factors. In addition, epidemiological studies show strong associations between asthma and infection with respiratory pathogens, including common respiratory viruses such as rhinoviruses, human respiratory syncytial virus, adenoviruses, coronaviruses and influenza viruses, as well as bacteria (including atypical bacteria) and fungi. In this Review, we describe the many roles of microorganisms in the risk of developing asthma and in the pathogenesis of and protection against the disease, and we discuss the mechanisms by which infections affect the severity and prevalence of asthma.

Ege, Markus J., M.D., Melanie Mayer, Ph.D., Anne-Cécile Normand, Ph.D., Jon Genuneit, M.D., William O.C.M. Cookson, M.D., D.Phil., Charlotte Braun-Fahrländer, M.D., Dick Heederik, Ph.D., Renaud Piarroux, M.D., Ph.D., and Erika von Mutius, M.D., for the GABRIELA Transregio 22 Study Group, 2011. Exposure to Environmental Microorganisms and Childhood Asthma. *N Engl J Med* 2011;364:701-9.

Background Children who grow up in environments that afford them a wide range of microbial exposures, such as traditional farms, are protected from childhood asthma and atopy. In previous studies, markers of microbial exposure have been inversely related to these conditions. Methods In two cross-sectional studies, we compared children living on farms with those in a reference group with respect to the prevalence of asthma and atopy and to the diversity of microbial exposure. In one study — PARSIFAL (Prevention of Allergy — Risk Factors for Sensitization in Children Related to Farming and Anthroposophic Lifestyle) — samples of mattress dust were screened for bacterial DNA with the use of single-strand conformation polymorphism (SSCP) analyses to detect environmental bacteria that cannot be measured by means of culture techniques. In the other study — GABRIELA (Multidisciplinary Study to Identify the Genetic and Environmental Causes of Asthma in the European Community [GABRIEL] Advanced Study) — samples of settled dust from children's rooms were evaluated for bacterial and fungal taxa with the use of culture techniques. Results In both studies, children who lived on farms had lower prevalences of asthma and atopy and were exposed to a greater variety of environmental microorganisms than the children in the reference group. In turn, diversity of microbial exposure was inversely related to the risk of asthma (odds ratio for PARSIFAL, 0.62; 95% confidence interval [CI], 0.44 to 0.89; odds ratio for GABRIELA, 0.86; 95% CI, 0.75 to 0.99). In addition, the presence of certain more circumscribed exposures was also inversely related to the risk of asthma; this included exposure to species in the fungal taxon eurotium (adjusted odds ratio, 0.37; 95% CI, 0.18 to 0.76) and to a variety of bacterial species, including *Listeria monocytogenes*, bacillus species, corynebacterium species, and others (adjusted odds ratio, 0.57; 95% CI, 0.38 to 0.86). Conclusions Children living on farms were exposed to a wider range of microbes than were children in the reference group, and this exposure explains a substantial fraction of the inverse relation between asthma and growing up on a farm. (Funded by the Deutsche Forschungsgemeinschaft and the European Commission.)

Ege, M. J. Ege, M. Mayer, K. Schwaiger, J. Mattes, G. Pershagen, M. van Hage, A. Scheynius<sup>5</sup>, J. Bauer & E. von Mutius, 2012. Environmental bacteria and childhood asthma. *Allergy* 67 (2012) 1565-1571

Background: We have previously found an inverse association of bacterial diversity with childhood asthma. It remains unclear whether certain bacteria account for the protective effect. Methods: The high variability of the bacterial 16S rRNA gene allows assessing diversity and specificity of bacterial communities by single-strand configuration

polymorphism (SSCP). DNA was extracted from mattress dust samples of 489 school-age children from rural and suburban regions in Germany. A fragment of the bacteria-specific 16S rRNA gene was amplified by PCR, digested to single-strand DNA, and subjected to electrophoresis. The resulting band patterns reflect the underlying DNA sequences. The individual bands were tested for associations with asthma, hay fever, and atopy in quantitative and qualitative multivariable analyses. Significantly associated bands were isolated and sequenced. The sequences were compared to a database, and distinct bacteria were identified. Results: Seven of 76 independent bands were found to be inversely associated with asthma, atopic sensitization, and hay fever with odds ratios ranging from 0.17 to 0.73. The bands contained the sequences of *Acinetobacter* sp., *Lactobacillus* spp., *Neisseria* spp., *Staphylococcus sciuri*, *Jeotgalicoccus* sp., *Corynebacterium* spp., and others. Conclusions: In a diverse microbial environment, certain bacteria may account for the protective effect on the development of asthma and atopy.

Egert M, Schmidt I, Bussey K, Breves R. 2009. A glimpse under the rim - the composition of microbial biofilm communities in domestic toilets. *J Appl Microbiol* 108(4):1167-74.

**Aim:** To determine the microbial composition of biofilms in domestic toilets by molecular means. **Methods and Results:** Genomic DNA was extracted from six biofilm samples originating from households around Düsseldorf, Germany. While no archaeal 16S rRNA or fungal ITS genes were detected by PCR, fingerprinting of bacterial 16S rRNA genes revealed a diverse community in all samples. These communities also differed considerably between the six biofilms. Using the Ribosomal Database Project (RDP) classifier tool, 275 cloned 16S rRNA gene sequences were assigned to 11 bacterial phyla and 104 bacterial genera. Only 15 genera (representing 121 sequences affiliated with Actinobacteria, Bacteroidetes, Planctomycetes and Proteobacteria) occurred in at least half of the samples or contributed at least 10% of the sequences in a single biofilm. These sequences were defined as 'typical' for toilet biofilms, and they were examined in more detail. On a 97% sequence similarity level, these sequences represented 56 species. Twelve of these were closely related to well-described bacterial species, and only two of them were categorized as belonging to risk group 2. No 16S rRNA genes of typical faecal bacteria were detected in any sample. Virtually all 'typical' clones were found to be closely related to bacteria or to sequences obtained from environmental sources, implicating that the flushing water is the main source of recruitment. **Conclusion:** In view of the great diversity of mostly yet-uncultured bacteria and the considerable differences between individual toilets, very general strategies appear to be most suited for the removal and prevention of toilet biofilms. **Significance and Impact of the Study:** For the first time, a molecular fingerprinting and cloning approach was used to monitor the species composition in biofilm samples taken from domestic toilets. Knowledge about the microbial composition of biofilms in domestic toilets is a prerequisite for developing and evaluating strategies for their removal and prevention.

Elguindi, Jutta, Xiuli Hao, Yanbing Lin, Hend A. Alwathnani, Gehong Wei and Christopher Rensing, 2011. Advantages and challenges of increased antimicrobial copper use and copper mining. *Appl Microbiol Biotechnol* (2011) 91:237-249

Copper is a highly utilized metal for electrical, automotive, household objects, and more recently as an effective antimicrobial surface. Copper-containing solutions applied to fruits and vegetables can prevent bacterial and fungal infections. Bacteria, such as *Salmonellae* and *Cronobacter sakazakii*, often found in food contamination, are rapidly killed on contact with copper alloys. The antimicrobial effectiveness of copper alloys in the healthcare environment against bacteria causing hospital-acquired infections such as methicillin-resistant *Staphylococcus aureus* (MRSA), *Escherichia coli* O157:H7, and *Clostridium difficile* has been described recently. The use of copper and copper-containing materials will continue to expand and may lead to an increase in copper mining and production. However, the copper mining and manufacturing industry and the consumer do not necessarily enjoy a favorable relationship. Open pit mining, copper mine tailings, leaching products, and deposits of toxic metals in the environment often raises concerns and sometimes public outrage. In addition, consumers may fear that copper alloys utilized as antimicrobial surfaces in food production will lead to copper toxicity in humans. Therefore, there is a need to mitigate some of the negative effects of increased copper use and copper mining. More thermo-tolerant, copper ion-resistant microorganisms could improve copper leaching and lessen copper groundwater contamination. Copper ion-resistant bacteria associated with plants might be useful in biostabilization and phytoremediation of copper-contaminated environments. In this review, recent progress in microbiological and biotechnological aspects of microorganisms in contact with copper will be presented and discussed, exploring their role in the improvement for the industries involved as well as providing better environmental outcomes.

Escombe, A. Roderick, David A. J. Moore, Robert H. Gilman, William Pan, Marcos Navincopa, Eduardo Ticona, Carlos Martinez, Luz Caviedes, Patricia Sheen, Armando Gonzalez, Catherine J. Noakes, Jon S. Friedland, Carlton A. Evans, 2008. The Infectiousness of Tuberculosis Patients Coinfected with HIV. *PLoS Med* 5(9): e188. doi:10.1371/journal.pmed.0050188

**Background** The current understanding of airborne tuberculosis (TB) transmission is based on classic 1950s studies in which guinea pigs were exposed to air from a tuberculosis ward. Recently we recreated this model in Lima, Peru, and in this paper we report the use of molecular fingerprinting to investigate patient infectiousness in the current era of HIV infection and multidrug-resistant (MDR) TB. **Methods and Findings** All air from a mechanically ventilated negative-pressure HIV-TB ward was exhausted over guinea pigs housed in an airborne transmission study facility on the roof. Animals had monthly tuberculin skin tests, and positive reactors were removed for autopsy and organ culture for *M. tuberculosis*. Temporal exposure patterns, drug susceptibility testing, and DNA fingerprinting of patient and animal TB strains defined infectious TB patients. Relative patient infectiousness was calculated using the Wells-Riley model of airborne infection. Over 505 study days there were 118 ward admissions of 97 HIV-positive pulmonary TB patients. Of 292 exposed guinea pigs, 144 had evidence of TB disease; a further 30 were tuberculin skin test positive only. There was marked variability in patient infectiousness; only 8.5% of 118 ward admissions by TB patients were shown by DNA fingerprinting to have caused 98% of the 125 characterised cases of secondary animal TB. 90% of TB transmission occurred from inadequately treated MDR TB patients. Three highly infectious MDR TB patients produced 226, 52, and 40 airborne infectious units (quanta) per hour. **Conclusions** A small number of inadequately treated MDR TB patients coinfecting with HIV were responsible for almost all TB transmission, and some patients were highly infectious. This result highlights the importance of rapid TB drug-susceptibility testing to allow prompt initiation of effective treatment, and environmental control measures to reduce ongoing TB transmission in crowded health care settings. TB infection control must be prioritized in order to prevent health care facilities from disseminating the drug-resistant TB that they are attempting to treat.

Ettenauer, Jörg D., Guadalupe Piñar, Ksenija Lopandic, Bernhard Spangl, Günther Ellersdorfer, Christian Voithl, Katja Sterflinger, 2012. Microbes on building materials - Evaluation of DNA extraction protocols as common basis for molecular analysis. *Science of the Total Environment* 439 (2012) 44-53

The study of microbial life in building materials is an emerging topic concerning biodeterioration of materials as well as health risks in houses and at working places. Biodegradation and potential health implications associated with microbial growth in our residues claim for more precise methods for quantification and identification. To date, cultivation experiments are commonly used to gain insight into the microbial diversity. Nowadays, molecular techniques for the identification of microorganisms provide efficient methods that can be applied in this field. The efficiency of DNA extraction is decisive in order to perform a reliable and reproducible quantification of the microorganisms by qPCR or to characterize the structure of the microbial community. In this study we tested thirteen DNA extraction methods and evaluated their efficiency for identifying (1) the quantity of DNA, (2) the quality and purity of DNA and (3) the ability of the DNA to be amplified in a PCR reaction using three universal primer sets for the ITS region of fungi as well as one primer pair targeting the 16S rRNA of bacteria with three typical building materials — common plaster, red brick and gypsum cardboard. DNA concentration measurements showed strong variations among the tested methods and materials. Measurement of the DNA yield showed up to three orders of magnitude variation from the same samples, whereas A260/A280 ratios often prognosticated biases in the PCR amplifications. Visualization of the crude DNA extracts and the comparison of DGGE fingerprints showed additional drawbacks of some methods. The FastDNA Spin kit for soil showed to be the best DNA extraction method and could provide positive results for all tests with the three building materials. Therefore, we suggest this method as a gold standard for quantification of indoor fungi and bacteria in building materials.

Fairs, A, Wardlaw, AJ, Thompson, JR, and Pashley, CH 2010. Guidelines on Ambient Intramural Airborne Fungal Spores. *Journal of Investigational Allergology and Clinical Immunology*. 20 (6) 490-498.

**Objectives:** To generate baseline data for indoor airborne fungal spores in noncomplaint residential properties (with no moisture/mold-related problems) and to identify home characteristics indicative of elevated fungal levels. **Methods:** Air samples were collected onto petroleum jelly-coated slides from living rooms of 100 residential properties in Leicestershire, United Kingdom, using a Burkard continuous recording air sampler. The slides were examined by microscopy to determine fungal spore concentrations (spores/m<sup>3</sup> air/day). **Results:** Total indoor fungal spore

concentrations were approximately 16% of outdoor concentrations. Abundant indoor fungal genera include *Cladosporium*, *Sporobolomyces*, *Tilletiopsis*, and *Didymella*, all of which followed seasonal patterns of release and detection. No clear association was shown between outdoor-predominant fungi and home characteristics. In contrast, *Aspergillus*/*Penicillium*-type (Asp/ Pen-type) spores were common indoors and exceeded outdoor levels, with the highest concentrations detected in properties over 90 years old ( $P=.006$ ) and terraced properties ( $P=.003$ ). Conclusion: Asp/Pen-type spores are found in noncomplaint UK residential properties and mostly in old terraced houses. This study provides guidelines on acceptable levels of Asp/Pen-type spores and other abundant indoor fungal taxa that can be comparatively used in clinical evaluations of fungal exposure-related disease.

Fairs, Abbie, Joshua Agbetile, Michelle Bourne, Beverley Hargadon, William R Monteiro, Joseph P Morley, Richard E Edwards, Andrew J Wardlaw, Catherine H Pashley, 2012. Isolation of *Aspergillus fumigatus* from sputum is associated with elevated airborne levels in homes of patients with asthma. *Indoor Air Journal*, accepted 11/24/12.

Indoor bioaerosols, such as mold spores, have been associated with respiratory symptoms in patients with asthma; however, dose-response relationships and guidelines on acceptable levels are lacking. Furthermore, a causal link between mold exposure and respiratory infections or asthma remains to be established. The aim of this study was to determine indoor concentrations of *Aspergillus fumigatus* and a subset of clinically relevant fungi in homes of people with asthma, in relation to markers of airways colonization and sensitization. Air and dust samples were collected from the living room of 58 properties. Fungal concentrations were quantified using mold-specific quantitative PCR and compared with traditional microscopic analysis of air samples. Isolation of *A. fumigatus* from sputum was associated with higher airborne concentrations of the fungus in patient homes ( $P = 0.04$ ), and a similar trend was shown with *Aspergillus*/*Penicillium*-type concentrations analyzed by microscopy ( $P = 0.058$ ). No association was found between airborne levels of *A. fumigatus* and sensitization to this fungus, or dustborne levels of *A. fumigatus* and either isolation from sputum or sensitization. The results of this study suggest that the home environment should be considered as a potential source of fungal exposure and elevated home levels may predispose people with asthma to airways colonization.

Farhat, Maha, Marina Moletta-Denat, Jacques Frère, Séverine Onillon, Marie-Cécile Trouilhé and Enric Robine, 2012. Effects of Disinfection on *Legionella* spp., Eukarya, and Biofilms in a Hot Water System. *Appl. Environ. Microbiol.* 2012, 78(19):6850. DOI: 10.1128/AEM.00831-12.

*Legionella* species are frequently detected in hot water systems, attached to the surface as a biofilm. In this work, the dynamics of *Legionella* spp. and diverse bacteria and eukarya associated together in the biofilm, coming from a pilot scale 1 system simulating a real hot water system, were investigated throughout 6 months after two successive heat shock treatments followed by three successive chemical treatments. Community structure was assessed by a fingerprint technique, single-strand conformation polymorphism (SSCP). In addition, the diversity and dynamics of *Legionella* and eukarya were investigated by small-subunit (SSU) ribosomal cloning and sequencing. Our results showed that pathogenic *Legionella* species remained after the heat shock and chemical treatments (*Legionella pneumophila* and *Legionella anisa*, respectively). The biofilm was not removed, and the bacterial community structure was transiently affected by the treatments. Moreover, several amoebae had been detected in the biofilm before treatments (*Thecamoebae* sp., *Vannella* sp., and *Hartmanella vermiformis*) and after the first heat shock treatment, but only *H. vermiformis* remained. However, another protozoan affiliated with Alveolata, which is known as a host cell for *Legionella*, dominated the eukaryal species after the second heat shock and chemical treatment tests. Therefore, effective *Legionella* disinfection may be dependent on the elimination of these important microbial components. We suggest that eradicating *Legionella* in hot water networks requires better study of bacterial and eukaryal species associated with *Legionella* in biofilms.

Feazel, Leah M., Laura K. Baumgartner, Kristen L. Peterson, Daniel N. Frank, J. Kirk Harris, and Norman R. Pace, 2009. Opportunistic pathogens enriched in showerhead biofilms. *PNAS*, Vol 106:38, pp. 16393-16399.

The environments we humans encounter daily are sources of exposure to diverse microbial communities, some of potential concern to human health. In this study, we used culture-independent technology to investigate the microbial composition of biofilms inside showerheads as ecological assemblages in the human indoor environment. Showers are an important interface for human interaction with microbes through inhalation of aerosols, and

showerhead waters have been implicated in disease. Although opportunistic pathogens commonly are cultured from shower facilities, there is little knowledge of either their prevalence or the nature of other microorganisms that may be delivered during shower usage. To determine the composition of showerhead biofilms and waters, we analyzed rRNA gene sequences from 45 showerhead sites around the United States. We find that variable and complex, but specific, microbial assemblages occur inside showerheads. Particularly striking was the finding that sequences representative of non-tuberculous mycobacteria (NTM) and other opportunistic human pathogens are enriched to high levels in many showerhead biofilms, >100-fold above background water contents. We conclude that showerheads may present a significant potential exposure to aerosolized microbes, including documented opportunistic pathogens. The health risk associated with showerhead microbiota needs investigation in persons with compromised immune or pulmonary systems.

Feazel, Leah M, Charles E. Robertson, PhD; Vijay R. Ramakrishnan, MD; Daniel N. Frank, 2012. Microbiome Complexity and *Staphylococcus aureus* in Chronic Rhinosinusitis. *Laryngoscope*, 122:467-472, 2012

**Objectives/Hypothesis:** The aim of this study was to compare microbiological culture-based and culture-independent (16S rRNA gene sequencing) methodologies for pathogen identification in chronic rhinosinusitis (CRS) patients. We hypothesized that bacterial culture and DNA sequencing would yield largely concurrent results, although sequencing would detect greater bacterial diversity, and the sinonasal microbiomes of CRS patients would differ in composition and diversity compared with non-CRS controls. **Study Design:** Cross-sectional observational study. **Methods:** Middle meatus swabs from CRS patients collected during endoscopic sinus surgery were analyzed by both clinical culture and broad-range analysis of 16S rRNA gene pyrosequences. **Results:** A total of 21 swab samples from 15 CRS patients and five non-CRS controls were analyzed. One CRS patient was also swabbed 3 weeks postoperatively due to evidence of purulence during a clinical visit. All subjects had positive bacterial cultures, with a mean of 2.8 isolates per subject. The most prevalent cultivars were coagulase-negative staphylococci (15/20 specimens, 75%), *Staphylococcus aureus* (10/20, 50%), and *Propionibacterium acnes* (6/20, 30%). Among 57,407 pyrosequences generated, the most prevalent were from coagulase-negative staphylococci (21/21 specimens, 100%), *Corynebacterium* spp (18/21, 85.7%), *P. acnes* (16/21, 76.2%), and *S. aureus* (14/21, 66.7%). Bacterial diversity correlated with recent antibiotic use, asthma, prior sinus surgery, and relative abundance of *S. aureus*. **Conclusions:** DNA pyrosequencing revealed greater biodiversity than culture, although in most cases culture results represented a subset of the abundant DNA sequence types. CRS patients were characterized by altered microbial composition ( $P = .02$ ) and greater abundance of *S. aureus* ( $P = .03$ ).

Fernstrom, Aaron and Michael Goldblatt, 2013. Aerobiology and Its Role in the Transmission of Infectious Diseases. *Journal of Pathogens* Volume 2013, Article ID 493960, 13 pages <http://dx.doi.org/10.1155/2013/493960>

Aerobiology plays a fundamental role in the transmission of infectious diseases. As infectious disease and infection control practitioners continue employing contemporary techniques (e.g., computational fluid dynamics to study particle flow, polymerase chain reaction methodologies to quantify particle concentrations in various settings, and epidemiology to track the spread of disease), the central variables affecting the airborne transmission of pathogens are becoming better known. This paper reviews many of these aerobiological variables (e.g., particle size, particle type, the duration that particles can remain airborne, the distance that particles can travel, and meteorological and environmental factors), as well as the common origins of these infectious particles. We then review several real-world settings with known difficulties controlling the airborne transmission of infectious particles (e.g., office buildings, healthcare facilities, and commercial airplanes), while detailing the respective measures each of these industries is undertaking in its effort to ameliorate the transmission of airborne infectious diseases.

Fiedler Klaus, Edgar Schütz, Stefan Geh, 2001. Detection of microbial volatile organic compounds (MVOCs) produced by moulds on various materials. *Int. J. Hyg. Environ. Health* 204, 111 -121

Twelve fungal species were screened for microbial volatile organic compounds (MVOCs): *Aspergillus fumigatus*, *A. versicolor*, *A. niger*, *A. ochraceus*, *Trichoderma harzianum*, *T. pseudokoningii*, *Penicillium brevicompactum*, *P. chrysogenum*, *P. claviforme*, *P. expansum*, *Fusarium solani* and *Mucor* sp. More than 150 volatile substances derived from fungal cultures have been analysed by head-space solid-phase microextraction (HS-SPME). Each species had a defined MVOC profile which may be subjected to considerable modification in response to external factors such as cultivation on different substrata. The cultivation on different substrata changes the number and concentration of

MVOCs. Species-specific volatiles may serve as marker compounds for the selective detection of fungal species in indoor environments. Examination of MVOCs from indoor air samples may become an important method in indoor air hygiene for the detection of type and intensity of masked contamination by moulds.

Fierer and Jackson 2006. The diversity and biogeography of soil bacterial communities. PNAS, January 17, 2006 103(3) 626-631.

For centuries, biologists have studied patterns of plant and animal diversity at continental scales. Until recently, similar studies were impossible for microorganisms, arguably the most diverse and abundant group of organisms on Earth. Here, we present a continental-scale description of soil bacterial communities and the environmental factors influencing their biodiversity. We collected 98 soil samples from across North and South America and used a ribosomal DNA-fingerprinting method to compare bacterial community composition and diversity quantitatively across sites. Bacterial diversity was unrelated to site temperature, latitude, and other variables that typically predict plant and animal diversity, and community composition was largely independent of geographic distance. The diversity and richness of soil bacterial communities differed by ecosystem type, and these differences could largely be explained by soil pH ( $r^2 = 0.70$  and  $r^2 = 0.58$ , respectively;  $P < 0.0001$  in both cases). Bacterial diversity was highest in neutral soils and lower in acidic soils, with soils from the Peruvian Amazon the most acidic and least diverse in our study. Our results suggest that microbial biogeography is controlled primarily by edaphic variables and differs fundamentally from the biogeography of "macro" organisms.

Fierer, Noah, Zongzhi Liu, Mari Rodriguez-Hernandez, Rob Knight, Matthew Henn, and Mark T. Hernandez, 2008. Short-Term Temporal Variability in Airborne Bacterial and Fungal Populations. APPLIED AND ENVIRONMENTAL MICROBIOLOGY, Jan. 2008, p. 200-207.

Airborne microorganisms have been studied for centuries, but the majority of this research has relied on cultivation-dependent surveys that may not capture all of the microbial diversity in the atmosphere. As a result, our understanding of airborne microbial ecology is limited despite the relevance of airborne microbes to human health, various ecosystem functions, and environmental quality. Cultivation-independent surveys of small-subunit rRNA genes were conducted in order to identify the types of airborne bacteria and fungi found at a single site (Boulder, CO) and the temporal variability in the microbial assemblages over an 8-day period. We found that the air samples were dominated by ascomycete fungi of the Hypocreales order and a diverse array of bacteria, including members of the proteobacterial and Cytophaga-Flavobacterium-Bacteroides groups that are commonly found in comparable culture-independent surveys of airborne bacteria. Bacterium/fungus ratios varied by 2 orders of magnitude over the sampling period, and we observed large shifts in the phylogenetic diversity of bacteria present in the air samples collected on different dates, shifts that were not likely to be related to local meteorological conditions. We observed more phylogenetic similarity between bacteria collected from geographically distant sites than between bacteria collected from the same site on different days. These results suggest that outdoor air may harbor similar types of bacteria regardless of location and that the short-term temporal variability in airborne bacterial assemblages can be very large.

Fijan, Sabina, and Sonja Šostar Turk, 2012. Hospital Textiles, Are They a Possible Vehicle for Healthcare- Associated Infections? Int. J. Environ. Res. Public Health 2012, 9, 3330-3343; doi:10.3390/ijerph9093330

Textiles are a common material in healthcare facilities; therefore it is important that they do not pose as a vehicle for the transfer of pathogens to patients or hospital workers. During the course of use hospital textiles become contaminated and laundering is necessary. Laundering of healthcare textiles is most commonly adequate, but in some instances, due to inappropriate disinfection or subsequent recontamination, the textiles may become a contaminated inanimate surface with the possibility to transfer pathogens. In this review we searched the published literature in order to answer four review questions: (1) Are there any reports on the survival of microorganisms on hospital textiles after laundering? (2) Are there any reports that indicate the presence of microorganisms on hospital textiles during use? (3) Are there any reports that microorganisms on textiles are a possible source infection of patients? (4) Are there any reports that microorganisms on textiles are a possible source infection for healthcare workers?



FISCHER GUIDO, REGINA SCHWALBE, MANFRED MOLLER, RENE OSTROWSKI, AND WOLFGANG DOTT, 1999. SPECIES-SPECIFIC PRODUCTION OF MICROBIAL VOLATILE ORGANIC COMPOUNDS (MVOC) BY AIRBORNE FUNGI FROM A COMPOST FACILITY. *Chemosphere*, Vol. 39, No. 5, pp. 795-81

Thirteen airborne fungal species frequently isolated in composting plants were screened for microbial volatile organic compounds (MVOC), i.e., *Aspergillus candidus*, *A. fumigatus*, *A. versicolor*, *Emericella nidulans*, *Paecilomyces variotii*, *Penicillium brevicompactum*, *Penicillium clavigerum*, *Penicillium crustosum*, *Penicillium cyclopium*, *Penicillium expansum*, *Penicillium glabrum*, *Penicillium verruculosum*, and *Tritirachium oryzae*. Air samples from pure cultures were sorbed on Tenax GR and analyzed by thermal desorption in combination with GC/MS. Various hydrocarbons of different chemical groups and a large number of terpenes were identified. Some compounds such as 3-methyl-1-butanol and 1-octen-3-ol were produced by a number of species, whereas some volatiles were specific for single species. An inventory of microbial metabolites will allow identification of potential health hazards due to an exposure to fungal propagules and metabolites in the workplace. Moreover, species-specific volatiles may serve as marker compounds for the selective detection of fungal species in indoor domestic and working environments.

Fisk, William, Ekaterina A Eliseeva and Mark J Mendell, 2010. Association of residential dampness and mold with respiratory tract infections and bronchitis: a meta-analysis. *Environmental Health* 2010, 9:72 doi:10.1186/1476-069X-9-72.

Dampness and mold have been shown in qualitative reviews to be associated with a variety of adverse respiratory health effects, including respiratory tract infections. Several published meta-analyses have provided quantitative summaries for some of these associations, but not for respiratory infections. Demonstrating a causal relationship between dampness-related agents, which are preventable exposures, and respiratory tract infections would suggest important new public health strategies. We report the results of quantitative meta-analyses of published studies that examined the association of dampness or mold in homes with respiratory infections and bronchitis.

Flannigan, Brian, 2001. Deteriogenic Micro-organisms in Houses as a Hazard to Respiratory Health. *Int Biodeterioration & Biodegradation* 48 (2001) 41-54.

Although there is no doubt that high concentrations of airborne spores of actinomycetes and fungi associated with handling or processing of 'mouldy' materials cause occupational diseases, such as farmer's lung and maltworker's lung, which are classified as hypersensitivity pneumonitis or extrinsic allergic alveolitis, the evidence for the air spora outdoors causing asthma and hay fever is more equivocal and has been considered as being largely anecdotal. Evidence for mould-induced asthma resulting from exposure to spores in the home is similarly scant, although there have been recent reports which indicate a link between mould growth and respiratory health. There is increasing concern that in North America energy-saving measure (including increased insulation and reduced ventilation) affect the health of occupants of 'tight' buildings in which previously vented moisture and pollutants accumulate. In Europe, concern has heightened as the true scale of the twin problems of dampness and mould growth has become apparent, particularly in inadequately insulated houses. For example, in the UK probably 2-5 million of the stock of some 17 million houses are badly affected by dampness. In 60% of these cases the cause of the dampness is condensation, and an additional 2 million houses are affected to a lesser degree by condensation. The problem is particularly severe in areas where the climate is more rigorous, e.g. Scotland, and many tenants of local authority housing in such areas express concern that mould growth on damp walls may be a hazard to their health. The moulds which grow on damp walls and on furnishings, releasing spores into the indoor air, include some which are strongly deteriological, and this paper will consider the evidence for their involvement in problems of respiratory health.

Flores GE, Bates ST, Knights D, Lauber CL, Stombaugh J, et al. (2011) Microbial Biogeography of Public Restroom Surfaces. *PLoS ONE* 6(11): e28132. doi:10.1371/journal.pone.0028132

We spend the majority of our lives indoors where we are constantly exposed to bacteria residing on surfaces. However, the diversity of these surface-associated communities is largely unknown. We explored the biogeographical patterns exhibited by bacteria across ten surfaces within each of twelve public restrooms. Using high-throughput barcoded pyrosequencing of the 16S rRNA gene, we identified 19 bacterial phyla across all surfaces. Most sequences belonged to four phyla: Actinobacteria, Bacteroidetes, Firmicutes and Proteobacteria. The communities clustered into three general categories: those found on surfaces associated with toilets, those on the restroom floor, and those found

on surfaces routinely touched with hands. On toilet surfaces, gut-associated taxa were more prevalent, suggesting fecal contamination of these surfaces. Floor surfaces were the most diverse of all communities and contained several taxa commonly found in soils. Skin-associated bacteria, especially the Propionibacteriaceae, dominated surfaces routinely touched with our hands. Certain taxa were more common in female than in male restrooms as vagina-associated Lactobacillaceae were widely distributed in female restrooms, likely from urine contamination. Use of the SourceTracker algorithm confirmed many of our taxonomic observations as human skin was the primary source of bacteria on restroom surfaces. Overall, these results demonstrate that restroom surfaces host relatively diverse microbial communities dominated by human-associated bacteria with clear linkages between communities on or in different body sites and those communities found on restroom surfaces. More generally, this work is relevant to the public health field as we show that human-associated microbes are commonly found on restroom surfaces suggesting that bacterial pathogens could readily be transmitted between individuals by the touching of surfaces. Furthermore, we demonstrate that we can use high-throughput analyses of bacterial communities to determine sources of bacteria on indoor surfaces, an approach which could be used to track pathogen transmission and test the efficacy of hygiene practices.

Fogel, Matthew R., David R. Douglas, Cynthia A. Jumper and David C. Straus, 2008. Growth and Mycotoxin Production by *Chaetomium globosum* Is Favored in a Neutral pH. *Int. J. Mol. Sci.* 2008, 9, 2357-2365; DOI: 10.3390/ijms9122357

*Chaetomium globosum* is frequently isolated in water-damaged buildings and produces two mycotoxins called chaetoglobosins A and C when cultured on building material. In this study, the influence of ambient pH on the growth of *C. globosum* was examined on an artificial medium. This fungus was capable of growth on potato dextrose agar ranging in pH from 4.3 to 9.4 with optimal growth and chaetoglobosin C production occurring at a neutral pH. In addition, our results show that sporulation is favored in an acidic environment

Fox K, Fox A, Elssner T, Feigley C, Salzberg D. 2010. MALDI-TOF mass spectrometry speciation of staphylococci and their discrimination from micrococci isolated from indoor air of schoolrooms. *Journal of Environmental Monitoring* 12(4):917-23.

The focus of our work is the identification of medically relevant staphylococci from the environment; these organisms are among the major opportunistic pathogens associated with human disease. Andersen sampling was performed in schoolrooms during the school year. Eleven of thirty six isolates (all Gram-positive tetrads) were identified as staphylococci and 23 were characterized as micrococci. MALDI-TOF MS profiling was used as the first stage in the classification followed by standard biochemical tests including API Staph profiling. The staphylococcal isolates were each speciated; coagulase positive (*Staphylococcus aureus* [3 strains]) and coagulase negative: *Staphylococcus warneri* (4 isolates), *Staphylococcus hominis* (2), *Staphylococcus saprophyticus* (1) and *Staphylococcus cohnii* (1). *S. aureus* is most commonly found in the human nares but is frequently isolated from skin. The other staphylococcal species are among those most commonly isolated from human skin. Micrococci were much more frequently isolated from indoor air than reported by others for clinical samples. It is suggested that, without discrimination from micrococci, misidentification of staphylococci would be common on air sampling

Foxman, Betsy and Deborah Goldberg, 2008. Why the Human Microbiome Project Should Motivate Epidemiologists to Learn Ecology. *Epidemiology*, Volume 21, Number 6, November 2010, pp. 757-759.

If you are not an astronomer (amateur or otherwise), looking at the stars can be an exercise in frustration. Where are the constellations? The planets? A telescope doesn't necessarily help: you can see things more clearly, but without knowing where to look and what to look for, you can't tell what you are seeing. A similar problem arises as we consider the microorganisms that inhabit the human body. Our microbiota (previously called microflora) have been studied by high-throughput DNA sequencing of their genomes. Each of us carries at least 100 times more genes in our microbiota than in our personal genome.<sup>1</sup> There is so much there that it is hard to know where to look, and so the tendency is to explore more thoroughly what we already know, just as Galileo did when he first looked through a telescope. Galileo turned a telescope towards the moon and saw mountains; he looked at the Milky Way and saw separate stars; he looked at Jupiter and saw moons. But it took another century for astronomers to identify entirely new objects in the sky not proximate to those already known. The failure was not in the technology, but in pattern recognition. William Herschel—a musician turned astronomer—discovered a new way of seeing: reading the sky like a

musical score, he mapped patterns in the sky, enabling him to discern deviations from those patterns, such as the previously undetected planet of Uranus.

Frankel, Mika, Michael Timm, Erik Wind Hansen and Anne Mette Madsen, 2012. Comparison of Sampling methods for assessment of indoor microbial exposure. *Indoor Air*, 'Accepted Article', doi: 10.1111/j.1600-0668.2012.00770.x

Indoor microbial exposure has been related to allergy and respiratory disorders. However the lack of standardized sampling methodology is problematic when investigating dose-response relationships between exposure and health effects. In this study, different sampling methods were compared regarding their assessment of microbial exposures, including culturable fungi and bacteria, endotoxin, as well as the total inflammatory potential (TIP) of dust samples from Danish homes. The GSP filter sampler and BioSampler were used for sampling of airborne dust, whereas the Dust Fall Collector (DFC), the Electrostatic Dust Fall Collector (EDC) and vacuum cleaner were used for sampling of settled dust. The GSP assessed significantly higher microbial levels than the BioSampler, yet measurements from both samplers correlated significantly. Considerably higher levels of fungi, endotoxin and TIP were found in the EDC compared to the DFC, and regarding fungi, the EDC correlated more strongly and significantly to vacuumed dust than the DFC. Fungi in EDC- and vacuum dust correlated most strongly to airborne dust, and in particular the measurements from the EDC associated well with the GSP. Settled dust from the EDC was most representative of airborne dust and may thus be considered as a surrogate for assessment of indoor airborne microbial exposure.

Frankel, Mika, Gabriel Bekö, Michael Timm, Sine Gustavsen, Erik Wind Hansen and Anne Mette Madsen, 2012. Seasonal Variations of Indoor Microbial Exposures and Their Relation to Temperature, Relative Humidity, and Air Exchange Rate. *Appl. Environ. Microbiol.* 2012, 78(23):8289

Indoor microbial exposure has been related to adverse pulmonary health effects. Exposure assessment is not standardized, and various factors may affect the measured exposure. The aim of this study was to investigate the seasonal variation of selected microbial exposures and their associations with temperature, relative humidity, and air exchange rates in Danish homes. Airborne inhalable dust was sampled in five Danish homes throughout the four seasons of 1 year (indoors, n = 127; outdoors, n = 37). Measurements included culturable fungi and bacteria, endotoxin, N-acetyl-beta-D-glucosaminidase, total inflammatory potential, particles (0.75 to 15  $\mu\text{m}$ ), temperature, relative humidity, and air exchange rates. Significant seasonal variation was found for all indoor microbial exposures, excluding endotoxin. Indoor fungi peaked in summer (median, 235 CFU/m<sup>3</sup>) and were lowest in winter (median, 26 CFU/m<sup>3</sup>). Indoor bacteria peaked in spring (median, 2,165 CFU/m<sup>3</sup>) and were lowest in summer (median, 240 CFU/m<sup>3</sup>). Concentrations of fungi were predominately higher outdoors than indoors, whereas bacteria, endotoxin, and inhalable dust concentrations were highest indoors. Bacteria and endotoxin correlated with the mass of inhalable dust and number of particles. Temperature and air exchange rates were positively associated with fungi and N-acetyl-beta-D-glucosaminidase and negatively with bacteria and the total inflammatory potential. Although temperature, relative humidity, and air exchange rates were significantly associated with several indoor microbial exposures, they could not fully explain the observed seasonal variations when tested in a mixed statistical model. In conclusion, the season significantly affects indoor microbial exposures, which are influenced by temperature, relative humidity, and air exchange rates.

Fredricks, David N., 2001. Microbial Ecology of Human Skin in Health and Disease. *Journal of Investigative Dermatology Symposium Proceedings* 6:167-169

Cultivation of human skin reveals numerous bacteria and at least one fungus to be normal inhabitants of this ecosystem; however, most of our knowledge about the microbiology of human skin was acquired decades ago. Modern techniques employing nucleic acid-based microbial identification methods demonstrate the limitations of cultivation for appreciating microbial diversity in many ecosystems. The application of modern molecular methods to the study of skin may offer new perspectives on the resident microflora, and new insights into the causes of antibiotic responsive dermatologic conditions, such as acne and rosacea.

Fujimura, Kei E., Tine Demoor, Marcus Rauch, Ali A. Faruqi, Sihyug Jang, Christine C. Johnson, Homer A. Boushey, Edward Zoratti, Dennis Ownby, Nicholas W. Lukacs, and Susan V. Lynch, 2013. House dust exposure mediates gut microbiome Lactobacillus enrichment and airway immune defense against allergens and virus infection. [www.pnas.org/cgi/doi/10.1073/pnas.1310750111](http://www.pnas.org/cgi/doi/10.1073/pnas.1310750111)

Exposure to dogs in early infancy has been shown to reduce the risk of childhood allergic disease development, and dog ownership is associated with a distinct house dust microbial exposure. Here, we demonstrate, using murine models, that exposure of mice to dog-associated house dust protects against ovalbumin or cockroach allergen-mediated airway pathology. Protected animals exhibited significant reduction in the total number of airway T cells, down-regulation of Th2-related airway responses, as well as mucin secretion. Following dog-associated dust exposure, the cecal microbiome of protected animals was extensively restructured with significant enrichment of, amongst others, *Lactobacillus johnsonii*. Supplementation of wild-type animals with *L. johnsonii* protected them against both airway allergen challenge or infection with respiratory syncytial virus. *L. johnsonii*-mediated protection was associated with significant reductions in the total number and proportion of activated CD11c+/CD11b+ and CD11c+/CD8+ cells, as well as significantly reduced airway Th2 cytokine expression. Our results reveal that exposure to dog-associated household dust results in protection against airway allergen challenge and a distinct gastrointestinal microbiome composition. Moreover, the study identifies *L. johnsonii* as a pivotal species within the gastrointestinal tract capable of influencing adaptive immunity at remote mucosal surfaces in a manner that is protective against a variety of respiratory insults

Galvin S., A. Dolan, O. Cahill, S. Daniels, H. Humphreys, 2012. Microbial monitoring of the hospital environment: why and how? *Journal of Hospital Infection* 82 (2012) 143e151

**Background:** The purpose of microbial monitoring of the inanimate environment surrounding a patient can be two-fold; to monitor hygiene standards and also to examine for the presence of specific nosocomial pathogens which may be the source of an outbreak. While both purposes involve routine culture of microorganisms, the methods used for each can differ in order to provide optimal results. The main difference between both purposes is the need for enumeration, site specificity for an aerobic colony count (ACC) for hygiene assessments, and the need to simply detect the presence or absence of multi-resistant nosocomial pathogens for infection control surveillance. **Aim:** To access current methods used in research studies and during outbreak investigations to detect nosocomial pathogens in the inanimate environment in the clinical setting. **Methods:** A Pubmed search of published literature was performed. **Findings:** Microbial monitoring of the environment can involve the use of swabs, sponges, contact plates and dip slides coupled with a variety of enrichment broths and selective media. The use of molecular methods such as polymerase chain reaction (PCR) can potentially provide a faster turnaround time, resulting in the quicker implementation of infection prevention and control cleaning and disinfection regimens. However, the optimal methods for performing a microbial hygiene evaluation or detecting specific bacterial pathogens are not generally agreed. **Conclusion:** There is a need for agreed standards on the optimal methods, frequency of environmental sampling and acceptable levels of surface contamination within the healthcare system

Gauzere, Carole Marina Moletta-Denat, Faisal Bousta, Stephane Moularat, Genevieve Oriol, Sebastien Ritoux, Jean-Jacques Godon, Enric Robine, 2012. Reliable Procedure for Molecular Analysis of Airborne Microflora in Three Indoor Environments: An Office and Two Different Museum Contexts. *Clean – Soil, Air, Water* 2013, 41 (3), 226–234.

Biological aerosols from air constitute a significant source of exposure to microorganisms in public places. Airborne microorganisms are involved in the development of certain respiratory symptoms, allergies, or infections among users and occupants. Various sampling instruments have commonly been used in aerobiology to collect bacteria and fungi suspended in the air. The objective of this study was to develop a reliable procedure for sampling in indoor public environments presenting different levels of occupancy, airborne bacteria and fungi to be subjected to molecular analysis (bacteria and fungi quantitative PCR, capillary electrophoresis single strand conformation polymorphism fingerprinting). Four different sampling devices were tested in situ in an office building (open-plan type) and the sampling strategy chosen was tested in two museum contexts. In accordance with the drawbacks involved to our study (quantitative and qualitative aspects, cost, and overcrowding), cyclone device appeared to be most suitable. The results underline the effectiveness of this high-volume aerosol sampling device for both qualitative and quantitative molecular analysis. Four in situ sampling collections were carried out in 1 day in the Louvre Museum to study quantitative and qualitative variations of airborne bacterial and fungal diversity. The quantitative results revealed a similar order of magnitude for the numbers of both bacteria and fungi. In the Louvre Museum, the samples yielded between  $3.7 \times 10^4$  and  $4.1 \times 10^4$  genome equivalent (GE) bacteria/m<sup>3</sup> air and between  $5.0 \times 10^4$  and  $5.9 \times 10^4$  GE fungi/m<sup>3</sup> air and in the Decorative Arts Museum between,  $2.1 \times 10^4$  and  $2.5 \times 10^4$  GE bacteria/m<sup>3</sup> air and between  $1.4 \times 10^4$  and  $1.7 \times 10^4$  GE fungi/m<sup>3</sup> air. The results also indicate that the dominant bacterial community displayed a stable structure over a short period of time whereas dominant eukaryotic airborne community appeared more variable.

Gauzere, Carole, Marina Moletta-Denata, H el ene Blanquart, St ephane Ferreira, St ephane Moularat, Jean-Jacques Godon, Enric Robine, 2013. Stability of airborne microbes in the Louvre Museum over time. *Indoor Air* doi: 10.1111/ina.12053

The microbial content of air has as yet been little described, despite its public health implications, and there remains a lack of environmental microbial data on airborne microflora in enclosed spaces. In this context, the aim of this study was to characterise the diversity and dynamics of airborne microorganisms in the Louvre Museum using high-throughput molecular tools, and to underline the microbial signature of indoor air in this human-occupied environment. This microbial community was monitored for a six month during occupied time. The quantitative results revealed variations in the concentrations of less than one logarithm, with average values of 103 and 104 *E. coli*/A. *fumigatus* genome equivalent per m<sup>3</sup> for bacteria and fungi, respectively. Our observations highlight the stability of the indoor airborne bacterial diversity over time, while the corresponding eukaryote community was less stable. Bacterial diversity characterised by pyrosequencing 454 showed high diversity dominated by the Proteobacteria which represented 51.1%, 46.9% and 38.4% of sequences, for each of the 3 air samples sequenced. A common bacterial diversity was underlined, corresponding to 58.4 % of the sequences. The core species were belonging mostly to the Proteobacteria and Actinobacteria, and to the genus *Paracoccus* spp., *Acinetobacter* sp., *Pseudomonas* sp., *Enhydrobacter* sp., *Sphingomonas* sp., *Staphylococcus* sp. and *Streptococcus* sp.

GERBA, CHARLES P., CRAIG WALLIS, AND JOSEPH L. MELNICK, 1975. Microbiological Hazards of Household Toilets: Droplet Production and the Fate of Residual Organisms. *Applied MICROBIOLOGY*, Aug. 1975, p. 229-237.

Large numbers of bacteria and viruses when seeded into household toilets were shown to remain in the bowl after flushing, and even continual flushing could not remove a persistent fraction. This was found to be due to the adsorption of the organisms to the porcelain surfaces of the bowl, with gradual elution occurring after each flush. Droplets produced by flushing toilets were found to harbor both bacteria and viruses which had been seeded. The detection of bacteria and viruses falling out onto surfaces in bathrooms after flushing indicated that they remain airborne long enough to settle on surfaces throughout the bathroom. Thus, there is a possibility that a person may acquire an infection from an aerosol produced by a toilet.

Giannantonio, DJ, Kurth, JC, Kurtis, KE, Sobecky, PA 2009. Effects of concrete properties and nutrients on fungal colonization and fouling. *International Biodeterioration & Biodegradation* 63 (2009) 252-259

This study describes the fouling of concrete surfaces by diverse fungal genera under controlled laboratory conditions. A circulating flow-through chamber was designed for testing the effects of different concrete compositions and exogenously added nutrients on fungal colonization and fouling. Fungal strains belonging to the genera *Alternaria*, *Cladosporium*, *Epicoccum*, *Fusarium*, *Mucor*, *Penicillium*, *Pestalotiopsis*, and *Trichoderma* were cultured directly from visibly fouled concrete structures and used individually and in a mix to inoculate mortar tiles varying in cement composition, supplementary cementitious material additions, water-to-cement ratio, and surface roughness. A strong positive relationship was observed between the water-to-cement ratio and the amount of biofouling. In addition, cement containing photocatalytic titanium dioxide and exposed to artificial sunlight strongly inhibited fungal colonization and fouling. Mortar tiles coated with form-release oil and incubated with sterile rainwater were also capable of supporting fungal colonization. Our results indicate that the fouling of concrete surfaces by fungi can be influenced by variations in concrete composition variations and available nutrients

Gilbert, J., and Meyer, F., 2012. "Modeling the Earth Microbiome" *Microbe*. 7(2): 64-69.

Globally, microbial cells are 1 billion times more abundant than stars in the universe. Such numbers make it a daunting task to understand microbial complexity in useful ways. Because cataloguing this vastness does not immediately provide useful products, we should design surveys with specific questions that will help lead to specific products while also refining those questions.

Gilkeson, C.A., M.A. Camargo-Valero, L.E. Pickin, C.J. Noakes, 2013. Measurement of ventilation and airborne infection risk in large naturally ventilated hospital wards. *Building and Environment* 65 (2013) 35-48

Airborne pathogens pose a significant threat to human health and this is especially the case in hospital environments which house patients with weakened immune systems. Good ventilation design can reduce risk, however quantifying ventilation performance and its influence on infection risk is difficult, particularly for large naturally ventilated environments with multiple openings. This study applies a pulse-injection gas tracer method to assess potential infection risk and local ventilation rates in a naturally-ventilated environment. Experiments conducted in a 200 m<sup>3</sup> cross-ventilated Nightingale ward show that local external wind speeds in the range 1-4 m/s lead to indoor ventilation rates of between 3.4 and 6.5 air changes per hour (ACH). Natural ventilation is shown to be effective in open wards with an even distribution of potential airborne infection risk throughout patient locations. Comparison with a partitioned ward highlighted the potential for protecting neighbouring patients with physical partitions between beds, however, higher tracer concentrations are present in both the vicinity and downstream of the source. Closing the windows to represent winter conditions dramatically increases infection risk, with relative exposure to the tracer increased fourfold compared to the scenarios with the windows open. Extract fans are shown to alleviate this problem suggesting that a hybrid approach utilising the respective strengths of natural and mechanical ventilation may offer the best year-round solution in this and similar settings.

Giovannangelo, M., U. Gehring<sup>1,2</sup>, E. Nordling<sup>3</sup>, M. Oldenwening<sup>1</sup>, G. Terpstra<sup>1</sup>, T. Bellander<sup>3,4</sup>, G. Hoek<sup>1</sup>, J. Heinrich<sup>2</sup>, B. Brunekreef<sup>1,5</sup> 2007 Determinants of house dust endotoxin in three European countries - the AIRALLERG study *Indoor Air* 17: 70-79

The comparison of endotoxin levels between study populations and countries is limited as a result of differences in sampling, extraction, and storage procedures. The objective of this study is to assess the levels and determinants of endotoxin in mattress and living room floor dust samples from three European countries, namely, Germany, the Netherlands, and Sweden, using a standardized sampling, storage, and analysis protocol. The mattress and living room floor dust was collected from the homes of 1065 German, Dutch, and Swedish (pre-)school children. All the samples were collected in the cool season and analyzed for endotoxin in a central laboratory. The determinants were assessed by a standardized questionnaire. The endotoxin concentrations in mattress and living room floor dust were found to be the highest in German homes and lowest in the Swedish ones. Differences between the geometric means were small (factor 1.1- 1.7). Most of the associations between endotoxin concentrations and potential determinants were not statistically significant and heterogeneous across countries. However, keeping pets and having more than four persons living in the home were consistently associated with up to 1.7-fold higher endotoxin concentrations in mattress and floor dust. Furthermore, having carpets or rugs, and opening the windows frequently was associated with up to 3.4-fold and 1.3-fold higher endotoxin concentrations in living room floor dust, respectively. The proportion of variance explained by the questionnaire variables was generally low. In conclusion, the data on housing characteristics did not accurately predict the endotoxin concentrations in house dust, and could only partly explain the differences between countries.

Giovannangelo M, Nordling E, Gehring U, Oldenwening M, Bellander T, Heinrich J, Hoek G, Brunekreef B. 2007. Variation of biocontaminant levels within and between homes - the AIRALLERG study. *J Expo Sci Environ Epidemiol* 17(2):134-40.

Few epidemiological studies report on reliability of exposure measurements even though this significantly influences the results of correlation and regression analysis often used in these studies. Poor reliability of exposure measurement reduces the ability to detect a true association between a certain component and health outcome variables. The aim of this study was to determine the ratio of the within-home and between-home components of variance of a number of biocontaminants measured in house dust in the framework of an international study conducted in the Netherlands, Germany and Sweden (the AIRALLERG study). To this end, duplicate dust samples were collected from children's beds and from living room floors in over 100 homes. Samples were taken at the same point in time. Variables considered were the dust mass collected in mg/m<sup>2</sup> and the concentrations of the house dust mite allergens Der p 1 and Der f 1, cat allergen Fel d 1, endotoxin, (1→3)-β-D-glucan and extracellular polysaccharides, all per gram of dust and per square meter of sampling surface. An analysis of variance showed that the within-home variance was small compared to the between-home variance for most variables (mostly less than half) with the exception of glucan on mattresses, when expressed in µg/g. Investigation of variation over time is needed for a more complete assessment of the use of these variables in epidemiological analyses of exposure-response relationships.

Goebes MD, Boehm AB, Hildemann LM. 2011. Contributions of foot traffic and outdoor concentrations to indoor airborne aspergillus. *Aerosol Sci Technol* 45(3):352-63

Aspergillus is a mold genus that can cause allergies, asthma, and pulmonary infections in sensitive people; its particles are common in indoor air. Two potential contributors to indoor Aspergillus particles were examined in this field study: human activity (walking over carpet), and outdoor Aspergillus concentrations. Filtered air samples were collected outdoors and inside two carpeted hallways in public buildings, while measuring indoor foot traffic. Aspergillus concentrations were analyzed using quantitative Polymerase Chain Reaction (qPCR). A bivariate model was used to predict indoor Aspergillus concentrations based on foot traffic and outdoor Aspergillus concentrations. For 3 of 4 scenarios, most of the variation in indoor Aspergillus could be explained by the combined effect of outdoor Aspergillus concentrations and foot traffic, with particularly strong correlations during peak traffic times. In addition, indoor Aspergillus was significantly associated with outdoor Aspergillus in 2 of 4 scenarios, and with foot traffic in 2 of 4 scenarios. For 2 of 3 sampling campaigns, Aspergillus did not have a significant association either with gravimetric particulate matter  $\leq 5 \mu\text{m}$  (PM<sub>5</sub>), or with optically measured PM of 0.75-1  $\mu\text{m}$ , 1-2  $\mu\text{m}$ , 2-3.5  $\mu\text{m}$ , or 3.5-5  $\mu\text{m}$ . Controlled experiments, examining whether the foot traffic contribution was due to resuspension from carpeting or to shedding from clothing and/or human bodies, saw a significant increase in Aspergillus levels from resuspension. Although an increase was also seen for clothing over Tyvek suits, it was not statistically significant.

Golofit-Szymczak M and Gorny RL. 2010. Bacterial and fungal aerosols in air-conditioned office buildings in Warsaw, Poland-the winter season. *Int J Occup Saf Ergonomics* 16(4):465-76.

The microbial quality of the working environment was assessed in winter in air-conditioned office buildings in Warsaw. The average indoor concentrations of bacterial and fungal aerosols were low ( $<10^3 \text{ cfu}\cdot\text{m}^{-3}$ ), below Polish proposals for threshold limit values in public service buildings. Even during cold months, if the air-conditioning system works properly, people remain the main source of bacterial aerosol in offices, whereas infiltration of outdoor air remains a major mechanism responsible for their fungal contamination. An analysis of the bioaerosol size distribution showed that microbial propagules that reach both the upper and lower respiratory tract may evoke numerous adverse health effects from irritation and asthmatic reactions to allergic inflammation. A comparative analysis of viable and total airborne microbial counts showed that viable micro-organisms accounted for up to 0.3% of the total number of microbial propagules. Hence, a comprehensive hygienic assessment of office workplaces should include an efficient control of both these elements.

Gomes, C., J. Freihaut, W. Bahnfleth, 2007. Resuspension of allergen-containing particles under mechanical and aerodynamic disturbances from human walking. *Atmospheric Environment* 41 (2007) 5257-5270.

This study presents and develops a controlled and characterized method to explore the influence of specific occupant activity on the aerosolization of allergen-containing particles. Indoor allergen-related diseases are primarily inhalation sensitized and developed, suggesting an aerobiological pathway of allergen-containing carrier particles from dust reservoir to occupant respiration. But the pathways are not well understood or quantified. The influence of occupant walking on particle aerosolization is simulated by a system in which complex floor disturbances are deconvoluted into aerodynamic and mechanical components. Time resolved particle size distributions are measured for particles resuspended from representative samples of flooring materials and different types of floor disturbances in an environmentally controlled experimental chamber. Results indicate aerodynamic disturbances, relative to mechanical, dominate the particle resuspension behavior. Dust type, dust load and floor type showed marginal influences on a normalized surface loading basis. Humidity effects were not clear since during experiments the floor samples may not have reached moisture partitioning equilibrium with the controlled air humidity. Average resuspension rates ranged from  $10^{-7}$  to  $10^{-3} \text{ min}^{-1}$ , having phenomenological consistency with previous, large room or chamber investigations, suggesting the method can be utilized to develop a database for particle resuspension rates.

Gonçalves, Ana B., R. Russell M. Paterson, Nelson Lima\_2006 Survey and significance of filamentous fungi from tap water *Int. J. Hyg. Environ.-Health* 209 (2006) 257-264

Fungi in drinking water are involved in the production of tastes and odours in water. Health problems are possible, originating from mycotoxins, animal pathogens and allergies. This report concerns the surveillance of mesophilic fungi in tap water and assessment of their potential for causing problems. The methods for the

determination of the filamentous fungi (ff) were filtering, swabbing and baiting. Tap water, half-strength corn meal, neopeptone-glucose rose Bengal aureomycin (NGRBA) and oomycete selective agars for the enumeration of colony forming units (cfu) were used. Samples were taken consecutively over 16 months. Filtration and NGRBA gave the highest ff counts. A total of 340 taxa were isolated. There appeared to be a negative correlation between bacterial and yeast (b/y) and ff counts. Highest counts were found in winter months for ff and in the warmer months for b/y. *Penicillium* (40.6%) and *Acremonium* (38.8%) were the most frequently isolated ff. There was a difference in the pattern of isolation of the key taxa with season: penicillia predominated in early summer and *Acremonium* in winter. *P. expansum* was isolated in high numbers in May 2004. This species is associated with the production of the mycotoxin patulin and the odour secondary metabolite geosmin. *P. brevicompactum* was detected throughout the sampling period and is known to produce the immunosuppressive drug mycophenolic acid. *Acremonium* is associated with ocentol production which is responsible for bad tastes and flavours. The remaining taxa were *Phialophora* sp. (4.1%), *Cladosporium* sp. (3.5%), *Rhizopus stolonifer* (2.9%), *Chaetomium* sp. (0.6%), *Alternaria* sp. (0.3%), *Aspergillus* sp. (0.3%), mycelia sterilia (2.6%) and unidentified (6.2%). It is emphasised that few *Aspergillus* and no *Fusarium* strains were isolated. *Rhizopus stolonifer* was obtained. However, none of the fungi isolated at mesophilic temperature used could be described as being involved with pathogenicity per se.

Gonzalez, Antonio, Jose C. Clemente, Ashley Shade, Jessica L. Metcalf, Sejin Song, Bharath Prithiviraj, Brent E. Palmer & Rob Knight, 2011. Our microbial selves: what ecology can teach us. *EMBO reports* VOL 12, NO 8, pp. 775-784

Advances in DNA sequencing have allowed us to characterize microbial communities—including those associated with the human body—at a broader range of spatial and temporal scales than ever before. We can now answer fundamental questions that were previously inaccessible and use well-tested ecological theories to gain insight into changes in the microbiome that are associated with normal development and human disease. Perhaps unsurprisingly, the ecosystems associated with our body follow trends identified in communities at other sites and scales, and thus studies of the microbiome benefit from ecological insight. Here, we assess human microbiome research in the context of ecological principles and models, focusing on diversity, biological drivers of community structure, spatial patterning and temporal dynamics, and suggest key directions for future research that will bring us closer to the goal of building predictive models for personalized medicine.

Gorny RL. 2004. Filamentous microorganisms and their fragments in indoor air - A review. *Annals of Agricultural and Environmental Medicine* 11(2):185-97.

The paper summarizes the current state of knowledge regarding the role of filamentous microorganisms (i.e., fungi and actinomycetes) and their submicrometer propagules (fragments) in formation of indoor bioaerosol. It discusses the importance of water damages in buildings and the role of humidity as a cause of fungal and actinomycetal contamination and subsequent deterioration of indoor spaces. The importance of the size of airborne microbial propagules for adverse health effects is broadly commented as well. Regarding the microbial fragments, the method of their release from the contaminated surfaces (including factors influencing their aerosolization, i.e., air velocity, colony structure, moisture conditions, vibration of the surface, time factor), modern measurement techniques and newly obtained results of the immunological reactivity of fragments are discussed. The novel ideas concerning the dynamic description of the release process of microbial propagules from their sources are also presented.

Gostincar C, Grube M, Gunde-Cimerman N. 2011. Evolution of fungal pathogens in domestic environments? *Fungal Biology* 115(10):1008-18.

Specific indoor environments select for certain stress-tolerant fungi and can drive their evolution towards acquiring medically important traits. Here we review the current knowledge in this area of research, focussing on the so-called black yeasts. Many of these melanised stress-tolerant organisms originate in unusual ecological niches in nature, and they have a number of preadaptations that make them particularly suited for growth on human-made surfaces and substrates. Several pathogenic species have been isolated recently from various domestic habitats. We argue that in addition to enriching for - potentially - pathogenic species, the selection pressure and stress acting on microorganisms in indoor environments are driving their evolution towards acquiring the missing virulence factors and further enhancing their stress tolerance and pathogenic potential. Some of the polyextremotolerant fungi are particularly problematic: they can grow at elevated temperatures, and so they have a higher potential to colonise warm-blooded organisms. As



several species of black fungi are already implicated in health problems of various kinds, their selection and possible evolution in human environments are of concern.

Grant, C., C. A. Hunter, B. Flannigan & A. F. Bravery, 1989. The Moisture Requirements of Moulds Isolated from Domestic Dwellings. *International Biodeterioration* 25 (1 1989) 259-284

Mould growth on the damp internal surface of buildings is estimated to occur in some 2.5 million dwellings in the UK. As moisture is regarded as the key factor in promoting mould growth in buildings. A study was carried out to determine the moisture requirements for growth of moulds isolated from domestic dwellings, with the intention of providing building operators and practitioners with the information on critical internal humidity levels. Nineteen species of moulds which occurred in at least 10% of domestic air samples were assessed for their ability to grow at different levels of water activity ( $A_w$ :  $A_w = RH/100$ ). Certain of these were selected for more detailed studies of their  $A_w$  requirements for growth on a range of building substrates including paint and woodchip wallpaper. The lowest  $A_w$  recorded for growth on malt extract agar was 0.76 (76% RH) for *Aspergillus repens*, while for *A. versicolor* and several *Penicillium* species the minimum value was 0.79. On woodchip wallpaper painted with an emulsion paint the  $A_w$  minimum for *A. versicolor* and *P. chrysogenum* was also found to be 0.79 at 25 °C although at a temperature of 12 °C which was closer to that found for wall surfaces in practice, the  $A_w$  minima were elevated to 0.87 for these two moulds. In general the study showed that increasing the temperature and the nutritional status of the substrate led to a reduction in the  $A_w$  requirements of the moulds. In building practice therefore the aim must be to maintain relative humidity and surface temperature conditions within dwellings at levels such that mould susceptible substrates remain below  $A_w$  0.80 to avoid development of mould growth.

Grass, Gregor, Christopher Rensing, and Marc Solioz, 2011. Metallic Copper as an Antimicrobial Surface. *Applied and Environmental Microbiology* Mar. 2011, p. 1541-1547

Bacteria, yeasts, and viruses are rapidly killed on metallic copper surfaces, and the term "contact killing" has been coined for this process. While the phenomenon was already known in ancient times, it is currently receiving renewed attention. This is due to the potential use of copper as an antibacterial material in health care settings. Contact killing was observed to take place at a rate of at least 7 to 8 logs per hour, and no live microorganisms were generally recovered from copper surfaces after prolonged incubation. The antimicrobial activity of copper and copper alloys is now well established, and copper has recently been registered at the U.S. Environmental Protection Agency as the first solid antimicrobial material. In several clinical studies, copper has been evaluated for use on touch surfaces, such as door handles, bathroom fixtures, or bed rails, in attempts to curb nosocomial infections. In connection to these new applications of copper, it is important to understand the mechanism of contact killing since it may bear on central issues, such as the possibility of the emergence and spread of resistant organisms, cleaning procedures, and questions of material and object engineering. Recent work has shed light on mechanistic aspects of contact killing. These findings will be reviewed here and juxtaposed with the toxicity mechanisms of ionic copper. The merit of copper as a hygienic material in hospitals and related settings will also be discussed.

Greatorex JS, Digard P, Curran MD, Moynihan R, Wensley H, et al. (2011) Survival of Influenza A(H1N1) on Materials Found in Households: Implications for Infection Control. *PLoS ONE* 6(11): e27932. doi:10.1371/journal.pone.0027932.

**Background:** The majority of influenza transmission occurs in homes, schools and workplaces, where many frequently touched communal items are situated. However the importance of transmission via fomites is unclear since few data exist on the survival of virus on commonly touched surfaces. We therefore measured the viability over time of two H1N1 influenza strains applied to a variety of materials commonly found in households and workplaces.  
**Methodology and Principal Findings:** Influenza A/PuertoRico/8/34 (PR8) or A/Cambridge/AHO4/2009 (pandemic H1N1) viruses were inoculated onto a wide range of surfaces used in home and work environments, then sampled at set times following incubation at stabilised temperature and humidity. Virus genome was measured by RT-PCR; plaque assay (for PR8) or fluorescent focus formation (for pandemic H1N1) was used to assess the survival of viable virus.  
**Conclusions/Significance:** The genome of either virus could be detected on most surfaces 24 h after application with relatively little drop in copy number, with the exception of unsealed wood surfaces. In contrast, virus viability dropped much more rapidly. Live virus was recovered from most surfaces tested four hours after application and from some nonporous materials after nine hours, but had fallen below the level of detection from all surfaces at 24 h. We conclude

that influenza A transmission via fomites is possible but unlikely to occur for long periods after surface contamination (unless reinoculation occurs). In situations involving a high probability of influenza transmission, our data suggest a hierarchy of priorities for surface decontamination in the multi-surface environments of home and hospitals.

Greig, J.D., M.B. Lee, and J.E. Harris, 2011. Review of enteric outbreaks in prisons: Effective infection control interventions. *Public Health* 125 (2011) 222-228

**Objectives:** To identify documented outbreaks, worldwide, of enteric illness in correctional facilities over the last 10 years to understand the epidemiology of the outbreaks and explicitly identify effective infection control measures. **Study design:** Review of literature and outbreak investigation reports. **Methods:** Computer-aided searches of literature databases and systematic searches of government websites were completed to identify relevant outbreak reports. Reference lists were hand-searched to validate the electronic search methodology. Reports identified through personal communications with public health officials were also included. **Results:** Of the 72 outbreaks meeting the inclusion criteria, 76% and 21% were associated with bacterial agents and viral agents, respectively. The majority of outbreaks were associated with *Salmonella* (n = 20), *Clostridium perfringens* (n = 14), norovirus (n = 14), pathogenic *Escherichia coli* (n = 10) and *Campylobacter* spp. (n = 5). Transmission was primarily foodborne (67%). During an outbreak, the most common control measures included limiting movements of ill inmates and staff, and their exclusion from kitchen duty. The most common retrospectively reported preventative recommendations included monitoring food temperatures and effective infection control procedures. **Conclusions:** It is essential to monitor food temperatures to prevent enteric outbreaks in prisons. Training in safe food handling should be offered to inmates who work in the kitchen. Enteric outbreaks are best controlled by effective infection control practices, while active surveillance and early diagnosis may prevent further spread of illness

Grice, Elizabeth A. Grice, Heidi H. Kong, Sean Conlan, Clayton B. Deming, Joie Davis, Alice C. Young, NISC Comparative Sequencing Program, Gerard G. Bouffard, Robert W. Blakesley, Patrick R. Murray, Eric D. Green, Maria L. Turner, Julia A. Segre, 2009. Topographical and Temporal Diversity of the Human Skin Microbiome. *Science* 324, 1190

Human skin is a large, heterogeneous organ that protects the body from pathogens while sustaining microorganisms that influence human health and disease. Our analysis of 16S ribosomal RNA gene sequences obtained from 20 distinct skin sites of healthy humans revealed that physiologically comparable sites harbor similar bacterial communities. The complexity and stability of the microbial community are dependent on the specific characteristics of the skin site. This topographical and temporal survey provides a baseline for studies that examine the role of bacterial communities in disease states and the microbial interdependencies required to maintain healthy skin.

Grice, Elizabeth A. and Julia A. Segre, 2011. The skin microbiome. *Nature* 9: April, pp. 244-253.

The skin is the human body's largest organ, colonized by a diverse milieu of microorganisms, most of which are harmless or even beneficial to their host. Colonization is driven by the ecology of the skin surface, which is highly variable depending on topographical location, endogenous host factors and exogenous environmental factors. The cutaneous innate and adaptive immune responses can modulate the skin microbiota, but the microbiota also functions in educating the immune system. The development of molecular methods to identify microorganisms has led to an emerging view of the resident skin bacteria as highly diverse and variable. An enhanced understanding of the skin microbiome is necessary to gain insight into microbial involvement in human skin disorders and to enable novel antimicrobial and antimicrobial therapeutic approaches for their treatment.

Gupta, Jitendra K., Chao-Hsin Lin, Qingyan Chen, 2012. Risk assessment of airborne infectious diseases in aircraft cabins. *Indoor Air* 2012; 22: 388–395.

Passengers in an aircraft cabin can have different risks of infection from airborne infectious diseases such as influenza, severe acute respiratory syndrome (SARS), and tuberculosis (TB) because of the non-uniform airflow in an aircraft cabin. The current investigation presents a comprehensive approach to assessing the spatial and temporal distributions of airborne infection risk in an aircraft cabin. A case of influenza outbreak was evaluated in a 4-h flight in a twin-aisle, fully occupied aircraft cabin with the index passenger seated at the center of the cabin. The approach considered the characteristics of the exhalation of the droplets carrying infectious agents from the index passenger, the

dispersion of these droplets, and the inhalation of the droplets by susceptible passengers. Deterministic and probabilistic approaches were used to quantify the risks based on the amount of inhaled influenza virus RNA particles and quanta, respectively. The probabilistic approach indicated that the number of secondary infection cases can be reduced from 3 to 0 and 20 to 11, for influenza cases if N95 respirator masks are used by the passengers. The approach and methods developed can easily be implemented in other enclosed spaces such as buildings, trains, and buses to assess the infection risk.

Gutarowska, Beata and Magorzata Piotrowska, 2007. Methods of mycological analysis in buildings. *Building and Environment* 42 (2007) 1843-1850.

Due to their properties and common occurrence, fungi constitute the most frequent cause of biodeterioration of building materials and a serious health hazard to occupants. The authors present the methods of mycological analysis used to assess contamination caused by moulds and their metabolites in buildings. The article focuses on culture-based methods for analysing mould activity in dividing walls and indoor air. The article also covers chemical methods for the determination of, e.g., ergosterol, volatile mould metabolites, as well as toxicity in buildings based on mycotoxin and cytotoxicity evaluation in MTT assays. In order to estimate the degree of mould contamination or activity as well as health hazard, several complementary methods should be applied.

Gutarowska, Beata and Agata CZYZOWSKA, 2010. The ability of filamentous fungi to produce acids on indoor building materials. *Annals of Microbiology*, 59 (4) 807-813.

Sixty two filamentous fungi isolated from paint coatings, wallpaper, carton-gypsum board, and indoor air in buildings were screened for acid activity. It was found that 64.5% of strains produce acids on medium with bromo-cresol purple, where 18% of the strains were distinguished by very high acid activity (acid activity coefficient  $Q = 1.32-2.83$ ), including the species: *Aspergillus niger*, *Aspergillus versicolor*, *Penicillium expansum*, *Penicillium brevicompactum*, *Penicillium chrysogenum*, *Cladosporium cladosporioides*, *Stachybotrys chartarum*, *Mucor globosus*, *Ulocladium chartarum* and *Alternaria alternata*. Research indicated that filamentous fungi considerably decrease the pH of the medium when that medium containing building material. The greatest acid production and pH decrease of the medium was observed during the growth of filamentous fungi in a medium with mortar, while the production of acids was less in a medium with cartongypsum board, gypsum, and wallpaper. Filamentous fungi produced succinic, oxalic, malic and fumaric acids in the medium with indoor building materials. It was stated that the type of building material affects the spectrum and quantity of organic acids produced by filamentous fungi.

Gutarowska, B., M. Sulyok, and R. Krska, 2010. A Study of the Toxicity of Moulds Isolated from Dwellings. *Indoor Built Environ*, 19:6, pp. 668-675.

An analysis of the toxicity of moulds isolated from 34 dwellings with mould-affected walls was performed. During the analysis 74 moulds strains were isolated, 17.5% of them were toxic. Detailed analysis by high performance liquid chromatography/tandem mass spectrometry of six toxic strains proved their ability to grow on building materials and produce mycotoxins. It was confirmed that the toxins stachybotrylactam, sterigmatocystin and roquefortin were produced on gypsum board and concrete by *Stachybotrys chartarum*, *Aspergillus versicolor* and *Penicillium chrysogenum*, respectively. This is also the first report on the production of aflatoxin B1 and G1 by *A. flavus* on building materials. Extracts from *A. versicolor*, *A. flavus*, *P. chrysogenum* growing on building materials were found to have cytotoxic potential. It was found that some mycotoxin production may be reduced or may even vanish, when moulds grow on building materials. However, taking into consideration the appreciable amounts of some mycotoxins that were still produced on the building materials investigated, the study indicated a toxic risk in the mould-affected buildings analysed.

Hägerhed-Engman, Linda, Carl-Gustaf Bornehag & Jan Sundell, 2009. Building characteristics associated with moisture related problems in 8,918 Swedish dwellings. *International Journal of Environmental Health Research* Volume 19, Issue 4, pp. 251-265.

Moisture problems in buildings have in a number of studies been shown to increase the risk for respiratory symptoms. The study Dampness in Buildings and Health (DBH) was initiated with the aim to identify health relevant

exposures related to dampness in buildings. A questionnaire study about home environment with a focus on dampness problems and health was conducted in one county of Sweden (8,918 homes, response rate 79%). Building characteristics that were associated with one or more of the dampness indicators were for single-family houses, older houses, flat-roofed houses built in the 1960s and 1970s, houses with a concrete slab on the ground that were built before 1983. Moreover, tenancy and earlier renovation due to mould or moisture problems was strongly associated with dampness. A perception of dry air was associated with window-pane condensation, e.g. humid indoor air.

Hall, Caroline Breese, 2007. The Spread of Influenza and Other Respiratory Viruses: Complexities and Conjectures. *Clinical Infectious Diseases* 2007; 45:353-9

Since ancient times, the abrupt appearance and spread of maladies has demanded and defied explanation by mankind. In 400 b.c., Hippocrates suggested that the environment, including water and air, were important, and in the second century a.d., Galen suggested that outbreaks of illnesses were caused by inhaled air. For centuries thereafter, the prime theories proposed that illnesses arose from mystical influences and noxious effluvia borne by air [1]. The widespread devastation inflicted by plagues was thought to result from inhaling the putrescent vapors of decaying corpses. This belief in "miasmas" (derived from the Greek word for pollution) engendered perhaps the first infection-control procedures. The unfortunate souls assigned to handle the corpses were gowned in long robes with hoods to which were attached beaks stuffed with herbs, which were intended to filter the miasmas from the air (figure 1)

Halloran SK, Wexler AS, Ristenpart WD (2012) A Comprehensive Breath Plume Model for Disease Transmission via Expiratory Aerosols. *PLoS ONE* 7(5): e37088. doi:10.1371/journal.pone.0037088.

The peak in influenza incidence during wintertime in temperate regions represents a longstanding, unresolved scientific question. One hypothesis is that the efficacy of airborne transmission via aerosols is increased at lower humidities and temperatures, conditions that prevail in wintertime. Recent work with a guinea pig model by Lowen et al. indicated that humidity and temperature do modulate airborne influenza virus transmission, and several investigators have interpreted the observed humidity dependence in terms of airborne virus survivability. This interpretation, however, neglects two key observations: the effect of ambient temperature on the viral growth kinetics within the animals, and the strong influence of the background airflow on transmission. Here we provide a comprehensive theoretical framework for assessing the probability of disease transmission via expiratory aerosols between test animals in laboratory conditions. The spread of aerosols emitted from an infected animal is modeled using dispersion theory for a homogeneous turbulent airflow. The concentration and size distribution of the evaporating droplets in the resulting "Gaussian breath plume" are calculated as functions of position, humidity, and temperature. The overall transmission probability is modeled with a combination of the time-dependent viral concentration in the infected animal and the probability of droplet inhalation by the exposed animal downstream. We demonstrate that the breath plume model is broadly consistent with the results of Lowen et al., without invoking airborne virus survivability. The results also suggest that, at least for guinea pigs, variation in viral kinetics within the infected animals is the dominant factor explaining the increased transmission probability observed at lower temperatures.

Hamada N and Abe N. 2010. Growth characteristics of four fungal species in bathrooms. *Biocontrol Sci* 15(3):111-5.

The growth of four fungal species (four isolates) from bathrooms was examined under various environmental conditions. These fungi were found several times in bathrooms and washing machines, but not in other indoor environments such as house dust or windows. The four species (*Ramichloridium strelitziae*, *Cyphellophora laciniata*, *Phoma fimeti* and *Exophiala* sp.) were identified using DNA and morphological analyses. These bathroom fungi were able to consume surfactants, soap and shampoo, but were unable to grow well in high-temperature or dry conditions. Soap and shampoo seem to affect fungal flora in the bathroom.

Hanley, BP and B Borup, 2010. Aerosol influenza transmission risk contours: A study of humid tropics versus winter temperate zone. *Virology Journal* 2010, 7:98.

Background: In recent years, much attention has been given to the spread of influenza around the world. With the continuing human outbreak of H5N1 beginning in 2003 and the H1N1 pandemic in 2009, focus on influenza and other respiratory viruses has been increased. It has been accepted for decades that international travel via jet aircraft is

a major vector for global spread of influenza, and epidemiological differences between tropical and temperate regions observed. Thus we wanted to study how indoor environmental conditions (enclosed locations) in the tropics and winter temperate zones contribute to the aerosol spread of influenza by travelers. To this end, a survey consisting of 632 readings of temperature (T) versus relative humidity (RH) in 389 different enclosed locations air travelers are likely to visit in 8 tropical nations were compared to 102 such readings in 2 Australian cities, including ground transport, hotels, shops, offices and other publicly accessible locations, along with 586 time course readings from aircraft. Results: An influenza transmission risk contour map was developed for T versus RH. Empirical equations were created for estimating: 1. risk relative to temperature and RH, and 2. time parameterized influenza transmission risk. Using the transmission risk contours and equations, transmission risk for each country's locations was compared with influenza reports from the countries. Higher risk enclosed locations in the tropics included new automobile transport, luxury buses, luxury hotels, and bank branches. Most temperate locations were high risk. Conclusion: Environmental control is recommended for public health mitigation focused on higher risk enclosed locations. Public health can make use of the methods developed to track potential vulnerability to aerosol influenza. The methods presented can also be used in influenza modeling. Accounting for differential aerosol transmission using T and RH can potentially explain anomalies of influenza epidemiology in addition to seasonality in temperate climates.

Hanski, Ilkka Hanski, Leena von Hertzen, Nanna Fyhrquist, Kaisa Koskinen, Kaisa Torppa, Tiina Laatikainen, Piia Karisola, Petri Auvinen, Lars Paulin, Mika J. Mäkelä, Erkki Vartiainen, Timo U. Kosunen, Harri Alenius, and Tari Haahtela, 2012. Environmental biodiversity, human microbiota, and allergy are interrelated. *PNAS* 109:21, 8334-8339.

Rapidly declining biodiversity may be a contributing factor to another global megatrend—the rapidly increasing prevalence of allergies and other chronic inflammatory diseases among urban populations worldwide. According to the “biodiversity hypothesis,” reduced contact of people with natural environmental features and biodiversity may adversely affect the human commensal microbiota and its immunomodulatory capacity. Analyzing atopic sensitization (i.e., allergic disposition) in a random sample of adolescents living in a heterogeneous region of 100 × 150 km, we show that environmental biodiversity in the surroundings of the study subjects’ homes influenced the composition of the bacterial classes on their skin. Compared with healthy individuals, atopic individuals had lower environmental biodiversity in the surroundings of their homes and significantly lower generic diversity of gammaproteobacteria on their skin. The functional role of the Gram-negative gammaproteobacteria is supported by *in vitro* measurements of expression of IL-10, a key anti-inflammatory cytokine in immunologic tolerance, in peripheral blood mononuclear cells. In healthy, but not in atopic, individuals, IL-10 expression was positively correlated with the abundance of the gammaproteobacterial genus *Acinetobacter* on the skin. These results raise fundamental questions about the consequences of biodiversity loss for both allergic conditions and public health in general.

Harrison, J, C.A.C. Pickering, E.B. Faragher, P.K.C. Austwick, S.A. Little and L. Lawton, 1992. An investigation of the relationship between microbial and particulate indoor air pollution and the sick building syndrome. *Respiratory Medicine*, Volume 86, Issue 3, May 1992, Pages 225-235

The sick building syndrome has been the subject of research for approximately 10 years. Although it is often suggested that symptoms in office workers are due to circulating micro-organisms or particles, epidemiological studies investigating the relationship between them have been lacking. This cross-sectional study has combined medical and aerobiological assessments of offices in Great Britain and has found that, although airborne particulates and micro-organisms are unlikely to be the sole cause of the sick building syndrome, positive associations between symptom prevalence rates and levels of airborne viable bacteria and fungi within groups of buildings with similar ventilation systems, suggest a possible causal link that should be explored.

Hernberg, Samu, Penpatra Sripaiboonkij, Reginald Quansah, Jouni J.K. Jaakkola, Maritta S. Jaakkola, 2014. Indoor molds and lung function in healthy adults. *Respiratory Medicine* (2014) xx, 1-8.

Hewitt KM, Gerba CP, Maxwell SL, Kelley ST (2012) Office Space Bacterial Abundance and Diversity in Three Metropolitan Areas. *PLoS ONE* 7(5): e37849. doi:10.1371/journal.pone.0037849

People in developed countries spend approximately 90% of their lives indoors, yet we know little about the source and diversity of microbes in built environments. In this study, we combined culture-based cell counting and multiplexed pyrosequencing of environmental ribosomal RNA (rRNA) gene sequences to investigate office space bacterial diversity in three metropolitan areas. Five surfaces common to all offices were sampled using sterile double-tipped swabs, one tip for culturing and one for DNA extraction, in 30 different offices per city (90 offices, 450 total samples). 16S rRNA gene sequences were PCR amplified using bar-coded "universal" bacterial primers from 54 of the surfaces (18 per city) and pooled for pyrosequencing. A three-factorial Analysis of Variance (ANOVA) found significant differences in viable bacterial abundance between offices inhabited by men or women, among the various surface types, and among cities. Multiplex pyrosequencing identified more than 500 bacterial genera from 20 different bacterial divisions. The most abundant of these genera tended to be common inhabitants of human skin, nasal, oral or intestinal cavities. Other commonly occurring genera appeared to have environmental origins (e.g., soils). There were no significant differences in the bacterial diversity between offices inhabited by men or women or among surfaces, but the bacterial community diversity of the Tucson samples was clearly distinguishable from that of New York and San Francisco, which were indistinguishable. Overall, our comprehensive molecular analysis of office building microbial diversity shows the potential of these methods for studying patterns and origins of indoor bacterial contamination. "[H]umans move through a sea of microbial life that is seldom perceived except in the context of potential disease and decay." - Feazel et al. (2009).

Hoang, Chi P., Kerry A. Kinney, Richard L. Corsi, Paul J. Szaniszló, 2010. Resistance of green building materials to fungal growth. *International Biodeterioration & Biodegradation* 64 (2010) 104 - 113.

While the market for "green" building materials has been expanding rapidly, the susceptibility of these materials to fungal growth is not well understood. The relative fungal resistance of four pairs of green building materials and their conventional analogs was assessed. An artificial inoculation protocol was used to investigate the effects of external nutrient levels, host material, and spore levels on the susceptibility of building materials to *Aspergillus niger*. Also, a natural inoculation protocol was utilized to evaluate the resistance of the building materials to colonization by common indoor fungi. Increasing spore levels and the presence of external nutrients promoted the growth of *A. niger* on the surface of drywall, conventional ceiling tile, and gypsum wallboard. Following natural inoculation, a strong correlation was found to exist between the equilibrium moisture content (EMC) of organic-based materials and the time until 50% of the total surface area of a material specimen was covered by fungi (T50%). Fungal growth rates on the top, back, and side surfaces of coated or composite building materials were quite different. The results suggest that the presence of organic matter in a given building material and its EMC are more important predictors of fungal susceptibility than is the label of "green" or "nongreen".

Holme, J., L. Hagerhed-Engman, J. Mattsson, J. Sundell, C.-G. Bornehag, 2010. Culturable mold in indoor air and its association with moisture-related problems and asthma and allergy among Swedish children. *Indoor Air* 2010; 20: 329–340.

In a nested case-control study with 198 children with asthmatic and allergic symptoms (cases) and 202 healthy controls in Värmland, Sweden, we have investigated the relationship between mold spore exposure (mean colony-forming unit) indoor and (i) different indexes of moldy odor indoor (observed by professional inspectors and reported by parents), (ii) visible signs of dampness in the homes of the children (observed and reported), and (iii) doctor-diagnosed asthma/allergy in children. No association was found between the spore concentration indoor and moldy odor and signs of visible dampness in the homes. When a semi-quantitative method in distinguishing between moldy houses or non-moldy houses was used, there were no significant differences between the observed indexes of moldy odor or visible signs of dampness (both observed and reported). No association could be found between the spore concentration in indoor air and asthma/allergy in the children.

Horner, W. Elliott, Anthony G. Worthan, and Philip R. Morey, 2004. Air- and Dustborne Mycoflora in Houses Free of Water Damage and Fungal Growth. *APPLIED AND ENVIRONMENTAL MICROBIOLOGY*, Nov. 2004, p. 6394-6400.

Typically, studies on indoor fungal growth in buildings focus on structures with known or suspected water damage, moisture, and/or indoor fungal growth problems. Reference information on types of culturable fungi and total fungal levels are generally not available for buildings without these problems. This study assessed 50 detached single-

family homes in metropolitan Atlanta, Ga., to establish a baseline of "normal and typical" types and concentrations of airborne and dustborne fungi in urban homes which were predetermined not to have noteworthy moisture problems or indoor fungal growth. Each home was visually examined, and samples of indoor and outdoor air and of indoor settled dust were taken in winter and summer. The results showed that rankings by prevalence and abundance of the types of airborne and dustborne fungi did not differ from winter to summer, nor did these rankings differ when air samples taken indoors were compared with those taken outdoors. Water indicator fungi were essentially absent from both air and dust samples. The air and dust data sets were also examined specifically for the proportions of colonies from ecological groupings such as leaf surface fungi and soil fungi. In the analysis of dust for culturable fungal colonies, leaf surface fungi constituted a considerable portion (>20%) of the total colonies in at least 85% of the samples. Thus, replicate dust samples with less than 20% of colonies from leaf surface fungi are unlikely to be from buildings free of moisture or mold growth problems.

Horner WE. 2006. Managing building-related aspergillus exposure. *Medical Mycology* 44:S33-8.

Aspergillus exposure is difficult to avoid. Indoor dust contains spores and thermotolerant molds may colonize damp or water-damaged building materials or components. Dust control should be part of diligent maintenance since disturbing dusts, especially during building renovation, can expose occupants to spores. Colonization of HVAC systems can shed spores into a building and expose occupants. Mold colonization warrants prompt and effective remediation, including removal of the colonization with associated debris and dusts without unduly exposing remediation workers, and while controlling fugitive dusts. Cleaning may suffice for non-porous surfaces, but colonized porous materials typically must be removed. Determining successful remediation can be challenging; the objective is not to sanitize, but a building in a 'normal and typical' state, a state that is often poorly defined. This is even more troublesome for colonized HVAC components and for health care facilities. Practical remediation assessment emphasizes inspection and then environmental monitoring. Air sampling may prove useful after inspection and monitoring, assuming prior consensus on the purpose of sampling and interpretation of results. Thoughtful design, careful construction and renovation, and diligent operation and maintenance of a building are all needed to minimize the exposure of building occupants to mold.

Hospodsky, Denina, Naomichi Yamamoto, and Jordan Peccia, 2010. Accuracy, Precision, and Method Detection Limits of Quantitative PCR for Airborne Bacteria and Fungi. *APPLIED AND ENVIRONMENTAL MICROBIOLOGY*, Nov. 2010, p. 7004-7012.

Real-time quantitative PCR (qPCR) for rapid and specific enumeration of microbial agents is finding increased use in aerosol science. The goal of this study was to determine qPCR accuracy, precision, and method detection limits (MDLs) within the context of indoor and ambient aerosol samples. *Escherichia coli* and *Bacillus atrophaeus* vegetative bacterial cells and *Aspergillus fumigatus* fungal spores loaded onto aerosol filters were considered. Efficiencies associated with recovery of DNA from aerosol filters were low, and excluding these efficiencies in quantitative analysis led to underestimating the true aerosol concentration by 10 to 24 times. Precision near detection limits ranged from a 28% to 79% coefficient of variation (COV) for the three test organisms, and the majority of this variation was due to instrument repeatability. Depending on the organism and sampling filter material, precision results suggest that qPCR is useful for determining dissimilarity between two samples only if the true differences are greater than 1.3 to 3.2 times (95% confidence level at  $n = 7$  replicates). For MDLs, qPCR was able to produce a positive response with 99% confidence from the DNA of five *B. atrophaeus* cells and less than one *A. fumigatus* spore. Overall MDL values that included sample processing efficiencies ranged from 2,000 to 3,000 *B. atrophaeus* cells per filter and 10 to 25 *A. fumigatus* spores per filter. Applying the concepts of accuracy, precision, and MDL to qPCR aerosol measurements demonstrates that sample processing efficiencies must be accounted for in order to accurately estimate bioaerosol exposure, provides guidance on the necessary statistical rigor required to understand significant differences among separate aerosol samples, and prevents undetected (i.e., nonquantifiable) values for true aerosol concentrations that may be significant.

Hospodsky, D. , J Qian , N Yamamoto, W NAZAROFF, J Peccia , 2012. Quantitative Microbial Population Characterization to Reveal Sources of Bacteria in Indoor Air. Presented at Healthy Buildings 2012, Brisbane, Australia

Exposure to specific airborne bacteria indoors is linked to infectious and noninfectious adverse health outcomes. However, the sources and origins of bacteria suspended in indoor air are not well understood. This study presents evidence for elevated concentrations of indoor airborne bacteria due to human occupancy, and investigates the sources

of these bacteria. Samples were collected in a university classroom while occupied and when vacant. The total particle mass concentration, bacterial genome concentration, and bacterial phylogenetic populations were characterized in indoor, outdoor, and ventilation duct supply air, as well as in the dust of ventilation system filters and in floor dust. Occupancy increased the total aerosol mass and bacterial genome concentration in indoor air PM<sub>10</sub> and PM<sub>2.5</sub> size fractions, with an increase of nearly two orders of magnitude in airborne bacterial genome concentration in PM<sub>10</sub>. On a per mass basis, floor dust was enriched in bacterial genomes compared to airborne particles. Quantitative comparisons between bacterial populations in indoor air and potential sources suggest that resuspended floor dust is an important contributor to bacterial aerosol populations during occupancy. Experiments that controlled for resuspension from the floor implies that direct human shedding may also significantly impact the concentration of indoor airborne particles. The high content of bacteria specific to the skin, nostrils, and hair of humans found in indoor air and in floor dust indicates that floors are an important reservoir of human-associated bacteria, and that the direct particle shedding of desquamated skin cells and their subsequent resuspension strongly influenced the airborne bacteria population structure in this human-occupied environment. Inhalation exposure to microbes shed by other current or previous human occupants may occur in communal indoor environments.

Hsu, J., C. Abad, M. Dinh, and Nasia Safdar, 2011. Prevention of Endemic Healthcare-Associated *Clostridium difficile* Infection: Reviewing the Evidence. *Am J Gastroenterol* 2010; 105:2327-2339; doi: 10.1038/ajg.2010.254

*Clostridium difficile* is the most common infectious cause of healthcare-associated diarrhea. Because of the increasing incidence and severity of endemic *C. difficile* infection (CDI), interventions to prevent healthcare-associated CDI are essential. We undertook a systematic review of interventions to reduce healthcare-associated CDI. **METHODS:** We searched multiple computerized databases, and manually searched for relevant articles to determine which interventions are useful in preventing CDI. Studies were required to be controlled in design and to report the incidence of endemic CDI as an outcome. Data on the patient population, intervention, study design, and outcomes were abstracted and reviewed using established criteria. **RESULTS:** Few randomized controlled trials exist in the area of CDI prevention. The interventions with the greatest evidence for the prevention of CDI include antimicrobial stewardship, glove use, and disposable thermometers. Environmental decontamination also may decrease CDI rates, although the level of evidence is not as strong as for the other proven interventions. Treatment of asymptomatic carriage of *C. difficile* is not recommended. There is insufficient evidence to make a recommendation for or against the use of probiotics. In cases of known or suspected CDI, hand hygiene with soap and water is preferred over use of waterless alcohol hand rub. Many nonrandomized trials included in our analysis used multiple interventions concurrently, making the independent role of each preventive strategy difficult to determine. We chose to include only studies that focused on endemic CDI because studies of outbreaks have used multiple strategies, making it difficult to measure the relative efficacy of each strategy. Environmental disinfection and probiotics need to be studied further to evaluate their roles in the prevention of CDI. Although there have been no studies assessing the utility of isolation and cohorting for the prevention of endemic CDI specifically, it is a widely used intervention for containment of this and other similar multidrug-resistant pathogens. **CONCLUSIONS:** Antimicrobial stewardship, glove use, hand hygiene, and disposable thermometers should be routinely used for the prevention of CDI. Environmental disinfection and probiotics should be studied further for their role in reducing CDI.

Hubner, Nils-Olaf, MD, Claudia Hübner, PhD, Axel Kramer, MD, PhD, and Ojan Assadian, 2011. Survival of Bacterial Pathogens on Paper and Bacterial Retrieval from Paper to Hands: Preliminary Results. *AJN*, December 2011, Vol. 111, No. 12

**Background:** Paper is omnipresent on hospital units, but few studies have examined the possible role of paper in the spread of nosocomial pathogens. **Objective:** To determine by laboratory investigation how long bacterial pathogens can survive on office paper and whether bacteria can be transferred from hands to paper and back to hands in a "worst-case scenario." **Methods:** Samples of four bacterial pathogens (*Escherichia coli*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Enterococcus hirae*) were prepared according to standard laboratory procedures. Sterile swatches of office paper were inoculated with the pathogens and bacterial survival was tested over seven days. To test the transmission of bacteria from one person's hands to paper and back to another person's hands, the fingertips of volunteers were inoculated with a nonpathogenic strain of *E. coli*; these volunteers then pressed the inoculum onto sterile paper swatches. Another group of volunteers whose hands had been moistened pressed their fingertips onto the contaminated paper swatches. Bacteria transferred to the moistened fingertips were cultivated according to standard



laboratory procedures. Results: The four tested organisms showed differences in length of survival depending on environmental room conditions, but were stable on paper for up to 72 hours and still cultivable after seven days. Test organisms were transferred to paper, survived on it, and were retransferred back to hands. Conclusion: Paper can serve as a vehicle for cross-contamination of bacterial pathogens in medical settings if current recommendations on hand hygiene aren't meticulously followed.

Human Microbiome Project Consortium 2012. A framework for human microbiome research. *Nature*, vol 486, pp 215-221

A variety of microbial communities and their genes (the microbiome) exist throughout the human body, with fundamental roles in human health and disease. The National Institutes of Health (NIH)-funded Human Microbiome Project Consortium has established a population-scale framework to develop metagenomic protocols, resulting in a broad range of quality-controlled resources and data including standardized methods for creating, processing and interpreting distinct types of high-throughput metagenomic data available to the scientific community. Here we present resources from a population of 242 healthy adults sampled at 15 or 18 body sites up to three times, which have generated 5,177 microbial taxonomic profiles from 16S ribosomal RNA genes and over 3.5 terabases of metagenomic sequence so far. In parallel, approximately 800 reference strains isolated from the human body have been sequenced. Collectively, these data represent the largest resource describing the abundance and variety of the human microbiome, while providing a framework for current and future studies

Hyvarinen, Anne, Teija Meklin, Asko Vepsäläinen, Aino Nevalainen, 2002. Fungi and actinobacteria in moisture-damaged building materials-concentrations and diversity. *International Biodeterioration & Biodegradation* 49 (2002) 27 - 37.

Modern building materials, once moistened, may provide ecological niches for various microbes that have not been well characterized. The aim of the current study was to determine whether fungal genera and actinobacteria were associated with seven types of moisture-damaged building materials by systematically describing the mycobiota and enumerating fungi and bacteria in these materials. Microbial analyses were obtained from 1140 visibly damaged samples of building material, viz. wood, paper, non-wooden building boards, ceramic products, mineral insulation materials, paints and glues, and plastics. Fungal and bacterial concentrations correlated well ( $r = 0.6$ ). The range of fungi and bacteria numbers was between 100 and  $10^8$  cfu g<sup>-1</sup> in all materials, but significant differences in counts were observed between materials. Highest median concentrations of fungi were observed in wooden and paper materials, and lowest in samples of mineral insulation, ceramic products, and paints and glues. Concentrations of viable bacteria in mineral insulation materials were significantly lower than in wood, paper, ceramic products and plastics. A rich variety of fungi was found in wooden materials, with *Penicillium* and yeasts occurring most frequently. In paper materials, a clear difference from wood was the more frequent occurrence of *Cladosporium* and *Stachybotrys*. The most distinctive finding in gypsum boards was that *Stachybotrys* was common. Ceramic products and paints and glues seemed to favour *Acremonium* and *Aspergillus versicolor*. Yeasts and members of the Sphaeropsidales occurred often in parallel in most materials. This study confirms that microbial growth occurs in many different building materials and shows associations between fungal genera and the type of material.

Ignatius T.S. Yu, M.B., B.S., M.P.H., Yuguo Li, Ph.D., Tze Wai Wong, M.B., B.S., Wilson Tam, M.Phil., Andy T. Chan, Ph.D., Joseph H.W. Lee, Ph.D., Dennis Y.C. Leung, Ph.D., and Tommy Ho, B.Sc., 2004. Evidence of Airborne Transmission of the Severe Acute Respiratory Syndrome Virus. *N Engl J Med* 2004;350:1731-9

There is uncertainty about the mode of transmission of the severe acute respiratory syndrome (SARS) virus. We analyzed the temporal and spatial distributions of cases in a large community outbreak of SARS in Hong Kong and examined the correlation of these data with the three-dimensional spread of a virus-laden aerosol plume that was modeled using studies of airflow dynamics. We determined the distribution of the initial 187 cases of SARS in the Amoy Gardens housing complex in 2003 according to the date of onset and location of residence. We then studied the association between the location (building, floor, and direction the apartment unit faced) and the probability of infection using logistic regression. The spread of the airborne, virus-laden aerosols generated by the index patient was modeled with the use of airflow-dynamics studies, including studies performed with the use of computational fluid-dynamics and multizone modeling. results The curves of the epidemic suggested a common source of the outbreak. All but 5 patients lived in seven buildings (A to G), and the index patient and more than half the other patients with SARS

(99 patients) lived in building E. Residents of the floors at the middle and upper levels in building E were at a significantly higher risk than residents on lower floors; this finding is consistent with a rising plume of contaminated warm air in the air shaft generated from a middle-level apartment unit. The risks for the different units matched the virus concentrations predicted with the use of multizone modeling. The distribution of risk in buildings B, C, and D corresponded well with the three-dimensional spread of virus-laden aerosols predicted with the use of computational fluid dynamics modeling. conclusions Airborne spread of the virus appears to explain this large community outbreak of SARS, and future efforts at prevention and control must take into consideration the potential for airborne spread of this virus.

Ihekweazu, Chikwe, Marina Basarab, Deborah Wilson, Isabel Oliver, David Dance, Robert George, Richard Pebody, 2010. Outbreaks of serious pneumococcal disease in closed settings in the post-antibiotic era: A systematic review. *Journal of Infection* (2010) 61, 21-27

**Objectives:** Since the introduction of antibiotics, pneumococcal disease is predominantly sporadic, with occasional outbreaks. Our objective was to review the epidemiology of reported outbreaks of serious pneumococcal disease in closed settings to inform the development of guidelines to manage such outbreaks. **Methods:** We systematically reviewed the literature for reported outbreaks of serious pneumococcal disease in closed settings to inform the development of guidelines in managing such outbreaks. **Results:** We identified 42 outbreaks reported in 39 papers: 14 in hospitals, 12 in long term care facilities, five outbreaks in households, four in military settings, three in child care settings and two each in homeless shelters and jails. The serotype/group most frequently associated with outbreaks was 14 (seven outbreaks) followed by 4 (five outbreaks) then serotypes/groups 1, 9 and 9 V each causing four outbreaks. The median outbreak size was four cases (2 - 46). The median duration was eight days, with 84% of cases occurring within 14 days of the first case. **Conclusion:** Outbreaks of serious pneumococcal disease are likely to continue happening requiring early recognition and implementation of public health measures in order to interrupt transmission. This study facilitated the development of the first UK interim guidelines for managing such outbreaks

Inamdar, Arati A., Muhammad M. Hossain, Alison I. Bernstein, Gary W. Miller, Jason R. Richardson, and Joan Wennstrom Bennett, 2013. Fungal-derived semiochemical 1-octen-3-ol disrupts dopamine packaging and causes neurodegeneration. *PNAS*, November 26, 2013, vol. 110, no. 48, 19561–19566.

Parkinson disease (PD) is the most common movement disorder and, although the exact causes are unknown, recent epidemiological and experimental studies indicate that several environmental agents may be significant risk factors. To date, these suspected environmental risk factors have been man-made chemicals. In this report, we demonstrate via genetic, biochemical, and immunological studies that the common volatile fungal semiochemical 1-octen-3-ol reduces dopamine levels and causes dopamine neuron degeneration in *Drosophila melanogaster*. Overexpression of the vesicular monoamine transporter (VMAT) rescued the dopamine toxicity and neurodegeneration, whereas mutations decreasing VMAT and tyrosine hydroxylase exacerbated toxicity. Furthermore, 1-octen-3-ol also inhibited uptake of dopamine in human cell lines expressing the human plasma membrane dopamine transporter (DAT) and human VMAT ortholog, VMAT2. These data demonstrate that 1-octen-3-ol exerts toxicity via disruption of dopamine homeostasis and may represent a naturally occurring environmental agent involved in parkinsonism

Ishoey, Thomas, Tanja Woyke, Ramunas Stepanauskas, Mark Novotny and Roger S Lasken, 2008. Genomic sequencing of single microbial cells from environmental samples. *Current Opinion in Microbiology* 2008, 11:198-204.

Recently developed techniques allow genomic DNA sequencing from single microbial cells [Lasken RS: Single-cell genomic sequencing using multiple displacement amplification. *Curr Opin Microbiol* 2007, 10:510-516]. Here, we focus on research strategies for putting these methods into practice in the laboratory setting. An immediate consequence of single-cell sequencing is that it provides an alternative to culturing organisms as a prerequisite for genomic sequencing. The microgram amounts of DNA required as template are amplified from a single bacterium by a method called multiple displacement amplification (MDA) avoiding the need to grow cells. The ability to sequence DNA from individual cells will likely have an immense impact on microbiology considering the vast numbers of novel organisms, which have been inaccessible unless culture-independent methods could be used. However, special approaches have been necessary to work with amplified DNA. MDA may not recover the entire genome from the single copy present in most bacteria. Also, some sequence rearrangements can occur during the DNA amplification reaction. Over the past two years many

research groups have begun to use MDA, and some practical approaches to single-cell sequencing have been developed. We review the consensus that is emerging on optimum methods, reliability of amplified template, and the proper interpretation of 'composite' genomes which result from the necessity of combining data from several single-cell MDA reactions in order to complete the assembly. Preferred laboratory methods are considered on the basis of experience at several large sequencing centers where >70% of genomes are now often recovered from single cells. Methods are reviewed for preparation of bacterial fractions from environmental samples, single-cell isolation, DNA amplification by MDA, and DNA sequencing.

Jaakkola, Maritta S., Reginald Quansah, Timo T. Hugg, Sirpa A. M. Heikkinen, and Jouni J. K. Jaakkola, 2013. Association of indoor dampness and molds with rhinitis risk: A systematic review and meta-analysis. *J ALLERGY CLIN IMMUNOL*, VOLUME 132, NUMBER 5, 1099-1110.

Jacobs, J. H., E. J. M. Krop, A. Borrás-Santos, J.-P. Zock, M. Taubel, A. Hyvärinen, J. Pekkanen, G. Doekes, D. J. J. Heederik, on behalf of the HITEA schools study consortium, 2014. Endotoxin levels in settled airborne dust in European schools: the HITEA school study. *Indoor Air* 2014; 24: 148–157

Indoor exposure to microbial agents is known to influence respiratory health. Besides home exposure, exposure in schools can affect respiratory health. In this study, we measured endotoxin in settled dust in primary schools in three European countries from three different geographical regions with different climates. Our aim was to characterize endotoxin levels in primary schools and evaluate associations with potential determinants. Endotoxin levels were repeatedly assessed in 23 schools in Spain (n = 7), the Netherlands (n = 10), and Finland (n = 6) using electrostatic dustfall collectors. In total, 645 measurements were taken in 237 classrooms. Endotoxin levels differed significantly between countries; Dutch schools had the highest levels, while Finnish schools showed the lowest levels. In each country, differences in endotoxin levels were observed between schools and over the sampling periods. Estimates improved after adjustment for sampling period. Factors affecting endotoxin levels in a school differed per country. In general, endotoxin levels were higher in lower grades and in classrooms with higher occupancy. School endotoxin levels may contribute significantly to total endotoxin exposure in children and teachers. As the correlation between the repeated measurements is reasonable, single endotoxin measurements form a reasonable basis for estimating annual endotoxin levels in schools.

Jarvis, Bruce B. and J. David Miller, 2005. Mycotoxins as harmful indoor air contaminants. *Appl Microbiol Biotechnol* (2005) 66: 367-372.

Fungal metabolites (mycotoxins) that pose a health hazard to humans and animals have long been known to be associated with mold-contaminated food and feed. In recent times, concerns have been raised about exposures to mycotoxin-producing fungi in indoor environments, e.g., damp homes and buildings. The principal mycotoxins that contaminate food and feed (aflatoxins, fumonisins, ochratoxin A, deoxynivalenol, zearalenone) are rarely if ever found in indoor environments, but their toxicological properties provide an insight into the difficulties of assessing the health effects of related mycotoxins produced by indoor molds. Although the *Penicillium* and *Aspergillus* genera of fungi are major contaminants of both food and feed products and damp buildings, the particular species and hence the array of mycotoxins are quite different in these environments. The mycotoxins of these indoor species and less common mycotoxins from *Stachybotrys* and *Chaetomium* fungi are discussed in terms of their health effects and the need for relevant biomarkers and long-term chronic exposure studies.

Johansson, E., S. Vesper, L. Levin, G. LeMasters, S. Grinshpun, T. Reponen, 2011. Streptomyces in house dust: associations with housing characteristics and endotoxin. *Indoor Air* 2011; 21: 300-310

In addition to mold, indoor bioaerosols also contain bacterial components that may have implications for human health. Endotoxin is a cell wall component in Gram-negative bacteria present at varying levels indoors that has been found to have respiratory health implications. *Streptomyces* is a large genus of Gram-positive bacteria, and some species have been shown to produce inflammatory reactions *in vitro* and *in vivo*. The aim of this study was to determine predictors of streptomyces levels in house dust and to compare the variation in streptomyces levels with that in

endotoxin levels. Dust was collected by floor vacuuming from 178 homes in the Cincinnati metropolitan area. Streptomyces levels were measured by quantitative PCR, and endotoxin was assayed by the Limulus amoebocyte lysate method. Associations between home characteristics and bacterial contaminants, expressed as concentration and load, were investigated through multiple regression analyses. The presence of two or more dogs was a strong predictor of both streptomyces and endotoxin levels. Season of dust collection and levels of outdoor molds were predictors of streptomyces but not endotoxin levels. In contrast, number of inhabitants was a significant predictor of endotoxin load only. Neither streptomyces nor endotoxin levels were associated with metrics of moisture damage.

Julian, Timothy R. Francisco J. Tamayo, James O. Leckie, and Alexandria B. Boehm, 2011. Comparison of Surface Sampling Methods for Virus Recovery from Fomites. APPLIED AND ENVIRONMENTAL MICROBIOLOGY, Oct. 2011, p. 6918-6925.

The role of fomites in infectious disease transmission relative to other exposure routes is difficult to discern due, in part, to the lack of information on the level and distribution of virus contamination on surfaces. Comparisons of studies intending to fill this gap are difficult because multiple different sampling methods are employed and authors rarely report their method's lower limit of detection. In the present study, we compare a subset of sampling methods identified from a literature review to demonstrate that sampling method significantly influences study outcomes. We then compare a subset of methods identified from the review to determine the most efficient methods for recovering virus from surfaces in a laboratory trial using MS2 bacteriophage as a model virus. Recoveries of infective MS2 and MS2 RNA are determined using both a plaque assay and quantitative reverse transcription-PCR, respectively. We conclude that the method that most effectively recovers virus from nonporous fomites uses polyester-tipped swabs prewetted in either one-quarter strength Ringer's solution or saline solution. This method recovers a median fraction for infective MS2 of 0.40 and for MS2 RNA of 0.07. Use of the proposed method for virus recovery in future fomite sampling studies would provide opportunities to compare findings across multiple studies.

Kanaani, Hussein, Megan Hargreaves, Zoran Ristovski, Lidia Morawska, 2009. Fungal spore fragmentation as a function of airflow rates and fungal generation methods. Atmospheric Environment 43 (2009) 3725-3735

The aim of this study was to characterise and quantify the fungal fragment propagules derived and released from several fungal species (*Penicillium*, *Aspergillus niger* and *Cladosporium cladosporioides*) using different generation methods and different air velocities over the colonies. Real time fungal spore fragmentation was investigated using an Ultraviolet Aerodynamic Particle Sizer (UVASP) and a Scanning Mobility Particle Sizer (SMPS). The study showed that there were significant differences ( $p < 0.01$ ) in the fragmentation percentage between different air velocities for the three generation methods, namely the direct, the fan and the fungal spore source strength tester (FSSST) methods. The percentage of fragmentation also proved to be dependent on fungal species. The study found that there was no fragmentation for any of the fungal species at an air velocity  $\leq 0.4 \text{ m s}^{-1}$  for any method of generation. Fluorescent signals, as well as mathematical determination also showed that the fungal fragments were derived from spores. Correlation analysis showed that the number of released fragments measured by the UVAPS under controlled conditions can be predicted on the basis of the number of spores, for *Penicillium* and *A. niger*, but not for *C. cladosporioides*. The fluorescence percentage of fragment samples was found to be significantly different to that of non-fragment samples ( $p < 0.0001$ ) and the fragment sample fluorescence was always less than that of the non-fragment samples. Size distribution and concentration of fungal fragment particles were investigated qualitatively and quantitatively, by both UVAPS and SMPS, and it was found that the UVAPS was more sensitive than the SMPS for measuring small sample concentrations, while the results obtained from the UVAPS and SMAS were not identical for the same samples.

Kelley, Scott T., Ulrike Theisen, Largus T. Angenent, Allison St. Amand and Norman R. Pace, 2004. Molecular Analysis of Shower Curtain Biofilm Microbes. Appl. Environ. Microbiol. 2004, 70(7):4187

Households provide environments that encourage the formation of microbial communities, often as biofilms. Such biofilms constitute potential reservoirs for pathogens, particularly for immune-compromised individuals. One household environment that potentially accumulates microbial biofilms is that provided by vinyl shower curtains. Over time, vinyl shower curtains accumulate films, commonly referred to as "soap scum," which microscopy reveals are constituted of lush microbial biofilms. To determine the kinds of microbes that constitute shower curtain biofilms and thereby to identify potential opportunistic pathogens, we conducted an analysis of rRNA genes obtained by PCR from

four vinyl shower curtains from different households. Each of the shower curtain communities was highly complex. No sequence was identical to one in the databases, and no identical sequences were encountered in the different communities. However, the sequences generally represented similar phylogenetic kinds of organisms. Particularly abundant sequences represented members of the  $\alpha$ -group of proteobacteria, mainly *Sphingomonas* spp. and *Methylobacterium* spp. Both of these genera are known to include opportunistic pathogens, and several of the sequences obtained from the environmental DNA samples were closely related to known pathogens. Such organisms have also been linked to biofilm formation associated with water reservoirs and conduits. In addition, the study detected many other kinds of organisms at lower abundances. These results show that shower curtains are a potential source of opportunistic pathogens associated with biofilms. Frequent cleaning or disposal of shower curtains is indicated, particularly in households with immune-compromised individuals.

"Kelley, Scott T and Jack A Gilbert, 2013. Studying the microbiology of the indoor

Environment. *Genome Biology* 2013, 14:202."

The majority of people in the developed world spend more than 90% of their lives indoors. Here, we examine our understanding of the bacteria that co-inhabit our artificial world and how they might influence human health.

Kembel, Steven W., Evan Jones, Jeff Kline, Dale Northcutt, Jason Stenson, Ann M Womack, Brendan JM Bohannon, G Z Brown and Jessica L Green, 2012. Architectural design influences the diversity and structure of the built environment microbiome. *The ISME Journal* (2012), 1-11

Buildings are complex ecosystems that house trillions of microorganisms interacting with each other, with humans and with their environment. Understanding the ecological and evolutionary processes that determine the diversity and composition of the built environment microbiome—the community of microorganisms that live indoors—is important for understanding the relationship between building design, biodiversity and human health. In this study, we used high-throughput sequencing of the bacterial 16S rRNA gene to quantify relationships between building attributes and airborne bacterial communities at a health-care facility. We quantified airborne bacterial community structure and environmental conditions in patient rooms exposed to mechanical or window ventilation and in outdoor air. The phylogenetic diversity of airborne bacterial communities was lower indoors than outdoors, and mechanically ventilated rooms contained less diverse microbial communities than did window-ventilated rooms. Bacterial communities in indoor environments contained many taxa that are absent or rare outdoors, including taxa closely related to potential human pathogens. Building attributes, specifically the source of ventilation air, airflow rates, relative humidity and temperature, were correlated with the diversity and composition of indoor bacterial communities. The relative abundance of bacteria closely related to human pathogens was higher indoors than outdoors, and higher in rooms with lower airflow rates and lower relative humidity. The observed relationship between building design and airborne bacterial diversity suggests that we can manage indoor environments, altering through building design and operation the community of microbial species that potentially colonize the human microbiome during our time indoors.

Kembel, Steven W., Martin Wu, Jonathan A. Eisen, Jessica L. Green, 2012. Incorporating 16S Gene Copy Number Information Improves Estimates of Microbial Diversity and Abundance. *PLoS Comput Biol* 8(10): e1002743. doi:10.1371/journal.pcbi.1002743

The abundance of different SSU rRNA ("16S") gene sequences in environmental samples is widely used in studies of microbial ecology as a measure of microbial community structure and diversity. However, the genomic copy number of the 16S gene varies greatly – from one in many species to up to 15 in some bacteria and to hundreds in some microbial eukaryotes. As a result of this variation the relative abundance of 16S genes in environmental samples can be attributed both to variation in the relative abundance of different organisms, and to variation in genomic 16S copy number among those organisms. Despite this fact, many studies assume that the abundance of 16S gene sequences is a surrogate measure of the relative abundance of the organisms containing those sequences. Here we present a method that uses data on sequences and genomic copy number of 16S genes along with phylogenetic placement and ancestral state estimation to estimate organismal abundances from environmental DNA sequence data. We use theory and simulations to demonstrate that 16S genomic copy number can be accurately estimated from the short reads typically obtained from high-throughput environmental sequencing of the 16S gene, and that organismal abundances in

microbial communities are more strongly correlated with estimated abundances obtained from our method than with gene abundances. We re-analyze several published empirical data sets and demonstrate that the use of gene abundance versus estimated organismal abundance can lead to different inferences about community diversity and structure and the identity of the dominant taxa in microbial communities. Our approach will allow microbial ecologists to make more accurate inferences about microbial diversity and abundance based on 16S sequence data.

Kettleleson, E., S. Kumar, T. Reponen, S. Vesper, D. Meheust, S. A. Grinshpun, A. Adhikari, 2013. *Stenotrophomonas*, *Mycobacterium*, and *Streptomyces* in home dust and air: associations with moldiness and other home/family characteristics. *Indoor Air* 2013; 23: 387–396.

Respiratory illnesses have been linked to children's exposures to water-damaged homes. Therefore, understanding the microbiome in waterdamaged homes is critical to preventing these illnesses. Few studies have quantified bacterial contamination, especially specific species, in water-damaged homes. We collected air and dust samples in twenty-one low-mold homes and twenty-one high-mold homes. The concentrations of three bacteria/genera, *Stenotrophomonas maltophilia*, *Streptomyces* sp., and *Mycobacterium* sp., were measured in air and dust samples using quantitative PCR (QPCR). The concentrations of the bacteria measured in the air samples were not associated with any specific home characteristic based on multiple regression models. However, higher concentrations of *S. maltophilia* in the dust samples were associated with water damage, that is, with higher floor surface moisture and higher concentrations of moisture-related mold species. The concentrations of *Streptomyces* and *Mycobacterium* sp. had similar patterns and may be partially determined by human and animal occupants and outdoor sources of these bacteria.

Khan AAH and Karuppayil SM. 2011. Practices contributing to biotic pollution in air-conditioned indoor environments. *Aerobiologia* 27(1):85-9.

Indoor environments play important roles in human health. The health hazards posed by polluted indoor environments include allergy, infections and toxicity. The term sick building syndrome (SBS) describes causes of building occupants experiencing adverse health effects that appear to be linked to the time spent in a building. Questionnaire-based data were collected from the people who live or work in air-conditioned (A/C) rooms. Responses of the occupants were analyzed to understand the practices contributing to biotic pollution of indoor air-conditioned environments. Our survey revealed some interesting facts about the users of A/C rooms and their practices that may be contributing to the indoor air quality. The allergy complaints and use of anti-allergy medicines were noted commonly among the occupants of government (Govt.) organizations and computer training centers where cleaning of room and A/C filters were not done periodically. Cleaning practices may reduce the complaints.

Khan A.S., S.J. Dancer, H. Humphreys, 2012. Priorities in the prevention and control of multidrug-resistant Enterobacteriaceae in hospitals. *Journal of Hospital Infection* 82 (2012) 85-93.

Background: Multidrug-resistant Enterobacteriaceae (MDE) are a major public health threat due to international spread and few options for treatment. Furthermore, unlike meticillin-resistant *Staphylococcus aureus* (MRSA), MDE encompass several genera and multiple resistance mechanisms, including extended-spectrum beta-lactamases and carbapenemases, which complicate detection in the routine diagnostic laboratory. Current measures to contain spread in many hospitals are somewhat ad hoc as there are no formal national or international guidelines. Aim: We sought to establish what should be the priorities for the prevention and control of MDE and what is feasible for implementation. We also identify areas for further research. Methods: We reviewed the published literature and other sources e.g. national agencies, for measures and interventions used to control MDE. Findings: Certain categories of at risk patients should be screened, especially in critical care areas, using appropriate laboratory methods. Standard and contact precautions are essential and hand hygiene compliance requires continued emphasis and high compliance levels. As MDE may persist on environmental surfaces for weeks, environmental decontamination could also be an effective control intervention. There are limited options for decolonisation with inadequate studies to date and antibiotic stewardship within and outside the hospital remains important. Conclusion: As there is a clear deficit in the evidence base to inform guidance on prevention and control, research in key areas, such as rapid detection, is urgently required.

Khoruts, Alexander MD, Johan Dicksved, PhD, Janet K. Jansson, PhD, and Michael J. Sadowsky PhD, 2010. Changes in the Composition of the Human Fecal Microbiome After Bacteriotherapy for Recurrent *Clostridium difficile*-associated Diarrhea. *J Clin Gastroenterol*, Volume 44, Number 5, pp. 354-360.

*Clostridium difficile*-associated disease (CDAD) is the major known cause of antibiotic-induced diarrhea and colitis, and the disease is thought to result from persistent disruption of commensal gut microbiota. Bacteriotherapy by way of fecal transplantation can be used to treat recurrent CDAD, which is thought to reestablish the normal colonic microflora. However, limitations of conventional microbiologic techniques have, until recently, precluded testing of this idea. In this study, we used terminal-restriction fragment length polymorphism and 16S rRNA gene sequencing approaches to characterize the bacterial composition of the colonic microflora in a patient suffering from recurrent CDAD before and after treatment by fecal transplantation from a healthy donor. Although the patient's residual colonic microbiota, prior to therapy was deficient in members of the bacterial divisions- Firmicutes and Bacteroidetes, transplantation had a dramatic impact on the composition of the patient's gut microbiota. By 14 days posttransplantation, the fecal bacterial composition of the recipient was highly similar to that of the donor and was dominated by *Bacteroides* spp. strains and an uncharacterized butyrate producing bacterium. The change in bacterial composition was accompanied by resolution of the patient's symptoms. The striking similarity of the recipient's and donor's intestinal microbiota following after bacteriotherapy suggests that the donor's bacteria quickly occupied their requisite niches resulting in restoration of both the structure and function of the microbial communities present.

Kildeso, J., H. Wurtz, K. F. Nielsen, P. Kruse, K. Wilkins, U. Thrane, S. Gravesen, P. A. Nielsen, T. Schneider, 2003. Determination of fungal spore release from wet building materials. *Indoor Air* 2003; 13: 148-155

The release and transport of fungal spores from water-damaged building materials is a key factor for understanding the exposure to particles of fungal origin as a possible cause of adverse health effects associated to growth of fungi indoors. In this study, the release of spores from nine species of typical indoor fungi has been measured under controlled conditions. The fungi were cultivated for a period of 4-6 weeks on sterilized wet wallpapered gypsum boards at a relative humidity (RH) of approximately 97%. A specially designed small chamber (P-FLEC) was placed on the gypsum board. The release of fungal spores was induced by well-defined jets of air impacting from rotating nozzles. The spores and other particles released from the surface were transported by the air flowing from the chamber through a top outlet to a particle counter and sizer. For two of the fungi (*Penicillium chrysogenum* and *Trichoderma harzianum*), the number of spores produced on the gypsum board and subsequently released was quantified. Also the relationship between air velocities from 0.3 to 3 m/s over the surface and spore release has been measured. The method was found to give very reproducible results for each fungal isolate, whereas the spore release is very different for different fungi under identical conditions. Also, the relationship between air velocity and spore release depends on the fungus. For some fungi a significant number of particles smaller than the spore size were released. The method applied in the study may also be useful for field studies and for generation of spores for exposure studies.

Kim KY and Kim CN. 2007. Airborne microbiological characteristics in public buildings of Korea. *Build Environ* 42(5):2188-96.

Characteristics of airborne bacteria and fungi were surveyed in the public buildings regulated in Korea, with the six-stage cascade impactor. The total concentrations of airborne bacteria and fungi were averaged to 404 and 382 cfu m<sup>-3</sup> in hospital, 931 and 536 cfu m<sup>-3</sup> in kindergarten, 294 and 334 cfu m<sup>-3</sup> in elderly welfare facility, and 586 and 371 cfu m<sup>-3</sup> in postpartum nurse center. Mean respirable concentrations of airborne bacteria and fungi were 194 and 292 cfu m<sup>-3</sup> in hospital, 358 and 347 cfu m<sup>-3</sup> in kindergarten, 134 and 266 cfu m<sup>-3</sup> in elderly welfare facility, and 254 and 289 cfu m<sup>-3</sup> in postpartum nurse center, respectively. Based on this results, total and respirable concentrations of airborne bacteria and fungi were significantly highest in kindergarten and lowest in elderly welfare facility (p<0.05). The ratios of indoor and outdoor concentration for airborne bacteria and fungi were below 1.0 in all the investigated public buildings regardless of size distribution. The dominant genera identified in the public buildings were *Staphylococcus* spp., *Micrococcus* spp., *Corynebacterium* spp., and *Bacillus* spp., for airborne bacteria and *Penicillium* spp., *Cladosporium* spp., and *Aspergillus* spp., for airborne fungi, respectively. Size distributions of airborne bacteria and fungi in terms of the dominant genera were not observed consistently except for *Staphylococcus* spp., which was detected mainly on the first stage (>7.0 μm) and second stage (4.7-7.0 μm), and *Penicillium* spp., and *Cladosporium* spp., showing the highest collection rate at stage 3 (3.3-4.7 μm) regardless of the kind of the public buildings

Kim K, Park J, Jang G, Kim C, Lee K. 2007. Assessment of bioaerosols in the public buildings of Korea. *Indoor Built Environ* 16(5):465-71.

The concentration of airborne bacteria and fungi in public buildings is regulated by law in Korea. Levels are investigated during the moderate seasons, spring (March-May) and autumn (September-November), using a six-stage cascade impactor. Total concentrations of airborne bacteria and fungi range from 290 to 940 cfu m<sup>-3</sup> and 330 to 540 cfu m<sup>-3</sup>, respectively. The levels of airborne bacteria and fungi are significantly highest in a kindergarten building and lowest in an elderly welfare facility ( $p < 0.05$ ). The ratio of respirable to total concentration range from 30 to 40% for airborne bacteria and from 55 to 70% for airborne fungi but there is no significant difference among the public buildings examined ( $p < 0.05$ ). The mean ratios of indoor and outdoor concentrations of airborne bacteria and fungi are below 1.0 regardless of the fraction of particle size and building type. The indoor concentration of airborne bacteria and fungi do not correlate significantly with indoor temperature and relative humidity ( $p < 0.05$ ). However, this does have a significant positive correlation with CO<sub>2</sub> and the number of people per area of the sampling site ( $I < 0.05$ ), which implies that the activity of residents has considerable effect on the levels of both airborne bacteria and fungi.

Ki Youn KIM, Yoon Shin KIM and Daekeun KIM, 2010. Distribution Characteristics of Airborne Bacteria and Fungi in the General Hospitals of Korea. *Industrial Health* 2010, 48, 236-243

The objective of this study is to provide fundamental data related to size-based characteristics of bioaerosol distributed in the general hospital. Measurement sites are main lobby, ICU, surgical ward and biomedical laboratory and total five times were sampled with six-stage cascade impactor. Mean concentrations of airborne bacteria and fungi were the highest in main lobby as followed by an order of surgical ward, ICU and biomedical laboratory. The predominant genera of airborne bacteria identified in the general hospital were *Staphylococcus* spp. (50%), *Micrococcus* spp. (15-20%), *Corynebacterium* spp. (5-20%), and *Bacillus* spp. (5-15%). On the other hand, the predominant genera of airborne fungi identified in the general hospital were *Cladosporium* spp. (30%), *Penicillium* spp. (20-25%), *Aspergillus* spp. (15-20%), and *Alternaria* spp. (10-20%). The detection rate was generally highest on stage 5 (1.1-2.1  $\mu\text{m}$ ) for airborne bacteria and on stage 1 (>7.0  $\mu\text{m}$ ) for airborne fungi

King, M.-F. King, C.J. Noakes, P.A. Sleight, M.A. Camargo-Valero, 2013. Bioaerosol deposition in single and two-bed hospital rooms: A numerical and experimental study. *Building and Environment* 59 (2013) 436e447

Aerial dispersion of pathogenic microorganisms and subsequent contamination of surfaces is well recognised as a potential transmission route for hospital acquired infection. Simulation approaches such as computational fluid dynamics (CFD) are increasingly used to model particle behaviour in indoor air and the results interpreted to infer infection risk. However there is little validation of such methods in the open literature. This paper considers the ability of CFD simulations to accurately predict spatial distributions of bioaerosol deposition in indoor environments and explores the influence that different room layouts have on deposition patterns. Spatial deposition of aerosolised *Staphylococcus aureus* was measured in an aerobiology test room arranged in three different layouts: an empty room, a single-bed and a two-bed hospital room. Comparison with CFD simulations using Lagrangian particle tracking demonstrates that a realistic prediction of spatial deposition is feasible, and that a Reynolds Stress (RSM) turbulence model yields significantly better results than the k- $\epsilon$  RNG turbulence model used in most indoor air simulations. Results for all layouts demonstrate that small particle bioaerosols are deposited throughout a room with no clear correlation between relative surface concentration and distance from the source. However, a physical partition separating patients is shown to be effective at reducing crosscontamination of neighbouring patient zones.

Klamer, Morten Elisabeth Morsing, Thor Husemoen, 2004. Fungal growth on different insulation materials exposed to different moisture regimes *International Biodeterioration & Biodegradation* 54 (2004) 277 - 282.

Commercially available paper, flax, glass wool and rock wool insulation materials were tested for sensitivity to moisture and the ability of fungi to grow on them under different moisture regimes. Three levels of moisture were used, ambient, simulated rain and water holding capacity. After wetting, the materials were inoculated with a mixture of fungi and incubated at 26°C in boxes with high moisture levels for 4 weeks. The greatest degree of fungal growth was observed on paper and flax insulation materials initially conditioned to ambient moisture levels. Paper and flax insulation were strongly affected by moisture, with all treatments showing losses in dry mass of approx. 20%, except for



paper subjected to simulated rain treatment in which the loss was 39%. Glass and rock wools were not sensitive to moisture and were resistant to fungal degradation, showing only traces of fungal growth and minimal loss in dry mass over 4 weeks.

Knibbs, Luke D., Congrong He, Caroline Duchaine, and Lidia Morawska, 2012. Vacuum Cleaner Emissions as a Source of Indoor Exposure to Airborne Particles and Bacteria. *Environ. Sci. Technol.* 2012, 46, 534-542.

Vacuuuming can be a source of indoor exposure to biological and nonbiological aerosols, although there are few data that describe the magnitude of emissions from the vacuum cleaner itself. We therefore sought to quantify emission rates of particles and bacteria from a large group of vacuum cleaners and investigate their potential determinants, including temperature, dust bags, exhaust filters, price, and age. Emissions of particles between 0.009 and 20  $\mu\text{m}$  and bacteria were measured from 21 vacuums. Ultrafine (<100 nm) particle emission rates ranged from  $4.0 \times 10^6$  to  $1.1 \times 10^{11}$  particles  $\text{min}^{-1}$ . Emission of 0.54-20  $\mu\text{m}$  particles ranged from  $4.0 \times 10^4$  to  $1.2 \times 10^9$  particles  $\text{min}^{-1}$ . PM<sub>2.5</sub> emissions were between  $2.4 \times 10^{-1}$  and  $5.4 \times 10^3$   $\mu\text{g min}^{-1}$ . Bacteria emissions ranged from 0 to  $7.4 \times 10^5$  bacteria  $\text{min}^{-1}$  and were poorly correlated with dust bag bacteria content and particle emissions. Large variability in emission of all parameters was observed across the 21 vacuums, which was largely not attributable to the range of determinant factors we assessed. Vacuum cleaner emissions contribute to indoor exposure to nonbiological and biological aerosols when vacuuming, and this may vary markedly depending on the vacuum used.

Knutsen, Alan P., MD, Robert K. Bush, MD, Jeffrey G. Demain, MD, David W. Denning, FRCP, FMedSci, Anupma Dixit, PhD, MPH, Abbie Fairs, MD, Paul A. Greenberger, MD, Barbara Kariuki, BS, MPH, Hirohito Kita, MD, Viswanath P. Kurup, PhD, Richard B. Moss, MD, Robert M. Niven, MD, Catherine H. Pashley, MD, Raymond G. Slavin, MD, Hari M. Vijay, PhD, MPH, and Andrew J. Wardlaw, MD, 2012. Fungi and allergic lower respiratory tract diseases. *J Allergy Clin Immunol* 2012;129:280-91

Asthma is a common disorder that in 2009 afflicted 8.2% of adults and children, 24.6 million persons, in the United States. In patients with moderate and severe persistent asthma, there is significantly increased morbidity, use of health care support, and health care costs. Epidemiologic studies in the United States and Europe have associated mold sensitivity, particularly to *Alternaria alternata* and *Cladosporium herbarum*, with the development, persistence, and severity of asthma. In addition, sensitivity to *Aspergillus fumigatus* has been associated with severe persistent asthma in adults. Allergic bronchopulmonary aspergillosis (ABPA) is caused by *A. fumigatus* and is characterized by exacerbations of asthma, recurrent transient chest radiographic infiltrates, coughing up thick mucus plugs, peripheral and pulmonary eosinophilia, and increased total serum IgE and fungus-specific IgE levels, especially during exacerbation. The airways appear to be chronically or intermittently colonized by *A. fumigatus* in patients with ABPA. ABPA is the most common form of allergic bronchopulmonary mycosis (ABPM); other fungi, including *Candida*, *Penicillium*, and *Curvularia* species, are implicated. The characteristics of ABPM include severe asthma, eosinophilia, markedly increased total IgE and specific IgE levels, bronchiectasis, and mold colonization of the airways. The term severe asthma associated with fungal sensitization (SAFS) has been coined to illustrate the high rate of fungal sensitivity in patients with persistent severe asthma and improvement with antifungal treatment. The immunopathology of ABPA, ABPM, and SAFS is incompletely understood. Genetic risks identified in patients with ABPA include HLA association and certain TH<sub>2</sub>-prominent and cystic fibrosis variants, but these have not been studied in patients with ABPM and SAFS. Oral corticosteroid and antifungal therapies appear to be partially successful in patients with ABPA. However, the role of antifungal and immunomodulating therapies in patients with ABPA, ABPM, and SAFS requires additional larger studies.

Koivula M, Kymalainen H, Virta J, Hakkarainen H, Hussein T, Komulainen J, Koponen H, Hautala M, Hameri K, Kanerva P, et al. 2005. Emissions from thermal insulations - part 2: Evaluation of emissions from organic and inorganic insulations RID A-8055-2011. *Build Environ* 40(6):803-14.

The aim of this study was to examine microbial, chemical and physical (particle) emissions from organic and inorganic thermal insulations with a multifunctional apparatus developed for this purpose. In addition, basic quality parameters of the insulation materials, including microbial content, ignition residue and density, were determined. The particular focus of the study was on bast fibrous insulations made of bast fibres of flax, linseed and hemp. The amounts of microbes in the dry insulations varied greatly, up to 107 cfu/g source. Several taxa of fungi were detected from the bast fibrous insulations, some of which may produce toxins in suitable conditions. The lowest microbial contents were

found in the commercial products. However, emissions of moulds from all insulations made from bast fibres were significant at 90% RH, whereas at lower RHs they were negligible. Only a minor amount of emissions was detected from the reference materials at any RH. Emissions of bacteria were negligible for all materials and conditions. The emission levels of VOCs were negligible for all materials except recycled wood. However, several components of the VOC emissions were identified. No significant emissions of particles were detected from thermal insulations made of bast fibres of flax and hemp. In the case of insulations, particularly those made of organic fibres, it is essential to follow good manufacturing practices and to keep the insulations in a dry place throughout the manufacturing and building process in order to minimize hygienic risks in insulations.

Kolodkin-Gal, Ilana, Diego Romero, Shugeng Cao, Jon Clardy, Roberto Kolter, Richard Losick, 2010. d-Amino Acids Trigger Biofilm Disassembly. *Science* 328, 627 (2010) DOI: 10.1126/science.1188628

Bacteria form communities known as biofilms, which disassemble over time. In our studies outlined here, we found that, before biofilm disassembly, *Bacillus subtilis* produced a factor that prevented biofilm formation and could break down existing biofilms. The factor was shown to be a mixture of D-leucine, D-methionine, D-tyrosine, and D-tryptophan that could act at nanomolar concentrations. D-Amino acid treatment caused the release of amyloid fibers that linked cells in the biofilm together. Mutants able to form biofilms in the presence of D-Amino acids contained alterations in a protein (YqxM) required for the formation and anchoring of the fibers to the cell. D-Amino acids also prevented biofilm formation by *Staphylococcus aureus* and *Pseudomonas aeruginosa*. D-amino acids are produced by many bacteria and, thus, may be a widespread signal for biofilm disassembly.

Kolter et al 1993. Stationary Phase of Bacterial Life cycle *Annu. Rev. Microbiol.* 1993.47:855-74.

In the natural environment bacteria seldom encounter conditions that permit periods of exponential growth. Rather, bacterial growth is characterized by long periods of nutritional deprivation punctuated by short periods that allow fast growth, a feature that is commonly referred to as the feast-or-famine lifestyle. In this chapter we review the recent advances made in our understanding of the molecular events that allow some gram-negative bacteria to survive prolonged periods of starvation. After an introductory description of the properties of starved gram-negative bacteria, the review presents three aspects of stationary phase: entry into stationary phase, responses during prolonged starvation, and reentry into the growth cycle.

Kolter, Roberto and E. Peter Greenberg 2006. The superficial life of microbes. *Nature* 443:300-302. 18 May 2006.

The social activities and organization of bacteria are crucial to their ecological success. But it is only in recent years that we have begun to study these secret societies. Most surfaces on this planet teem with microbial life, creating ecosystems of diverse organisms that flourish in slimy beds of their own making. The plaque encrusting our teeth, the slippery coating on river stones, the gunge clogging up water pipes or infected wounds: these are just a few examples of the microbial 'biofilms' that form anywhere there is a surface with a little moisture and some nutrients. Although microbes by and large live in such biofilm communities, most of our understanding of their physiology stems from experiments using liquid cultures of dispersed, free-swimming 'planktonic' cells. In the past decade, however, the number of studies performed on surface-associated microbes has increased dramatically. Today, we recognize that most, if not all, microbial species can form biofilms. The physiological differences between free-living individuals and communal biofilm-associated cells are becoming apparent, as are the regulatory mechanisms that underlie the switch between these two lifestyles.

Korpi A, Pasanen A, Pasanen P, Kalliokoski P. 1997. Microbial growth and metabolism in house dust. *Int Biodeterior Biodegrad* 40(1):19-27

Microbial growth and production of carbon dioxide (CO<sub>2</sub>) and microbial volatile organic compounds (MVOC) were investigated in house dust. According to CO<sub>2</sub> measurements, the metabolic activity increased after 11 days at 84-86% air relative humidity (RH) and after 3 days at 96-98% RH. Within 25 days, the concentration of fungal spores in house dust increased to about 45-fold at 84-86% RH resulting mainly from the growth of *Aspergillus*, *Eurotium* and *Penicillium*. At 96-98% RH, the proliferations were on average 1370- and 240-fold for fungi and bacteria, respectively. The dominating fungal genera were *Aspergillus* and *Penicillium*. The MVOC composition revealed that microbes can

utilize, for example, fatty acids and possibly aldehydes as carbon source resulting in the production of MVOC such as methyl ketones and alcohols. The main MVOC produced by microbes in house dust were 2-pentanone, 2-hexanone, 2-heptanone, limonene, 2-methylfuran, formaldehyde, acrolein and nonanal. Also, 3-octanone, 2-ethyl-1-hexanol, 1-octen-3-ol, 3-methyl-1-butanol, 3-methyl-2-butanol, camphene and  $\alpha$ -pinene can be considered to derive from microbial metabolism to some extent.

Korpi, Annei, Anna-Liisa Pasanen and Pertti Pasanen, 1998. Volatile Compounds Originating from Mixed Microbial Cultures on Building Materials under Various Humidity Conditions. *Appl. Environ. Microbiol.* 1998, 64(8):2914.

We examined growth of mixed microbial cultures (13 fungal species and one actinomycete species) and production of volatile compounds (VOCs) in typical building materials in outside walls, separating walls, and bathroom floors at various relative humidities (RHs) of air. Air samples from incubation chambers were adsorbed on Tenax TA and dinitrophenylhydrazine cartridges and were analyzed by thermal desorption-gas chromatography and high-performance liquid chromatography, respectively. Metabolic activity was measured by determining CO<sub>2</sub> production, and microbial concentrations were determined by a dilution plate method. At 80 to 82% RH, CO<sub>2</sub> production did not indicate that microbial activity occurred, and only 10% of the spores germinated, while slight increases in the concentrations of some VOCs were detected. All of the parameters showed that microbial activity occurred at 90 to 99% RH. The microbiological analyses revealed weak microbial growth even under drying conditions (32 to 33% RH). The main VOCs produced on the building materials studied were 3-methyl-1-butanol, 1-pentanol, 1-hexanol, and 1-octen-3-ol. In some cases fungal growth decreased aldehyde emissions. We found that various VOCs accompany microbial activity but that no single VOC is a reliable indicator of biocontamination in building materials.

Korpi A, Jarnberg J, Pasanen A. 2009. Microbial volatile organic compounds. *Crit Rev Toxicol* 39(2):139-93.

Microbial volatile organic compounds (MVOCs) are a variety of compounds formed in the metabolism of fungi and bacteria. Of more than 200 compounds identified as MVOCs in laboratory experiments, none can be regarded as exclusively of microbial origin or as specific for certain microbial species. Thus, the recognition of microbially contaminated areas by MVOC measurements is not successful with current methods. In this review, the basic physical and chemical properties of 96 typical MVOCs have been summarised. Of these, toxicological and exposure data were gathered for the 15 MVOCs most often analysed and reported in buildings with moisture and microbial damage. The most obvious health effect of MVOC exposure is eye and upper-airway irritation. However, in human experimental exposure studies, symptoms of irritation have appeared at MVOC concentrations several orders of magnitude higher than those measured indoors (single MVOC levels in indoor environments have ranged from a few ng/m<sup>3</sup> up to 1 mg/m<sup>3</sup>). This is also supported by dose-dependent sensory-irritation response, as determined by the American Society for Testing and Materials mouse bioassay. On the other hand, the toxicological database is poor even for the 15 examined MVOCs. There may be more potent compounds and other endpoints not yet evaluated

Korves, T. M., Y. M. Piceno, L. M. Tom, T. Z. DeSantis, B. W. Jones, G. L. Andersen, G. M. Hwang, 2012. Bacterial communities in commercial aircraft high-efficiency particulate air (HEPA) filters assessed by PhyloChip analysis. *Indoor Air* 2013; 23: 50-61.

Air travel can rapidly transport infectious diseases globally. To facilitate the design of biosensors for infectious organisms in commercial aircraft, we characterized bacterial diversity in aircraft air. Samples from 61 aircraft high-efficiency particulate air (HEPA) filters were analyzed with a custom microarray of 16S rRNA gene sequences (PhyloChip), representing bacterial lineages. A total of 606 subfamilies from 41 phyla were detected. The most abundant bacterial subfamilies included bacteria associated with humans, especially skin, gastrointestinal and respiratory tracts, and with water and soil habitats. Operational taxonomic units that contain important human pathogens as well as their close, more benign relatives were detected. When compared to 43 samples of urban outdoor air, aircraft samples differed in composition, with higher relative abundance of Firmicutes and Gammaproteobacteria lineages in aircraft samples, and higher relative abundance of Actinobacteria and Betaproteobacteria lineages in outdoor air samples. In addition, aircraft and outdoor air samples differed in the incidence of taxa containing human pathogens. Overall, these results demonstrate that HEPA filter samples can be used to deeply characterize bacterial diversity in aircraft air and suggest that the presence of close relatives of certain pathogens must be taken into account in probe design for aircraft biosensors.

Kramer A, Schwebke I, Kampf G. 2006. How long do nosocomial pathogens persist on inanimate surfaces? A systematic review. *Bmc Infectious Diseases* 6:130

**Background** Inanimate surfaces have often been described as the source for outbreaks of nosocomial infections. The aim of this review is to summarize data on the persistence of different nosocomial pathogens on inanimate surfaces. **Methods** The literature was systematically reviewed in MedLine without language restrictions. In addition, cited articles in a report were assessed and standard textbooks on the topic were reviewed. All reports with experimental evidence on the duration of persistence of a nosocomial pathogen on any type of surface were included. **Results** Most gram-positive bacteria, such as *Enterococcus* spp. (including VRE), *Staphylococcus aureus* (including MRSA), or *Streptococcus pyogenes*, survive for months on dry surfaces. Many gram-negative species, such as *Acinetobacter* spp., *Escherichia coli*, *Klebsiella* spp., *Pseudomonas aeruginosa*, *Serratia marcescens*, or *Shigella* spp., can also survive for months. A few others, such as *Bordetella pertussis*, *Haemophilus influenzae*, *Proteus vulgaris*, or *Vibrio cholerae*, however, persist only for days. Mycobacteria, including *Mycobacterium tuberculosis*, and spore-forming bacteria, including *Clostridium difficile*, can also survive for months on surfaces. *Candida albicans* as the most important nosocomial fungal pathogen can survive up to 4 months on surfaces. Persistence of other yeasts, such as *Torulopsis glabrata*, was described to be similar (5 months) or shorter (*Candida parapsilosis*, 14 days). Most viruses from the respiratory tract, such as corona, coxsackie, influenza, SARS or rhino virus, can persist on surfaces for a few days. Viruses from the gastrointestinal tract, such as astrovirus, HAV, polio- or rota virus, persist for approximately 2 months. Blood-borne viruses, such as HBV or HIV, can persist for more than one week. Herpes viruses, such as CMV or HSV type 1 and 2, have been shown to persist from only a few hours up to 7 days. **Conclusion** The most common nosocomial pathogens may well survive or persist on surfaces for months and can thereby be a continuous source of transmission if no regular preventive surface disinfection is performed.

Krauter, Paula and Arthur Biermann 2007. Reaerosolization of Fluidized Spores in Ventilation Systems. *APPLIED AND ENVIRONMENTAL MICROBIOLOGY*, Apr. 2007, p. 2165–2172 Vol. 73, No. 7

This project examined dry, fluidized spore reaerosolization in a heating, ventilating, and air conditioning duct system. Experiments using spores of *Bacillus atrophaeus*, a nonpathogenic surrogate for *Bacillus anthracis*, were conducted to delineate the extent of spore reaerosolization behavior under normal indoor airflow conditions. Short-term (five air-volume exchanges), long-term (up to 21,000 air-volume exchanges), and cycled (on-off) reaerosolization tests were conducted using two common duct materials. Spores were released into the test apparatus in turbulent airflow (Reynolds number, 26,000). After the initial pulse of spores (approximately  $10^{10}$  to  $10^{11}$  viable spores) was released, high-efficiency particulate air filters were added to the air intake. Airflow was again used to perturb the spores that had previously deposited onto the duct. Resuspension rates on both steel and plastic duct materials were between  $10^{-3}$  and  $10^{-5}$  per second, which decreased to 10 times less than initial rates within 30 min. Pulsed flow caused an initial spike in spore resuspension concentration that rapidly decreased. The resuspension rates were greater than those predicted by resuspension models for contamination in the environment, a result attributed to surface roughness differences. There was no difference between spore reaerosolization from metal and that from plastic duct surfaces over 5 hours of constant airflow. The spores that deposited onto the duct remained a persistent source of contamination over a period of several hours.

Kreiger, James, MD, MPH; David E. Jacobs, PhD, CIH; Peter J. Ashley, DrPH; Andrea Baeder, MPH; Ginger L. Chew, ScD; Dorr Dearborn, MD, PhD; H. Patricia Hynes, MA, MS; J. David Miller, PhD; Rebecca Morley, MSPP; Felicia Rabito, PhD; Darryl C. Zeldin, 2010. Housing Interventions and Control of Asthma-Related Indoor Biologic Agents: A Review of the Evidence. *J Public Health Management Practice*, 2010, 16(5) E-Supp, S11–S20

Subject matter experts systematically reviewed evidence on the effectiveness of housing interventions that affect health outcomes, primarily asthma, associated with exposure to moisture, mold, and allergens. Three of the 11 interventions reviewed had sufficient evidence for implementation: multifaceted, in-home, tailored interventions for reducing asthma morbidity; integrated pest management to reduce cockroach allergen; and combined elimination of moisture intrusion and leaks and removal of moldy items to reduce mold and respiratory symptoms. Four interventions needed more field evaluation, 1 needed formative research, and 3 either had no evidence of effectiveness or were ineffective. The 3 interventions with sufficient evidence all applied multiple, integrated strategies. This evidence review

shows that selected interventions that improve housing conditions will reduce morbidity from asthma and respiratory allergies.

Kuhn R, Trimble M, Hofer V, Lee M, Nassof R. 2005. Prevalence and airborne spore levels of stachybotrys spp. in 200 houses with water incursions in houston, texas. *Can J Microbiol* 51(1):25-8.

Two hundred homes with a history of water incursion were sampled for fungi to determine the prevalence and airborne spore levels of *Stachybotrys* spp. Sampling methods included room air, surface, and wall cavity air sampling. *Stachybotrys* spp. were detected with at least one of the methods in 58.5% of the houses tested, but only 9.6% of the room air samples contained *Stachybotrys* spores. Aerosolization of *Stachybotrys* spores was correlated with both wall cavity and surface contamination. However, after adjustment for the surface effect, *Stachybotrys* spores detected in wall cavities were not a significant factor contributing to spores detected in room air samples. We conclude that *Stachybotrys* spp. are commonly found on water-damaged building materials. In addition, the observations made in this study suggest that the impact on the living space air is low if the fungal spores are contained within a wall cavity.

Kumar M and Verma RK. 2010. Fungi diversity, their effects on building materials, occupants and control - a brief review. *J Sci Ind Res* 69(9):657-61

This study reviews fungal distribution, and effect of fungi on building materials and health of occupants. Techniques of fungal spore assessment, characterization, and quantification, and control of fungi are also discussed

Lai K. 2006. Hazard identification, dose-response and environmental characteristics of stachybotryotoxins and other health-related products from stachybotrys RID C-1531-2008. *Environ Technol* 27(3):329-35.

An extensive growth of *Stachybotrys* in water-damaged buildings is of great public health concern. It is inconclusive whether *Stachybotrys* is responsible for the reported health effects on the occupants in these contaminated environments. However, based on the veterinary, occupational and laboratory toxicity studies, it is reasonable to project that *Stachybotrys* can cause adverse health responses once the toxic level of the corresponding agents reached the target systems. In order to assess the risk to occupants in contaminated buildings, it is essential to outline and collect information for risk assessment. This review paper presents the current information in the format of hazard identification, dose-response and environmental characteristics and aims to discuss existing information with researchers and risk assessors and help to conduct risk characterization under different indoor conditions.

Lai, A.C.K., L.T. Wong, K.W. Mui, W.Y. Chan, H.C. Yu, 2012. An experimental study of bioaerosol (1-10  $\mu\text{m}$ ) deposition in a ventilated chamber. *Building and Environment* 56 (2012) 118-126.

Understanding of bioaerosols deposition in ventilated environments can significantly improve our current knowledge on exposure. This study presents an experimental and numerical analysis for bioaerosol deposition in a scaled ventilation chamber. Three different group sizes of common indoor airborne bioaerosols ranging from 1 to 10  $\mu\text{m}$ , (*Micrococcus luteus*, *Staphylococcus aureus*), (*Aspergillus niger*, *Penicillium citrinum*) and (*Rhizopus* sp.), were atomized and injected to a small chamber with three controllable ventilation flow rates varying from 1.7 h<sup>-1</sup> to 18.8 h<sup>-1</sup>. Twenty-eight (7 x 4) Petri dishes were placed at the bottom of the chamber and deposition was counted after inoculation. A commercial computational fluid dynamics tool was used to predict bioaerosol deposition. The results were compared with experiments and satisfactory agreements between them were observed. The results reveal that the larger the aerosol size, the shorter the deposition distance away from the inlet. The comparisons are further improved if non-spherical shape factor is considered.

LANG-YONA, NAAMA, YISHAI LEVIN, KAREN C. DANNEMILLER, ODED YARDEN, JORDAN PECCIA and YINON RUDICH, 2013. Changes in atmospheric CO<sub>2</sub> influence the allergenicity of *Aspergillus fumigatus*. *Global Change Biology* (2013) 19, 2381–2388, doi: 10.1111/gcb.12219

Increased susceptibility to allergies has been documented in the Western world in recent decades. However, a comprehensive understanding of its causes is not yet available. It is therefore essential to understand trends and mechanisms of allergy-inducing agents, such as fungal conidia. In this study, we investigated the hypothesis that environmental conditions linked to global atmospheric changes can affect the allergenicity of *Aspergillus fumigatus*, a

common allergenic fungal species in indoor and outdoor environments and in airborne particulate matter. We show that fungi grown under present-day CO<sub>2</sub> levels (392 ppm) exhibit 8.5 and 3.5 fold higher allergenicity compared to fungi grown at preindustrial (280 ppm) and double (560 ppm) CO<sub>2</sub> levels, respectively. A corresponding trend is observed in the expression of genes encoding for known allergenic proteins and in the major allergen Asp f1 concentrations, possibly due to physiological changes such as respiration rates and the nitrogen content of the fungus, influenced by the CO<sub>2</sub> concentrations. Increased carbon and nitrogen levels in the growth medium also lead to a significant increase in the allergenicity. We propose that climatic changes such as increasing atmospheric CO<sub>2</sub> levels and changes in the fungal growth medium may impact the ability of allergenic fungi such as *A. fumigatus* to induce allergies.

Lappalainen S, Kahkonen E, Loikkanen P, Palomaki E, Lindroos O, Reijula K. 2001. Evaluation of priorities for repairing in moisture-damaged school buildings in Finland. *Build Environ* 36(8):981-6

We concluded that by examining construction damages of buildings visually, noting the smell and measuring the moisture in surfaces of building materials was possible to decide the order of relative importance for repairings in water-damaged buildings. Also light evaluation of the exposure to fungi and bacteria was succeeded with those methods even if the evaluation was difficult in case of minor moisture damages. The operation of the HVAC systems had no correlation to the concentrations of fungi and bacteria in air, material and surfaces samples.

Lau, H.Y. and N.J. Ashbolt, 2009 The role of biofilms and protozoa in *Legionella* pathogenesis: implications for drinking water. *Journal of Applied Microbiology* 107 (2009) 368-378.

Current models to study *Legionella* pathogenesis include the use of primary macrophages and monocyte cell lines, various free-living protozoan species and murine models of pneumonia. However, there are very few studies of *Legionella* spp. pathogenesis aimed at associating the role of biofilm colonization and parasitization of biofilm microbiota and release of virulent bacterial cell/vacuoles in drinking water distribution systems. Moreover, the implications of these environmental niches for drinking water exposure to pathogenic legionellae are poorly understood. This review summarizes the known mechanisms of *Legionella* spp. proliferation within *Acanthamoeba* and mammalian cells and advocates the use of the amoeba model to study *Legionella* pathogenicity because of their close association with *Legionella* spp. in the aquatic environment. The putative role of biofilms and amoebae in the proliferation, development and dissemination of potentially pathogenic *Legionella* spp. is also discussed. Elucidating the mechanisms of *Legionella* pathogenicity development in our drinking water systems will aid in elimination strategies and procedural designs for drinking water systems and in controlling exposure to *Legionella* spp. and similar pathogens.

Lau, Josephine, William Bahnfleth, James Freihaut, 2008. Estimating the effects of ambient conditions on the performance of UVGI air cleaners. *Building and Environment* 44 (2009) 1362-1370.

Ultraviolet germicidal irradiation (UVGI) uses UVC radiation produced by low pressure mercury vapor lamps to control biological air contaminants. Ambient air velocity and temperature have a strong effect on lamp output by influencing the lamp surface cold spot temperature. In-duct UVGI systems are particularly susceptible to ambient effects due to the range of velocity and temperature conditions they may experience. An analytical model of the effect of ambient conditions on lamp surface temperature was developed for three common lamp types in cross flow from a convective-radiative energy balance assuming constant surface temperature. For one lamp type, a single tube standard output lamp, UVC output and cold spot temperature data were obtained under typical in-duct operating conditions. Over an ambient temperature range of 10-32.2 °C and an air velocity range of 0-3.25 m/s, measured cold spot temperature varied from 12.7 to 41.9 °C and measured lamp output varied by 68% of maximum. Surface temperatures predicted by the heat transfer model were 6-17 °C higher than corresponding measured cold spot temperatures, but were found to correlate well with cold spot temperature via a two-variable linear regression. When corrected using this relationship, the simple model predicted the cold spot temperature within 1 °C and lamp UVC output within ±5%. To illustrate its practical use, the calibrated lamp model was employed in a simulation of the control of a contaminant in a single-zone ventilation system by an in-duct UVGI device. In this example, failure to account for the impact of ambient condition effects resulted in under-prediction of average space concentration by approximately 20% relative to a constant output system operating at maximum UVC output.

Lee L, Tin S, Kelley ST. 2007. Culture-independent analysis of bacterial diversity in a child-care facility. *Bmc Microbiology* 7:27.

**Background** Child-care facilities appear to provide daily opportunities for exposure and transmission of bacteria and viruses. However, almost nothing is known about the diversity of microbial contamination in daycare facilities or its public health implications. Recent culture-independent molecular studies of bacterial diversity in indoor environments have revealed an astonishing diversity of microorganisms, including opportunistic pathogens and many uncultured bacteria. In this study, we used culture and culture-independent methods to determine the viability and diversity of bacteria in a child-care center over a six-month period. **Results** We sampled surface contamination on toys and furniture using sterile cotton swabs in four daycare classrooms. Bacteria were isolated on nutrient and blood agar plates, and 16S rRNA gene sequences were obtained from unique (one of a kind) colony morphologies for species identification. We also extracted DNA directly from nine representative swab samples taken over the course of the study from both toy and furniture surfaces, and used "universal" 16S rRNA gene bacterial primers to create PCR-based clone libraries. The rRNA gene clones were sequenced, and the sequences were compared with related sequences in GenBank and subjected to phylogenetic analyses to determine their evolutionary relationships. Culturing methods identified viable bacteria on all toys and furniture surfaces sampled in the study. *Bacillus* spp. were the most commonly cultured bacteria, followed by *Staphylococcus* spp., and *Microbacterium* spp. Culture-independent methods based on 16S rRNA gene sequencing, on the other hand, revealed an entirely new dimension of microbial diversity, including an estimated 190 bacterial species from 15 bacterial divisions. Sequence comparisons and phylogenetic analyses determined that the clone libraries were dominated by a diverse set of sequences related to *Pseudomonas* spp., as well as uncultured bacteria originally identified on human vaginal epithelium. Other sequences were related to uncultured bacteria from wastewater sludge, and many human-associated bacteria including a number of pathogens and opportunistic pathogens. Our results suggest that the child-care facility provided an excellent habitat for slime-producing *Pseudomonads*, and that diaper changing contributed significantly to the bacterial contamination. **Conclusion** The combination of culture and culture-independent methods provided powerful means for determining both viability and diversity of bacteria in child-care facilities. Our results provided insight into the source of contamination and suggested ways in which sanitation might be improved. Although our study identified a remarkable array of microbial diversity present in a single daycare, it also revealed just how little we comprehend the true extent of microbial diversity in daycare centers or other indoor environments

Lee, Se Hee, Doo Hwan Oh, Ji Young Jung, Jae Chan Kim and Che Ok Jeon, 2012. Comparative Ocular Microbial Communities in Humans with and without Blepharitis. *Ophthalmol Vis Sci.* 2012; 53:5585-5593.

**PURPOSE.** The aims of our study were to compare the ocular microbial communities of humans with and without blepharitis in an attempt to elucidate which microorganisms may cause blepharitis. **METHODS.** Bacterial 16S rRNA genes of eyelash and tear samples from seven blepharitis patients and four healthy controls were sequenced using a pyrosequencing method, and their bacterial community structures were compared bioinformatically. **RESULTS.** Phylotypic analysis demonstrated that eyelash and tear samples had highly diverse bacterial communities with many previously undescribed bacteria. Bacterial communities in eyelash samples from subjects with blepharitis were less diverse than those from healthy controls, while the bacterial communities of tear subjects with blepharitis were more diverse than those of healthy subjects. Statistical analyses using UniFrac and a principle coordinate analysis showed that the bacterial communities of tear samples from subjects with blepharitis were well clustered, regardless of individual, while the bacterial communities of all eyelash samples and healthy tear samples were not well clustered due to high interpersonal variability. Bioinformatic analysis revealed that *Propionibacterium*, *Staphylococcus*, *Streptophyta*, *Corynebacterium*, and *Enhydrobacter* were the common ocular bacteria. An increase of *Staphylococcus*, *Streptophyta*, *Corynebacterium*, and *Enhydrobacter*, and a decrease of *Propionibacterium* were observed from blepharitis subjects, in terms of the relative abundances. **CONCLUSIONS.** Higher abundances of *Streptophyta*, *Corynebacterium*, and *Enhydrobacter* in blepharitis subjects suggested that human blepharitis might be induced by the infestations of pollens, dusts, and soil particles. These results will provide valuable information for the prevention and treatment of human blepharitis based on ocular microbial flora.

Lemfack, Marie Chantal, Janette Nickel, Mathias Dunkel, Robert Preissner and Birgit Piechulla, 2013. mVOC: a database of microbial volatiles. *Nucleic Acids Research*, 2014, Vol. 42.

Scents are well known to be emitted from flowers and animals. In nature, these volatiles are responsible for inter- and intra-organismic communication, e.g. attraction and defence. Consequently, they influence and improve the establishment of organisms and populations in ecological niches by acting as single compounds or in mixtures. Despite the known wealth of volatile organic compounds (VOCs) from species of the plant and animal kingdom, in the past, less attention has been focused on volatiles of microorganisms. Although fast and affordable sequencing methods facilitate the detection of microbial diseases, however, the analysis of signature or fingerprint volatiles will be faster and easier. Microbial VOCs (mVOCs) are presently used as marker to detect human diseases, food spoilage or moulds in houses. Furthermore, mVOCs exhibited antagonistic potential against pathogens *in vitro*, but their biological roles in the ecosystems remain to be investigated. Information on volatile emission from bacteria and fungi is presently scattered in the literature, and no public and up-to-date collection on mVOCs is available. To address this need, we have developed mVOC, a database available online at <http://bioinformatics.charite.de/mvoc>.

Leong SC and Eccles R. 2009. A systematic review of the nasal index and the significance of the shape and size of the nose in rhinology. *Clin Otolaryngol* 34(3):191-8.

Objective of review: To determine if there is any clinical relevance of the shape and size of the nose in relation to physiology, pathology and surgery. Type of review: Systematic review. Search strategy: A structured search of PubMed was performed from 1966 to 2008 for each section of the review focusing on the ethnic variations in nasal index, the effect of climate of nasal shape, ethnic variations of nasal physiology and racial predilection for sinonasal pathology. Results: Nasal proportions do vary between ethnic groups but the size and shape of the nose does not define Caucasian, Asian and African races respectively. Anthropologists agree that the nasal variations are due to man's adaptation to the environment. However, this theory remains to be proven. Published data on nasal physiology have not shown significant differences between the ethnic groups despite obvious differences in nasal proportions. There is no evidence of ethnic specific predilection to disease due to anatomical variation, physiological vulnerability or genetic susceptibility. Rhinology research is often confounded by classifying populations according to race, as racial characteristics are not based on any scientific principles and the nasal index may be a more reliable discriminator. The only area in which the size and shape of the nose is of relevance is in aesthetic and reconstruction surgery. Conclusions: Nasal proportions are important aesthetically but appear to have little relevance to the rhinologist.

Leppanen, H. K., A. Nevalainen, A. Vepsalainen, M. Roponen, M. Taubel, O. Laine, P. Rantakokko, E. von Mutius, J. Pekkanen, A. Hyvarinen, 2014. Determinants, reproducibility, and seasonal variation of ergosterol levels in house dust. *Indoor Air* 2014; 24: 248–259.

Leung, W. T., G. N. Sze-To, C. Y. H. Chao, S. C. T. Yu, J. K. C. Kwan, 2012. Study on the interzonal migration of airborne infectious particles in an isolation ward using benign bacteria. *Indoor Air* 2013; 23: 148–161

Negative pressure isolation wards are essential infection control facilities against airborne transmissible diseases. Airborne infectious particles are supposed to be contained in the isolation room. However, negative pressure may break down by door-opening action or by human movement. Understanding the interzonal transport of airborne infectious particles in the isolation wards can aid the design and operation strategy of isolation facilities. In this work, the interzonal migration of airborne infectious particles by human movement was studied experimentally in an isolation ward. Artificial saliva solution with benign *E. coli* bacteria was aerosolized to simulate bacterium-laden infectious particles. The interzonal migration of aerosolized bacteria was characterized by biological air sampling. Less than 1% of airborne infectious particles were transported to the higher pressure zone when door was closed. With human movement, 2.7% of the particles were transported from the anteroom to the corridor. From high-to-low pressure zones, as much as 20.7% of airborne infectious particles were migrated. Only a minimal amount of particles was transported from the corridor to the positive pressure nurses station. Infection risk of tuberculosis of the healthcare workers and other occupants in the isolation wards were also assessed based on the measured migration ratios.

Li, A., Z. Liu, X. Zhu, Y. Liu and Q. Wang, The effect of air-conditioning parameters and deposition dust on microbial growth in supply air ducts, *Energy and Buildings* 42 (2010), pp. 449–454



To investigate the effect of air-conditioning parameters (including temperature, relative humidity and air velocity) and deposition dust on microbial growth in supply air duct, a complete test facility according to ASHRAE Standard 62.1-2007 was constructed. A series of experiments for testing microbial concentration (including bacteria and fungus) were conducted under different working conditions (such as different temperatures and relative humidity). The air velocity was constantly kept at 2.0 m/s. Orthogonal design was employed for the analysis of test data. The results indicated that air velocity attenuation down the direction of the supply air affected dust distribution at the bottom of duct, to some extent, and the number of microorganisms was positively correlated with the quantity of dust. In the range of temperature 22-32 degrees °C and relative humidity (RH) 40-90%, microbial growth significantly accelerated with higher temperature and RH increasing. The organic compounds composing the dust also had great impact on microbial growth. The basic researches are contributed to control the growth of microorganism and improve the indoor microenvironment in the air-conditioning room

Li, Sheng, Joseph N. S. Eisenberg, Ian H. Spicknall, and James S. Koopman, 2009. Dynamics and Control of Infections Transmitted From Person to Person Through the Environment. *American Journal of Epidemiology*, Vol. 170, No. 2, pp. 257-265.

The environment provides points for control of pathogens spread by food, water, hands, air, or fomites. These environmental transmission pathways require contact network formulations more realistically detailed than those based on social encounters or physical proximity. As a step toward improved assessment of environmental interventions, description of contact networks, and better use of environmental specimens to analyze transmission, an environmental infection transmission system model that describes the dynamics of human interaction with pathogens in the environment is presented. Its environmental parameters include the pathogen elimination rate,  $\mu$ , and the rate humans pick up pathogens,  $\rho$ , and deposit them,  $\alpha$ . The ratio,  $\rho N/\mu$  ( $N$  equals population size), indicates whether transmission is density dependent (low ratio), frequency dependent (high ratio), or in between. Transmission through frequently touched fomites, such as doorknobs, generates frequency-dependent patterns, while transmission through thoroughly mixed air or infrequently touched fomites generates density-dependent patterns. The environmental contamination ratio,  $\alpha/\gamma$ , reflects total agent deposition per infection and outbreak probability, where  $c$  is defined as the recovery rate. These insights provide theoretical contexts to examine the role of the environment in pathogen transmission and a framework to interpret environmental data to inform environmental interventions.

Li, Y., G. M. Leung, J. W. Tang, X. Yang, C. Y. H. Chao, J. Z. Lin, J. W. Lu, P. V. Nielsen, J. Niu, H. Qian, A.C. Sleight, H.-J. J. Su, J. Sundell, T. W. Wong, P. L. Yuen, 2007. Role of ventilation in airborne transmission of infectious agents in the built environment - a multidisciplinary systematic review. *Indoor Air* 2007; 17: 2-18

There have been few recent studies demonstrating a definitive association between the transmission of airborne infections and the ventilation of buildings. The severe acute respiratory syndrome (SARS) epidemic in 2003 and current concerns about the risk of an avian influenza (H5N1) pandemic, have made a review of this area timely. We searched the major literature databases between 1960 and 2005, and then screened titles and abstracts, and finally selected 40 original studies based on a set of criteria. We established a review panel comprising medical and engineering experts in the fields of microbiology, medicine, epidemiology, indoor air quality, building ventilation, etc. Most panel members had experience with research into the 2003 SARS epidemic. The panel systematically assessed 40 original studies through both individual assessment and a 2-day face-to-face consensus meeting. Ten of 40 studies reviewed were considered to be conclusive with regard to the association between building ventilation and the transmission of airborne infection. There is strong and sufficient evidence to demonstrate the association between ventilation, air movements in buildings and the transmission/spread of infectious diseases such as measles, tuberculosis, chickenpox, influenza, smallpox and SARS. There is insufficient data to specify and quantify the minimum ventilation requirements in hospitals, schools, offices, homes and isolation rooms in relation to spread of infectious diseases via the airborne route.

Liener K, Leiacker R, Lindemann J, Rettinger G, Keck T. 2003. Nasal mucosal temperature after exposure to cold, dry air and hot, humid air. *Acta Otolaryngol* 123(7):851-6.

Objective- To determine the influence of variations in the temperature and humidity of inhaled air on the nasal mucosal temperature at various sites in the nasal airways. Material and Methods- Fifteen volunteers were enrolled in the study. The temperature was measured on the mucosal surface of the nasal septum at the level of the nasal

vestibule, in the nasal valve area, anterior turbinate area and choanae. Temperature measurements were made using a miniaturized thermocouple. Continuous temperature readings were performed before and after 10 min of exposure to either cold, dry air, ambient air or hot, humid air. Results- Inhalation of cold, dry air significantly reduced the temperature of the septal mucosa at each location of measurement compared to the breathing of ambient air. Inhalation of hot, humid air significantly increased the septal mucosal temperature at all detection sites. Conclusions- The climatic condition of inhaled air can lead to significant changes in nasal mucosal temperature. As the nasal mucosa is important for nasal air conditioning, short-term exposure to air of extreme temperature and humidity can rapidly compromise nasal air conditioning

Ling, Alison L., Norman R. Pace, Mark T. Hernandez, and Timothy M. LaPara, 2013. Tetracycline Resistance and Class 1 Integron Genes Associated with Indoor and Outdoor Aerosols. *Environ. Sci. Technol.* 2013, 47, 4046–4052.

Genes encoding tetracycline resistance and the integrase of Class 1 integrons were enumerated using quantitative PCR from aerosols collected from indoor and outdoor environments. Concentrated animal feeding operations (CAFOs) and human-occupied indoor environments (two clinics and a homeless shelter) were found to be a source of airborne tet(X) and tet(W) genes. The CAFOs had 10- to 100-times higher concentrations of airborne 16S rRNA, tet(X), and tet(W) genes than other environments sampled, and increased concentrations of aerosolized bacteria correlated with increased concentrations of airborne resistance genes. The two CAFOs studied had statistically similar concentrations of resistance genes in their aerosol samples, even though antibiotic use was markedly different between the two operations. Additionally, tet(W) genes were recovered in outdoor air within 2 km of livestock operations, which suggests that antibiotic resistance genes may be transported via aerosols on local scales. The integrase gene (int11) from Class 1 integrons, which has been associated with multidrug resistance, was detected in CAFOs but not in human-occupied indoor environments, suggesting that CAFO aerosols could serve as a reservoir of multidrug resistance. In conclusion, our results show that CAFOs and clinics are sources of aerosolized antibiotic resistance genes that can potentially be transported via air movement.

Lipsitch, Marc and Ceclie Vibound, 2009. Influenza seasonality: Lifting the fog. *PNAS*, Vol 106:10, pp. 3645-3646.

Seasonal variation in the incidence of communicable diseases is among the oldest observations in population biology, dating back at least to ancient Greece, yet our understanding of the mechanisms underlying this phenomenon remains hazy at best. Influenza is perhaps the seasonal disease of most profound interest, because it is responsible for much of the seasonal variation in other infectious and noninfectious causes of morbidity and mortality (1-4). Influenza virus activity displays strong seasonal cycles in temperate areas of the world and less defined seasonality in tropical regions (5), suggesting that environmental factors may drive seasonal patterns. In a recent issue of *PNAS*, Shaman and Kohn (6) move us a step closer to understanding influenza seasonality by clarifying the impact of environmental factors on influenza virus transmission and survival. The authors demonstrate an impressive statistical association between vapor pressure, influenza transmission, and virus survival.

Lofgren, Eric, N. H. Fefferman, Y. N. Naumov, J. Gorski, and E. N. Naumova, 2007. Influenza Seasonality: Underlying Causes and Modeling Theories. *JOURNAL OF VIROLOGY*, June 2007, p. 5429-5436

Influenza (or "flu") leads to the hospitalization of more than 200,000 people yearly and results in 36,000 deaths from flu or flu-related complications in the United States (15), striking both the elderly and infant populations particularly hard (24). Two members of the Orthomyxoviridae family, the influenza A and B viruses, are the primary causes of this acute viral respiratory disease. Both viruses are characterized as enveloped viruses that contain eight negative-stranded RNA segments that encode 9 structural and 2 nonstructural proteins (influenza A virus) or 10 structural and 1 nonstructural protein (influenza B virus). Because of the higher levels of morbidity and mortality associated with influenza A virus, in part due to the large reservoir of the virus in aquatic birds, we will restrict ourselves to discussions of this virus.

Low, Swee Yang, Karen DANNEMILLER, Maosheng YAO, Naomichi YAMAMOTO and Jordan PECCIA, 2011. The allergenicity of *Aspergillus fumigatus* conidia is influenced by growth temperature. *Fungal Biology* (2011) 625 -632

Common indoor and outdoor environmental fungi such as *Aspergillus fumigatus* produce asexual spores containing a collection of proteins that can bind IgE antibodies and trigger allergic reactions. We characterized the impact of sporulation temperature on the IgE binding capacity (allergenicity) of *A. fumigatus* and explored the links between variable allergenicity and temperature-dependant expression of genes encoding these allergenic proteins. A 12-fold increase in *A. fumigatus* allergenicity per spore was observed when sporulation temperatures were decreased from 32 °C to 17 °C. Per spore protein mass and Asp f 1 allergen mass also followed this trend. Functional gene expression analysis of *A. fumigatus* sporulating cultures by real-time reverse-transcription PCR and gene expression microarrays revealed that a greater number of genes encoding known, major allergens are more highly expressed at lower sporulation temperatures. The results of this study indicate that environmental conditions at growth significantly influence the allergenicity of this common mould through the differential production of allergenic proteins, and highlight the importance of in vivo or in vitro allergenicity measurements for understanding environmental exposure to airborne allergenic fungi.

Lowen, Anice C., Samira Mubareka, Terrence M. Tumpey, Adolfo Garcí'a-Sastre, and Peter Palese, 2006. The guinea pig as a transmission model for human influenza viruses. *PNAS* 103:26

The severity of epidemic and pandemic influenza outbreaks is dictated in part by the efficiency with which the causative strain transmits between human hosts. The mechanisms underlying influenza virus spread are poorly understood, in part because of the lack of a convenient animal model to study this phenomenon. Indeed, despite extremely efficient transmission among humans and virulence in the mouse model, we have shown that even the 1918 pandemic influenza virus does not transmit between mice. We therefore evaluated the guinea pig as a model mammalian host for influenza virus. Using the recent human isolate A Panama 2007/99 (Pan/99) (H3N2) virus, we found that guinea pigs were highly susceptible to infection with the unadapted virus (ID<sub>50</sub> = 5 plaque-forming units). Pan/99 virus grew to high titers in the upper respiratory tract and was shed in nasal washings of infected animals. Moreover, influenza virus was transmitted from infected guinea pigs to noninfected guinea pigs housed in the same cage, an adjacent cage, and a cage placed 91 cm away. Our results demonstrate that influenza virus can pass between guinea pigs by means of droplet spread and thereby establish the suitability of the guinea pig as a model host for influenza virus transmission studies.

Lowen, Anice C., Samira Mubareka, John Steel, Peter Palese, 2007. Influenza Virus Transmission Is Dependent on Relative Humidity and Temperature. *PLoS Pathogens*, Vol 3:10, pp. 1470-1476

Using the guinea pig as a model host, we show that aerosol spread of influenza virus is dependent upon both ambient relative humidity and temperature. Twenty experiments performed at relative humidities from 20% to 80% and 5 °C, 20 °C, or 30 °C indicated that both cold and dry conditions favor transmission. The relationship between transmission via aerosols and relative humidity at 20 °C is similar to that previously reported for the stability of influenza viruses (except at high relative humidity, 80%), implying that the effects of humidity act largely at the level of the virus particle. For infected guinea pigs housed at 5 °C, the duration of peak shedding was approximately 40 h longer than that of animals housed at 20 °C; this increased shedding likely accounts for the enhanced transmission seen at 5 °C. To investigate the mechanism permitting prolonged viral growth, expression levels in the upper respiratory tract of several innate immune mediators were determined. Innate responses proved to be comparable between animals housed at 5 °C and 20 °C, suggesting that cold temperature (5 °C) does not impair the innate immune response in this system. Although the seasonal epidemiology of influenza is well characterized, the underlying reasons for predominant wintertime spread are not clear. We provide direct, experimental evidence to support the role of weather conditions in the dynamics of influenza and thereby address a long-standing question fundamental to the understanding of influenza epidemiology and evolution.

Lowen, Anice C., John Steel, Samira Mubareka, and Peter Palese, 2008. High Temperature (30°C) Blocks Aerosol but Not Contact Transmission of Influenza Virus. *JOURNAL OF VIROLOGY*, June 2008, p. 5650-5652.

Influenza causes significant morbidity in tropical regions; however, unlike in temperate zones, influenza in the tropics is not strongly associated with a given season. We have recently shown that influenza virus transmission in the guinea pig model is most efficient under cold, dry conditions, which are rare in the tropics. Herein, we report the lack of aerosol transmission at 30°C and at all humidities tested. Conversely, transmission via the contact route was equally

efficient at 30°C and 20°C. Our data imply that contact or short-range spread predominates in the tropics and offer an explanation for the lack of a well-defined, recurrent influenza season affecting tropical and subtropical regions of the world.

MacIntosh DL, Brightman HS, Baker BJ, Myatt TA, Stewart JH, McCarthy JF. 2006. Airborne fungal spores in a cross-sectional study of office buildings. *Journal of Occupational and Environmental Hygiene* 3(7):379-89

Airborne fungal spores were measured in 44 office buildings in the summer and winter throughout the continental United States, as part of the Building Assessment, Survey and Evaluation (BASE) program. Six indoor air and two outdoor air samples were collected on a single day from each building. The cross-sectional and repeated measure design afforded evaluation of between-building and within-building variability of fungal spore levels in buildings. Total fungal spore concentrations in indoor air ranged from < 24 to 1000 spores/m<sup>3</sup>, except for one building with natural ventilation where indoor levels were approximately 9000 spores/m<sup>3</sup>. Indoor air concentrations of total spores did not vary significantly between winter and summer or morning and afternoon monitoring periods or among climate zones or locations within a test area. Indoor-outdoor ratios of total spore concentrations typically ranged between 0.01 and 0.1 and were approximately seven times greater in winter than summer because of relatively low outdoor levels in the winter. The indoor-outdoor ratio of total spore concentrations for a building was consistent (reliability coefficient = 0.91) among repeated measures. Distributions of rank correlation coefficients for spore types in pairs of individual indoor-outdoor and indoor-indoor samples were weakly correlated (Spearman correlation = 0.2 on average). When spore type data were aggregated among samples from the same building, the central tendency of the rank correlation coefficients increased to 0.45. Rank correlation coefficients were also proportional to the number of spore types present in the samples that were compared. The BASE study provides normative data on concentrations of fungal spores that can aid in identification of problematic levels of mold in buildings.

Maclean, M., S.J. MacGregor, J.G. Anderson, G.A. Woolsey, J.E. Coia, K. Hamilton, I. Taggart, S.B. Watson, B. Thakker, G. Gettinby, 2010. Environmental decontamination of a hospital isolation room using high-intensity narrow-spectrum light. *Journal of Hospital Infection* 76 (2010) 247-251

The performance of a new decontamination technology, referred to as 'high-intensity narrow-spectrum light environmental decontamination system' (HINS-light EDS) was evaluated by a series of three studies carried out in a hospital isolation room used to treat burns patients. The ceiling-mounted HINS-light EDS emits high-intensity 405 nm light which, although bactericidal, is harmless to patients and staff thereby permitting continuous environmental disinfection throughout the day. Performance efficacy was assessed by contact agar plate sampling and enumeration of staphylococcal bacteria on environmental surfaces within the room before, during and after HINS-light EDS treatment. When the room was unoccupied, use of HINS-light EDS resulted in w90% reduction of surface bacterial levels and when the room was occupied by an MRSA-infected burns patient, reductions between 56% and 86% were achieved, with the highest reduction (86%) measured following an extended period of HINSlight EDS operation. In an on/off intervention study, surface bacterial levels were reduced by 62% by HINS-light EDS treatment and returned to normal contamination levels two days after the system was switched off. These reductions of staphylococci, including *Staphylococcus aureus* and methicillin-resistant *S. aureus*, by HINS-light EDS treatment were greater than the reductions achieved by normal infection control and cleaning activities alone. The findings provide strong evidence that HINS-light EDS, used as a supplementary procedure, can make a significant contribution to bacterial decontamination in clinical environments.

Maier, Raina M., Michael W. Palmer, Gary L. Andersen, Marilyn J. Halonen, Karen C. Josephson, Robert S. Maier, Fernando D. Martinez, Julia W. Neilson, Debra A. Stern, Donata Vercelli, and Anne L. Wright, 2010. Environmental Determinants of and Impact on Childhood Asthma by the Bacterial Community in Household Dust. *APPLIED AND ENVIRONMENTAL MICROBIOLOGY*, Apr. 2010, p. 2663-2667.

Asthma increased dramatically in the last decades of the 20th century and is representative of chronic diseases that have been linked to altered microbial exposure and immune responses. Here we evaluate the effects of environmental exposures typically associated with asthma protection or risk on the microbial community structure of household dust (dogs, cats, and day care). PCR-denaturing gradient gel analysis (PCR-DGGE) demonstrated that the bacterial community structure in house dust is significantly impacted by the presence of dogs or cats in the home ( $P = 0.0190$  and  $0.0029$ , respectively) and by whether or not children attend day care ( $P = 0.0037$ ). In addition, significant

differences in the dust bacterial community were associated with asthma outcomes in young children, including wheezing ( $P = 0.0103$ ) and specific IgE ( $P = 0.0184$ ). Our findings suggest that specific bacterial populations within the community are associated with either risk or protection from asthma.

Mann, Ethan E. & Daniel J. Wozniak, 2012. *Pseudomonas* biofilm matrix composition and niche biology. *FEMS Microbiol Rev* 36 (2012) 893-916

Biofilms are a predominant form of growth for bacteria in the environment and in the clinic. Critical for biofilm development are adherence, proliferation, and dispersion phases. Each of these stages includes reinforcement by, or modulation of, the extracellular matrix. *Pseudomonas aeruginosa* has been a model organism for the study of biofilm formation. Additionally, other *Pseudomonas* species utilize biofilm formation during plant colonization and environmental persistence. Pseudomonads produce several biofilm matrix molecules, including polysaccharides, nucleic acids, and proteins. Accessory matrix components shown to aid biofilm formation and adaptability under varying conditions are also produced by pseudomonads. Adaptation facilitated by biofilm formation allows for selection of genetic variants with unique and distinguishable colony morphology. Examples include rugose small-colony variants and wrinkly spreaders (WS), which over produce Psl/Pel or cellulose, respectively, and mucoid bacteria that over produce alginate. The well-documented emergence of these variants suggests that pseudomonads take advantage of matrix-building subpopulations conferring specific benefits for the entire population. This review will focus on various polysaccharides as well as additional *Pseudomonas* biofilm matrix components. Discussions will center on structure-function relationships, regulation, and the role of individual matrix molecules in niche biology

MARRAKCHI, SLAHEDDINE AND HOWARD I. MAIBACH, 2007. Biophysical parameters of skin: map of human face, regional, and age-related differences. *Contact Dermatitis* 2007: 57: 28–34

The face showed anatomical variation on reaction to chemicals, which could be related to differences in biophysical specificities of the skin. The aim of this study was to establish a map of the face for 6 biophysical parameters. 10 young human volunteers (24–34 years) and 10 old volunteers (66–83 years) were studied to prepare a map of the human face based on regional variations and age-related differences by measuring various biophysical parameters. 7 locations on the face, neck, and forearm were investigated. Skin blood flow, transepidermal water loss (TEWL), stratum corneum hydration (capacitance), temperature, pH, and sebum content of the skin surface were measured. In both groups, skin blood flow in the nose showed the highest value. Perioral and nasolabial areas showed the highest TEWL values. The neck showed the highest capacitance value. The highest skin temperature was detected in the neck in the young group and in the nasolabial area in the old group. The chin showed the most alkaline pH in both groups. Nasolabial area showed the highest sebum content in the young group, as did the chin in the old group. These baseline values provide a framework to build on for ascertaining disease and intervention-related effects.

Mason S, Cortes D, Horner WE. 2010. Detection of gaseous effluents and by-products of fungal growth that affect environments (RP-1243). *Hvac&R Research* 16(2):109-21

Musty odors, often associated with damp or water-damaged buildings, originate from the release of microbial volatile organic compounds (MVOCs) from mold growing on building materials and construction substrates. Chemical analysis of air samples is a feasible way to supplement conventional bioaerosol techniques during building investigations. Analytical methodologies for MVOCs are straightforward; however, development of a scientifically validated method to measure unique MVOCs that indicate with high confidence the presence of hidden mold regardless of the amount of mold present remains a challenge. Laboratory studies identified and quantified specific MVOCs associated with various mold species and MVOCs generated by specific molds growing on selected building materials in simulated, realistic conditions. This research determined that numerous MVOCs are released from active mold growth and are dependent on both the type of mold and the host substrate. MVOC profiles generated by 32 combinations of various molds and materials were determined, but only a few of these compounds demonstrated effectiveness in field/building studies. Certain mold-selective MVOCs were identified as potential indicators for specific mold, including methoxybenzene for *Stachybotrys chartarum* and benzothiazole and menthol for *Chaetomium globosum*. These studies provided a firm foundation for continued research of mold-specific MVOC markers as indicators of hidden mold and as predictors of potential mold sources in problem buildings

McBain, Andrew J., Robert G. Bartolo, Carl E. Catrenich, Duane Charbonneau, Ruth G. Ledder, Alexander H. Rickard, Sharon A. Symmons, and Peter Gilbert, 2003. Microbial Characterization of Biofilms in Domestic Drains and the Establishment of Stable Biofilm Microcosms. *Appl. Environ. Microbiol.* 2003, 69(1):177.

We have used heterotrophic plate counts, together with live-dead direct staining and denaturing gradient gel electrophoresis (DGGE), to characterize the eubacterial communities that had formed as biofilms within domestic sink drain outlets. Laboratory microcosms of these environments were established using excised biofilms from two separate drain biofilm samples to inoculate constant-depth film fermentors (CDFS). Drain biofilms harbored 9.8 to 11.3 log<sub>10</sub> cells of viable enteric species and pseudomonads/g, while CDFS-grown biofilms harbored 10.6 to 11.4 log<sub>10</sub> cells/g. Since live-dead direct staining revealed various efficiencies of recovery by culture, samples were analyzed by DGGE, utilizing primers specific for the V2-V3 region of eubacterial 16S rDNA. These analyses showed that the major PCR amplicons from in situ material were represented in the microcosms and maintained there over extended periods. Sequencing of amplicons resolved by DGGE revealed that the biofilms were dominated by a small number of genera, which were also isolated by culture. One drain sample harbored the protozoan *Colpoda maupasi*, together with rhabditid nematodes and bdelloid rotifers. The microcosm enables the maintenance of stable drain-type bacterial communities and represents a useful tool for the modeling of this ecosystem.

McBRIDE, MOLLIE E., W. CHRISTOPHER DUNCAN, AND J. M. KNOX, 1977. The Environment and the Microbial Ecology of Human Skin. *APPLIED AND ENVIRONMENTAL MICROBIOLOGY*, Mar. 1977, p. 603-608.

Microbial flora of the skin of three human population groups representing different natural environments was examined quantitatively and qualitatively to determine whether environmental differences in temperature and humidity can influence the microbial flora of normal skin. Five anatomical skin sites—hands, back, axillae, groin, and feet—were sampled from 10 subjects working in a high-humidity, high-temperature environment, 10 subjects from a low-temperature, high-humidity environment, and 10 subjects working in a moderate-temperature and low-humidity environment. Bacterial populations were significantly larger from the back, axillae, and feet in individuals from the high-temperature and high-humidity environment as compared to the moderate-temperature, low-humidity environment. High humidity and low temperature had no significant effect on total populations, but this group showed a higher frequency of isolation of fungi, and gram-negative bacteria from the back and feet. Although there was an indication that increase in the environmental humidity could result in an increased frequency of isolation of gram-negative bacteria, there was no evidence that an increase in either temperature or humidity altered the relative proportions of gram-negative bacteria in the predominantly gram-positive microbial flora found on normal skin. It was concluded that, although climatic changes may cause fluctuation in microbial populations from certain sites, they are not a major influence on the ecology of the microbial flora of normal skin in the natural environment. The variables introduced by studying individuals in their natural environment and the influence of these on the results are discussed.

McDevitt, James J., David L. MacIntosh and Theodore A. Myatt, 2008. Removal of influenza viral aerosols by high efficiency electrostatic air cleaner and implications for household infection transmission. *Indoor Air* 2008, 17-22 August 2008, Copenhagen, Denmark - Paper ID: 1063.

The objectives of this study were to evaluate the effectiveness of a high efficiency in-duct air cleaner at removing airborne influenza, and apply these results to a multi-zone IAQ model to evaluate the effectiveness of controlling household secondary infection transmission. For the removal efficiency tests, we aerosolized influenza and collected air samples upstream and downstream of the air cleaner. We measured a removal efficiency of greater than 99% using a reverse transcription quantitative polymerase chain reaction (RT-qPCR) assay. We used the model to estimate the airborne influenza concentration and a modified Wells-Riley equation to estimate the risk of infection. In a quarantine scenario, the risk of influenza infection was reduced 30-fold with the use of high efficiency filtration. This study demonstrates the utility of RT-qPCR assays for evaluating air cleaner viral removal efficiency and applies these results to demonstrate that a high efficiency in-duct air cleaner may modify the effectiveness of quarantine strategies.

McDevitt, James, Stephen Rudnick, Melvin First, and John Spengler, 2010. Role of Absolute Humidity in the Inactivation of Influenza Viruses on Stainless Steel Surfaces at Elevated Temperatures. *APPLIED AND ENVIRONMENTAL MICROBIOLOGY*, June 2010, Vol. 76, No. 12. p. 3943-3947

Influenza virus has been found to persist in the environment for hours to days, allowing for secondary transmission of influenza via inanimate objects known as fomites. We evaluated the efficacy of heat and moisture for the decontamination of surfaces for the purpose of preventing of the spread of influenza. Aqueous suspensions of influenza A virus were deposited onto stainless steel coupons, allowed to dry under ambient conditions, and exposed to temperatures of 55°C, 60°C, or 65°C and relative humidity (RH) of 25%, 50%, or 75% for up to 1 h. Quantitative virus assays were performed on the solution used to wash the viruses from these coupons, and results were compared with the solution used to wash coupons treated similarly but left under ambient conditions. Inactivation of influenza virus on surfaces increased with increasing temperature, RH, and exposure time. Reductions of greater than 5 logs of influenza virus on surfaces were achieved at temperatures of 60 and 65°C, exposure times of 30 and 60 min, and RH of 50 and 75%. Our data also suggest that absolute humidity is a better predictor of surface inactivation than RH and allows the prediction of survival using two parameters rather than three. Modest amounts of heat and adequate moisture can provide effective disinfection of surfaces while not harming surfaces, electrical systems, or mechanical components, leaving no harmful residues behind after treatment and requiring a relatively short amount of time.

McGinnis MR. 2007. Indoor mould development and dispersal. *Medical Mycology* 45(1):1-9.

Indoor mould development can occur following the accumulation of free water associated with a susceptible building material. Upon entry of viable fungal propagules from outdoors, the fungus becomes attached to a susceptible substrate. Vegetative growth begins if the appropriate environmental conditions exist, the primary ones being ample free water and a susceptible substrate that can provide the necessary nutrients for fungal growth. Extracellular fungal enzymes are released into the immediate environment surrounding the fungus from which nutrients are absorbed resulting in biodeterioration of building materials. As the fungal vegetative growth expands, fungal reproductive propagules such as conidia, ascospores, basidiospores, and viable hyphal units develop that are typically carried by air currents to new sites within the indoor environment. The indoor fungal ecologic niche is a complex ecosystem where different fungal species interact among themselves and with bacteria, insects, and mites.

Meadow, J. F., A. E. Altrichter, S. W. Kembel, J. Kline, G. Mhuireach, M. Moriyama, D. Northcutt, T. K. O'Connor, A. M. Womack, G. Z. Brown, J. L. Green and B. J. M. Bohannon, 2014. Indoor airborne bacterial communities are influenced by ventilation, occupancy, and outdoor air source. *Indoor Air* 2014; 24: 41–48

Architects and engineers are beginning to consider a new dimension of indoor air: the structure and composition of airborne microbial communities. A first step in this emerging field is to understand the forces that shape the diversity of bioaerosols across space and time within the built environment. In an effort to elucidate the relative influences of three likely drivers of indoor bioaerosol diversity – variation in outdoor bioaerosols, ventilation strategy, and occupancy load – we conducted an intensive temporal study of indoor airborne bacterial communities in a high-traffic university building with a hybrid HVAC (mechanically and naturally ventilated) system. Indoor air communities closely tracked outdoor air communities, but human-associated bacterial genera were more than twice as abundant in indoor air compared with outdoor air. Ventilation had a demonstrated effect on indoor airborne bacterial community composition; changes in outdoor air communities were detected inside following a time lag associated with differing ventilation strategies relevant to modern building design. Our results indicate that both occupancy patterns and ventilation strategies are important for understanding airborne microbial community dynamics in the built environment.

Meadow, James F., Adam E. Altrichter, Steven W. Kembel, Jeff Kline, Gwynne Mhuireach, Maxwell Moriyama, Dale Northcutt, Timothy K. O'Connor, Ann M. Womack, G. Z. Brown, Jessica L. Green, Brendan J. M. Bohannon, 2013. Indoor Airborne Bacterial Communities Are Influenced By Ventilation, Occupancy, and Outdoor Air Source. Accepted for Publication *Indoor Air*.

Architects and engineers are beginning to consider a new dimension of indoor air: the structure and composition of airborne microbial communities. A first step in this emerging field is to understand the forces that shape the diversity of bioaerosols across space and time within the built environment. In an effort to elucidate the relative influences of three likely drivers of indoor bioaerosol diversity – variation in outdoor bioaerosols, ventilation strategy, and occupancy load – we conducted an intensive temporal study of indoor airborne bacterial communities in a high-traffic university building with a hybrid HVAC (mechanically- and naturally-ventilated) system. Indoor air communities closely tracked outdoor air communities, but human-associated bacterial genera were more than twice as abundant in

indoor air compared to outdoor air. Ventilation had a demonstrated effect on indoor airborne bacterial community composition; changes in outdoor air communities were detected inside following a time lag associated with differing ventilation strategies relevant to modern building design. Our results indicate that both occupancy patterns and ventilation strategies are important for understanding airborne microbial community dynamics in the built environment.

Meadow, James F Meadow, Adam E Altrichter, Steven W Kembel, Maxwell Moriyama, Timothy K O'Connor, Ann M Womack, G Z Brown, Jessica L Green and Brendan J M Bohannon, 2014. Bacterial communities on classroom surfaces vary with human contact. *Microbiome* 2014, 2:7

Background: Humans can spend the majority of their time indoors, but little is known about the interactions between the human and built-environment microbiomes or the forces that drive microbial community assembly in the built environment. We sampled 16S rRNA genes from four different surface types throughout a university classroom to determine whether bacterial assemblages on each surface were best predicted by routine human interactions or by proximity to other surfaces within the classroom. We then analyzed our data with publicly-available datasets representing potential source environments. Results: Bacterial assemblages from the four surface types, as well as individual taxa, were indicative of different source pools related to the type of human contact each surface routinely encounters. Spatial proximity to other surfaces in the classroom did not predict community composition. Conclusions: Our results indicate that human-associated microbial communities can be transferred to indoor surfaces following contact, and that such transmission is possible even when contact is indirect, but that proximity to other surfaces in the classroom does not influence community composition.

Medina-Ramón, Mercedes, Antonella Zanobetti, and Joel Schwartz, 2006. The Effect of Ozone and PM10 on Hospital Admissions for Pneumonia and Chronic Obstructive Pulmonary Disease: A National Multicity Study. *American Journal of Epidemiology* Vol. 163, No. 6, pp. 579-588

A case-crossover study was conducted in 36 US cities to evaluate the effect of ozone and particulate matter with an aerodynamic diameter of  $\leq 10 \mu\text{m}$  (PM10) on respiratory hospital admissions and to identify which city characteristics may explain the heterogeneity in risk estimates. Respiratory hospital admissions and air pollution data were obtained for 1986-1999. In a meta-analysis based on the city-specific regression models, several city characteristics were evaluated as effect modifiers. During the warm season, the 2-day cumulative effect of a 5-ppb increase in ozone was a 0.27% (95% confidence interval (CI): 0.08, 0.47) increase in chronic obstructive pulmonary disease admissions and a 0.41% (95% CI: 0.26, 0.57) increase in pneumonia admissions. Similarly, a 10- $\mu\text{g}/\text{m}^3$  increase in PM10 during the warm season resulted in a 1.47% (95% CI: 0.93, 2.01) increase in chronic obstructive pulmonary disease at lag 1 and a 0.84% (95% CI: 0.50, 1.19) increase in pneumonia at lag 0. Percentage of households with central air conditioning reduced the effect of air pollution, and variability of summer apparent temperature reduced the effect of ozone on chronic obstructive pulmonary disease. The study confirmed, in a large sample of cities, that exposure to ozone and PM10 is associated with respiratory hospital admissions and provided evidence that the effect of air pollution is modified by certain city characteristics.

Meheust, Delphine, Jean-Pierre Gangneux, Tiina Reponen, Larry Wymer, Stephen Vesper, Pierre Le Cann, 2012. Correlation between Environmental Relative Moldiness Index (ERMI) values in French dwellings and other measures of fungal contamination. *Science of the Total Environment* 438 (2012) 319–324

The Environmental Relative Moldiness Index (ERMI) is a DNA-based metric developed to describe the fungal contamination in US dwellings. Our goal was to determine if the ERMI values in dwellings in north western France were correlated with other measures of fungal contamination. Dust and air samples were obtained from 40 dwellings and analyzed by quantitative PCR and/or by culturing. These dwellings were also inspected and the amount of visible fungal growth estimated in  $\text{m}^2$ . The ERMI values in these dwellings ranged from  $-2.7$  to  $28.8$  and the fungal contamination estimates ranged from 0 to  $20 \text{m}^2$ . The 40 dwellings were divided into those with a low ( $<6$ ) or high ( $>8$ ) ERMI values ( $n=20$  in each). The average ERMI value was  $15.70$  for the high ERMI compared to  $2.68$  for the low ERMI dwellings. ERMI values were correlated (significant Kendall's tau values) with concentrations of fungi in air samples analyzed by QPCR or culturing. ERMI values were also correlated (significant Kendall's tau values) with the visible estimates of fungal contamination. Older dwellings were more likely to have higher ERMI values. These results suggest that the ERMI dust sample, which is quick and easy to collect, may be useful in making decisions about reducing fungal exposures in homes.



Memarzadeh, Farhad, 2011. Literature Review of the Effect of Temperature and Humidity on Viruses. ASHRAE Trans, Volume 117. Part 2, ML-11-024.

An extensive literature review of more than 120 papers was conducted on the effect of humidity and temperature on the transmission of infectious viruses. This review targets influenza viruses to be transmitted through the air as well as direct and indirect contact. Evidence is cited from both direct and indirect study results examining environmental conditions that affect infectious disease aerosol transmission in enclosed environments. These results will have a major influence on the choice of infection control measures in indoor environments as well as an associated cost for equipment and renovations to the ventilation system or room design.

Mendell, Mark J., Anna G. Mirer, Kerry Cheung, My Tong, and Jeroen Douwes, 2011. Respiratory and Allergic Health Effects of Dampness, Mold, and Dampness-Related Agents: A Review of the Epidemiologic Evidence. *ehponline.org* doi: 10.1289/ehp.1002410 (available at <http://dx.doi.org/>)

**Objectives** - Many studies have shown consistent associations between evident indoor dampness or mold and respiratory or allergic health effects, but causal links remain unclear. Findings on measured microbiologic factors have received little review. We conducted an updated, comprehensive review on these topics. **Data Sources** - We reviewed eligible peer-reviewed epidemiologic studies or quantitative meta-analyses, up to late 2009, on dampness, mold, or other microbiologic agents and respiratory or allergic effects. **Data Extraction** - We evaluated evidence for causation or association between qualitative/subjective assessments of dampness or mold (considered together) and specific health outcomes. We separately considered evidence for associations between specific quantitative measurements of microbiologic factors and each health outcome. **Data Synthesis** - Evidence from epidemiologic studies and meta-analyses showed indoor dampness or mold to be associated consistently with increased asthma development and exacerbation, current and ever diagnosis of asthma, dyspnea, wheeze, cough, respiratory infections, bronchitis, allergic rhinitis, eczema, and upper respiratory tract symptoms. Associations were found in allergic and nonallergic individuals. Evidence strongly suggested causation of asthma exacerbation in children. Suggestive evidence was available for few specific measured microbiologic factors and was in part equivocal, suggesting both adverse and protective associations with health. **Conclusions** - Evident dampness or mold had consistent positive associations with multiple allergic and respiratory effects. Measured microbiologic agents in dust had limited suggestive associations, including both positive and negative associations for some agents. Thus, while prevention and remediation of indoor dampness and mold are likely to reduce health risks, current evidence does not support measuring specific indoor microbiologic factors to guide health-protective actions.

Menetrez, F. M. Y., Foarde, K. K., Dean, T. R., Betancourt, D. A. 2010. The effectiveness of UV irradiation on vegetative bacteria and fungi surface contamination. *Chemical Engineering Journal*, Vol. 157, No. 2-3. (01 March 2010), pp. 443-450.

Ultraviolet irradiation has been used in the indoor environment to eliminate or control infectious diseases in medical care facilities. Heating, ventilating, and air-conditioning (HVAC) system components such as duct-liners, cooling coils, drip pans, interior insulation and areas subjected to high levels of moisture can create an environment which is prone to biological contamination on surfaces. The movement of indoor air being dominated by HVAC system operation can carry biological contaminants which can expose large numbers of building occupants to bioaerosols. The use of germicidal ultraviolet lamps (UVGI) in commercial and residential HVAC systems has increased. UVGI treatment has focused on HVAC component internal surfaces and airflow. A method to determine the antimicrobial efficacy of UVGI irradiation was developed and tested on the surface of agar plates with four species of vegetative bacteria and seven species of fungi. The percent kill and the kinetics of the rate of killing,  $k$  value, were calculated for each organism.

Mentese, Sibel, Munevver Arisoy, Abbas Yousefi Rad, and Gulen Gullu, 2009. Bacteria and Fungi Levels in Various Indoor and Outdoor Environments in Ankara, Turkey. *Clean* 2009, 37 (6), 487 - 493.

In this study, different types of indoor environments (primary school, kindergarten, cafeteria, restaurant, dormitory, dwelling, office, sport salon, library, classroom, and laboratory) and their outdoor environments were investigated in terms of bioaerosol contamination. A total of 120 environments were investigated in Ankara, Turkey. The single-stage Andersen sampler was used for viable bioaerosol sampling. During the sampling, indoor and outdoor

temperature, relative humidity, and CO<sub>2</sub> concentration were measured. Total bacteria counts (TBC) and fungi concentrations varied on a large scale within and between the sampling site groups (10-103 CFU/m<sup>3</sup>). The highest TBC levels were measured in kindergartens, primary schools, restaurants, high schools, and homes, while the highest mold levels were measured in kitchens, bathrooms, and offices. *Micrococcus* spp., *Staphylococcus auricularis*, and *Bacillus* spp. were predominant bacteria species and *Penicillium* spp., *Aspergillus* spp., and *Cladosporium* spp. were the most observed mold genera detected in the samples. Indoor-to-outdoor (I/O) ratios of the observed fungi counts were calculated as approximately around 1, and for bacteria counts these ratios were higher than 1. There was no statistical difference between indoor and outdoor mold levels, while a significant difference was found between indoor and outdoor bacteria levels ( $p < 0.001$ ). A significant correlation between indoor CO<sub>2</sub> and bioaerosols indicates insufficient ventilation.

MILLER, J. DAVID, PHILIP D. HAISLEY AND JAMES H. REINHARDT. 2000. Air Sampling Results in Relation to Extent of Fungal Colonization of Building Materials in Some Water-Damaged Buildings. *Indoor Air* 2000; 10: 146–151

We studied the extent and nature of fungal colonization of building materials in 58 naturally ventilated apartments that had suffered various kinds of water damage in relation to air sampling done before the physical inspections. The results of air samples from each apartment were compared by rank order of species with pooled data from outdoor air. Approximately 90% of the apartments that had significant amounts of fungi in wall cavities were identified by air sampling. There was no difference in the average fungal colony forming unit values per m<sup>3</sup> between the 15 apartments with the most fungal contamination and the 15 with the least. In contrast, the prevalence of samples with fungal species significantly different than the pooled outdoor air between the more contaminated versus the less contaminated apartments was approximately 10-fold. We provide information on methods to document fungal contamination in buildings.

Monds, Russell D., O'Toole, George A. 2009. The developmental model of microbial biofilms: ten years of a paradigm up for review *Trends In Microbiology* 17:2, pp 73-87

For the past ten years, the developmental model of microbial biofilm formation has served as the major conceptual framework for biofilm research; however, the paradigmatic value of this model has begun to be challenged by the research community. Here, we critically evaluate recent data to determine whether biofilm formation satisfies the criteria requisite of a developmental system. We contend that the developmental model of biofilm formation must be approached as a model in need of further validation, rather than utilized as a platform on which to base empirical research and scientific inference. With this in mind, we explore the experimental approaches required to further our understanding of the biofilm phenotype, highlighting evolutionary and ecological approaches as a natural complement to rigorous mechanistic studies into the causal basis of biofilm formation. Finally, we discuss a second model of biofilm formation that serves as a counterpoint to our discussion of the developmental model. Our hope is that this article will provide a platform for discussion about the conceptual underpinnings of biofilm formation and the impact of such frameworks on shaping the questions we ask, and the answers we uncover, during our research into these microbial communities.

Monto, Arnold, S., 2002. The Seasonality of Rhinovirus Infections and Its Implications for Clinical Recognition. *CLINICAL THERAPEUTICS*, VOL. 24, NO. 12, 1987-1997

Background: Rhinoviruses are the most common cause of acute respiratory infections. Isolation of rhinoviruses occurs in a distinct and consistent seasonal pattern that can be used to help determine whether an acute respiratory illness is caused by a rhinovirus. Objective: This article reviews information on the seasonality of rhinovirus infection derived from early and recent studies of rhinovirus occurrence and treatment. Methods: PubMed was searched from 1965 to the present to identify all potentially relevant papers. The search terms used were rhinovirus and seasonality. A total of 1998 papers were screened. Results: Rhinoviruses comprise more than three quarters of viruses circulating in early autumn. In some years and perhaps some geographic areas, spring is an even more important time for rhinovirus transmission. Although overall rates of respiratory illness are lower in summer, rhinoviruses are the most frequently isolated virus at this time of year. Other viral agents, including influenza viruses and respiratory syncytial virus (particularly with parainfluenza virus), predominate in the winter. Thus, for most of the year, rhinoviruses are the cause of the majority of acute viral respiratory infections. Conclusion: Understanding the seasonal incidence of rhinovirus

infection may help determine how best to employ currently available antirhinoviral agents in patients presenting with symptoms of an acute viral respiratory infection.

Moon HJ and Yoon YR. 2010. Investigation of physical characteristics of houses and occupants' behavioural factors for mould infestation in residential buildings. *Indoor Built Environ* 19(1):57-64.

Mould growth can deteriorate indoor air quality in buildings. To alleviate problems in the built environment, accurate understanding of the risk factors associated for mould infestation is required. This study aimed at identifying the key risk factors that could affect mould growth on interior surfaces in residential buildings in Korea. Both the physical characteristics of buildings and the behaviour of occupants were recognised as key concerns. A questionnaire survey had been conducted randomly on a national basis for this research. The questionnaire included building-related factors, and occupants' activities and behaviour. A total of 314 completed questionnaires were collected and processed for statistical analysis. The association of mould growth with locations and types (apartments, multiplex houses, and detached houses) of the residential buildings were tested. The relationships between mould growth and activity factors, for example, bathing, washing clothes, and opening windows were also considered. Apartments were shown to be more vulnerable to mould growth in comparison to other types of residential buildings. The results were compared with findings from other regions in the world to further understand the effects of these key factors.

Moon, Hyeun Jun, Kyeong Min Kim, Seung Ho Ryu, 2012. The effect of hygric properties of porous mineral based wallpapers on mould germination and growth. *Proceedings of Healthy Buildings 2012, Brisbane, Queensland, Australia*

The hygrothermal properties of building materials are related to condensation phenomena and biological contaminants such as fungi infestations, especially in building environments. The purpose of this study was to discover the relationships between adsorption/desorption content and mould germination/growth on wallpapers made of porous mineral materials. An experiment study was conducted to characterize the adsorption /desorption content of six wallpapers made of porous mineral materials, PVC, acrylic resin and corn starch. The specimens of wallpapers were inoculated with fungi. The correlation between adsorption/desorption content and mould germination/growth was analyzed. The wallpapers with high adsorption/desorption content retarded mould germination and growth.

Morawska, L., 2006. Droplet fate in indoor environments, or can we prevent the spread of infection? *Indoor Air* 2006; 16: 335-347

When considering how people are infected and what can be done to prevent the infections, answers from many disciplines are sought: microbiology, epidemiology, medicine, engineering, and physics. There are many pathways to infection spread, and among the most significant from the epidemiological point of view is airborne transport. Microorganisms can become airborne when droplets are generated during speech, coughing, sneezing, vomiting, or atomization of feces during sewage removal. The fate of the droplets is governed by the physical principles of transport, with droplet size being the most important factor affecting their dispersion, deposition on surfaces and determining the survival of microorganisms within the droplets. In addition, physical characteristics of the indoor environment as well as the design and operation of building ventilation systems are of critical importance. Do we understand the mechanisms of infection spread and can we quantify the droplet dynamics under various indoor conditions? Unfortunately no, as this aspect of infection spread has attracted surprisingly little scientific interest. However, investigations of numerous cases in which a large number of people were infected show how critical the physics of microorganism spread can be. This paper reviews the state of knowledge regarding mechanisms of droplet spread and solutions available to minimize the spread and prevent infections.

Moritz, Miriam M., Hans-Curt Flemming, Jost Wingender, 2010. Integration of *Pseudomonas aeruginosa* and *Legionella pneumophila* in drinking water biofilms grown on domestic plumbing materials. *International Journal of Hygiene and Environmental Health* 213 (2010) 190-197.

Drinking water biofilms were grown on coupons of plumbing materials, including ethylene-propylenediene-monomer (EPDM) rubber, silane cross-linked polyethylene (PE-X b), electron-ray cross-linked PE (PE-X c) and copper under constant flow-through of cold tap water. After 14 days, the biofilms were spiked with *Pseudomonas aeruginosa*, *Legionella pneumophila* and *Enterobacter nimipressuralis* (10<sup>6</sup> cells/mL each). The test bacteria were environmental

isolates from contamination events in drinking water systems. After static incubation for 24 h, water flow was resumed and continued for 4 weeks. Total cell count and heterotrophic plate count (HPC) of biofilms were monitored, and *P. aeruginosa*, *L. pneumophila* and *E. nimipressuralis* were quantified, using standard culture-based methods or culture-independent fluorescence in situ hybridization (FISH). After 14 days total cell counts and HPC values were highest on EPDM followed by the plastic materials and copper. *P. aeruginosa* and *L. pneumophila* became incorporated into drinking water biofilms and were capable to persist in biofilms on EPDM and PE-X materials for several weeks, while copper biofilms were colonized only by *L. pneumophila* in low culturable numbers. *E. nimipressuralis* was not detected in any of the biofilms. Application of the FISH method often yielded orders of magnitude higher levels of *P. aeruginosa* and *L. pneumophila* than culture methods. These observations indicate that drinking water biofilms grown under cold water conditions on domestic plumbing materials, especially EPDM and PE-X in the present study, can be a reservoir for *P. aeruginosa* and *L. pneumophila* that persist in these habitats mostly in a viable but non-culturable state

Moschandreas, DJ, Pagilla, KR, Storino, LV, 2003. Time and space uniformity of indoor bacteria concentrations in Chicago area residences. *AEROSOL SCIENCE AND TECHNOLOGY*, 37: 899-906.

The objective of this article is to assess spatial and temporal variation of indoor gram-positive bacteria and *Staphylococcus* sp. in 20 urban residences. At each residence, air was sampled at one outdoor site and four indoor sites (rooms) to assess spatial variation and once each season for five consecutive seasons to assess temporal variation. All temporal and spatial comparisons were performed using data obtained by the Andersen sampling technique. A secondary objective of this study is to evaluate relationships among several sampling methods used to measure bacteria levels; since differences in the measured concentrations are expected, the focus is to discern if corresponding measurements relate to each other. Not surprisingly, comparisons among the four sampling systems revealed statistically significant differences, although levels correlated relatively well. Using data only from the Andersen samplers, we conclude that seasonal variation is residence dependent with typically higher summer levels, but a clear pattern of variation could not be established. Room-to-room difference is not statistically significant, but the basement levels render the basement a distinct microenvironment. Indoor concentrations exceeded corresponding outdoor concentrations 75% of the time. *Staphylococcus* accounts for approximately 27% of the average indoor bacteria levels. The highest levels of gram-positive bacteria are found in the kitchen. The presence of multiple indoor sources with variable emission rates in multiple indoor locations results in bacteria levels that vary with time and space

Moularat Stéphane, Marion Hulin, Enric Robine, Isabella Annesi-Maesano, Denis Caillaud, 2011. Airborne fungal volatile organic compounds in rural and urban dwellings Detection of mould contamination in 94 homes determined by visual inspection and airborne fungal volatile organic compounds method. *Science of the Total Environment*. 409. 2005-2009

Moulds can both degrade the materials and structures they colonise and contribute to the appearance of symptoms and diseases in the inhabitants of contaminated dwellings. Only few data have compared the levels of contamination in urban and rural environments and the results are not consistent. The aim of this study was to use a fungal contamination index, based on the detection of specific Microbial Volatile Organic Compounds (MVOC), to determine the exposure to moulds of individuals living in urban and rural dwellings. For this purpose, 94 dwellings (47 in an urban setting in Clermont-Ferrand and 47 in rural areas of the Auvergne region, France) were studied. By demonstrating marked disparities between the proportion of visible contamination (19%) and that of active, visible and/or hidden contamination (59%) and the fact that almost all visible contamination was identified by MVOC, we were able to show that use of the index seemed relevant to confirm the actual presence of fungal contamination in a dwelling. Furthermore, it was possible to demonstrate a relationship between moulds and the presence of water on surfaces (condensation, infiltrations, water damage, etc.). A higher proportion of positive fungal contamination index in rural homes was observed compared to the proportion in urban ones (68% versus 49%;  $p < 0.05$ ).

Mourtzoukou EG and Falagas ME. 2007. Exposure to cold and respiratory tract infections. *International Journal of Tuberculosis and Lung Disease* 11(9):938-43.

There is a constant increase in hospitalizations and mortality during winter months; cardiovascular diseases as well as respiratory infections are responsible for a large proportion of this added morbidity and mortality. Exposure to cold has often been associated with increased incidence and severity of respiratory tract infections. The data available suggest that exposure to cold, either through exposure to low environmental temperatures or during induced

hypothermia, increases the risk of developing upper and lower respiratory tract infections and dying from them; in addition, the longer the duration of exposure the higher the risk of infection. Although not all studies agree, most of the available evidence from laboratory and clinical studies suggests that inhaled cold air, cooling of the body surface and cold stress induced by lowering the core body temperature cause pathophysiological responses such as vasoconstriction in the respiratory tract mucosa and suppression of immune responses, which are responsible for increased susceptibility to infections. The general public and public health authorities should therefore keep this in mind and take appropriate measures to prevent increases in morbidity and mortality during winter due to respiratory infections

Muise, Brad, Dong-Chul Seo, E. Earl Blair and Trent Applegate, 2010. Mold spore penetration through wall service outlets: a pilot study. *Environ Monit Assess* (2010) 163:95-104 DOI 10.1007/s10661-009-0819-7

A pilot study was conducted to estimate fungal spore penetration for wall service outlets subjected to a constant air pressure. During the laboratory experiment, a wall chamber was fabricated, and telephone, electrical, and cable service outlets were installed. *Penicillium chrysogenum* spores were aerosolized into the chamber that was held under pressure. Spores that penetrated the outlets were funneled into an impinger for microscopic enumeration. Thirty trials were conducted for each of the five outlets (N = 150), and the wall chamber was decontaminated between trials. Results of an analysis of variance suggest wall service outlets allow spore penetration. The penetration factor for the telephone outlet was significantly greater than all other outlets ( $p < 0.05$ ), and there was no difference in penetration between electrical outlets with and without plugs. Penetration factor differences were attributed to air leakage rates across the outlets. Due to the experimental design and equipment limitations, further research is needed to support these findings.

Murphy, Courtney R., Samantha J. Eells, Victor Quan, Diane Kim, Ellena Peterson, Loren G. Miller, and Susan S. Huang, 2012. Methicillin-Resistant *Staphylococcus aureus* Burden in Nursing Homes Associated with Environmental Contamination of Common Areas. *J Am Geriatr Soc MRSA*, June, Vol. 60, No. 6, pp. 1012-1018

Objectives To determine whether environmental cleaning and contamination are associated with variation in the prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA) between nursing homes. Design Prospective study of environmental contamination and cleaning quality. Setting Nursing home. Participants Ten California nursing homes. Measurements Nursing homes were categorized into two groups based upon high and low differences in MRSA point prevalence and admission prevalence (delta prevalence) from nares screenings of nursing home residents. Environmental cleaning and infection control practices were evaluated by culturing common area objects for MRSA, assessing removal of intentionally applied marks visible only under ultraviolet (UV) light, and administering surveys on infection control and cleaning. Results Overall, 16% (78/500) of objects were MRSA positive, and 22% (129/577) of UV-visible marks were removed. A higher proportion of MRSA-positive objects was found in the high (19%) than in low (10%) nursing home groups ( $P = .005$ ). Infection control and cleaning policies varied, including the frequency of common room cleaning (median 2.5 times daily, range 1-3 times daily) and time spent cleaning per room (median 18 minutes, range 7- 45 minutes). In multivariate models, MRSA-positive objects were associated with high delta prevalence nursing homes (odds ratio (OR) = 2.8,  $P = .005$ ), less time spent cleaning each room (OR = 2.9,  $P < .001$ ), and less-frequent cleaning of common rooms (OR=1.5,  $P = .01$ ). Conclusion Substantial variation was found in MRSA environmental contamination, infection control practices, and cleaning quality. MRSA environmental contamination was associated with greater differences between MRSA point and admission prevalence, less-frequent common room cleaning, and less time spent cleaning per room, which suggests that modifying cleaning practices may reduce MRSA environmental contamination and burden in nursing homes.

Murtoniemi, T. ,M.-R. Hirvonen, A. Nevalainen, M. Suutari, 2003. The relation between growth of four microbes on six different plasterboards and biological activity of spores. *Indoor Air* 2003; 13: 65-73

Microbial growth on water-damaged building materials is commonly associated with adverse health effects in the occupants. We examined the growth of *Stachybotrys chartarum*, *Aspergillus versicolor*, *Penicillium spinulosum*, and *Streptomyces californicus*, isolated from water-damaged buildings, on six different brands of plasterboards. The microbial growth was compared with the biological activity of the spores, that is the potential to induce cytotoxicity and proinflammatory mediators in RAW264.7 macrophages. These results showed that the microbial growth on plasterboard depended on both the microbial strain and the brand of plasterboard used. The biological activity of spores appeared to

be regulated by different growth conditions on plasterboards so that good microbial growth was associated with a low bioactivity of the spores, whereas the spores collected from plasterboard supporting only weak growth usually were biologically active. Cytotoxicity of either *S. chartarum* or *A. versicolor* did not correlate with any particular growth conditions or induced inflammatory responses. Instead, there were positive correlations between cytotoxicity and levels of induced proinflammatory cytokines for *P. spinulosum* and *S. californicus*. These data suggest that both the microbial growth on plasterboard and the resulting bioactivity of spores vary and might be affected by changing the growth conditions provided by the plasterboards.

Myatt, Theodore A., Sebastian L. Johnston, Zhengfa Zuo, Matthew Wand, Tatiana Kebabdz, Stephen Rudnick and Donald K. Milton, 2004. Detection of Airborne Rhinovirus and Its Relation to Outdoor Air Supply in Office Environments. *Am J Respir Crit Care Med* Vol 169. pp 1187-1190.

Rhinoviruses are major causes of morbidity in patients with respiratory diseases; however, their modes of transmission are controversial. We investigated detection of airborne rhinovirus in office environments by polymerase chain reaction technology and related detection to outdoor air supply rates. We sampled air from 9 A.M. to 5 P.M. each workday, with each sample run for 1 work week. We directly extracted RNA from the filters for nested reverse transcriptase- polymerase chain reaction analysis of rhinovirus. Nasal lavage samples from building occupants with upper respiratory infections were also collected. Indoor carbon dioxide (CO<sub>2</sub>) concentrations were recorded every 10 minutes as a surrogate for outdoor air supply. To increase the range of CO<sub>2</sub> concentrations, we adjusted the outdoor air supply rates every 3 months. Generalized additive models demonstrated an association between the probability of detecting airborne rhinovirus and a weekly average CO<sub>2</sub> concentration greater than approximately 100 ppm, after controlling for covariates. In addition, one rhinovirus from a nasal lavage contained an identical nucleic acid sequence similar to that in the building air collected during the same week. These results suggest that occupants in buildings with low outdoor air supply may have an increased risk of exposure to infectious droplet nuclei emanating from a fellow building occupant.

Myatt, Theodore A, Matthew H Kaufman, Joseph G Allen, David L MacIntosh, M Patricia Fabian, James J McDevitt, 2010. Modeling the airborne survival of influenza virus in a residential setting: the impacts of home humidification. *Environmental Health* 2010, 9:55.

Background: Laboratory research studies indicate that aerosolized influenza viruses survive for longer periods at low relative humidity (RH) conditions. Further analysis has shown that absolute humidity (AH) may be an improved predictor of virus survival in the environment. Maintaining airborne moisture levels that reduce survival of the virus in the air and on surfaces could be another tool for managing public health risks of influenza. Methods: A multi-zone indoor air quality model was used to evaluate the ability of portable humidifiers to control moisture content of the air and the potential related benefit of decreasing survival of influenza viruses in single family residences. We modeled indoor AH and influenza virus concentrations during winter months (Northeast US) using the CONTAM multi-zone indoor air quality model. A two-story residential template was used under two different ventilation conditions - forced hot air and radiant heating. Humidity was evaluated on a room-specific and whole house basis. Estimates of emission rates for influenza virus were particle-size specific and derived from published studies and included emissions during both tidal breathing and coughing events. The survival of the influenza virus was determined based on the established relationship between AH and virus survival. Results: The presence of a portable humidifier with an output of 0.16 kg water per hour in the bedroom resulted in an increase in median sleeping hours AH/RH levels of 11 to 19% compared to periods without a humidifier present. The associated percent decrease in influenza virus survival was 17.5 - 31.6%. Distribution of water vapor through a residence was estimated to yield 3 to 12% increases in AH/RH and 7.8-13.9% reductions in influenza virus survival. Conclusion: This modeling analysis demonstrates the potential benefit of portable residential humidifiers in reducing the survival of aerosolized influenza virus by controlling humidity indoors.

Naftali S, Rosenfeld M, Wolf M, Elad D. 2005. The air-conditioning capacity of the human nose. *Ann Biomed Eng* 33(4):545-53.

The nose is the front line defender of the respiratory system. Unsteady simulations in three-dimensional models have been developed to study transport patterns in the human nose and its overall air-conditioning capacity. The results suggested that the healthy nose can efficiently provide about 90% of the heat and the water fluxes required to condition

the ambient inspired air to near alveolar conditions in a variety of environmental conditions and independent of variations in internal structural components. The anatomical replica of the human nose showed the best performance and was able to provide 92% of the heating and 96% of the moisture needed to condition the inspired air to alveolar conditions. A detailed analysis explored the relative contribution of endonasal structural components to the air-conditioning process. During a moderate breathing effort, about 11% reduction in the efficacy of nasal air-conditioning capacity was observed.

Nardell, E. and A. Dharmadhikari, 2010. Turning off the spigot: reducing drug-resistant tuberculosis transmission in resource-limited settings. *INT J TUBERC LUNG DIS* 14(10):1233-1243

Ongoing transmission and re-infection, primarily in congregate settings, is a key factor fueling the global multidrug-resistant/extensively drug-resistant tuberculosis (MDR/XDR-TB) epidemic, especially in association with the human immunodeficiency virus. Even as efforts to broadly implement conventional TB transmission control measures begin, current strategies may be incompletely effective under the overcrowded conditions extant in high-burden, resource-limited settings. Longstanding evidence suggesting that TB patients on effective therapy rapidly become non-infectious and that unsuspected, untreated TB cases account for the most transmission makes a strong case for the implementation of rapid point-of care diagnostics coupled with fully supervised effective treatment. Among the most important decisions affecting transmission, the choice of an MDR-TB treatment model that includes community-based treatment may offer important advantages over hospital or clinic-based care, not only in cost and effectiveness, but also in transmission control. In the community, too, rapid identification of infectious cases, especially drug-resistant cases, followed by effective, fully supervised treatment, is critical to stopping transmission. Among the conventional interventions available, we present a simple triage and separation strategy, point out that separation is intimately linked to the design and engineering of clinical space and call attention to the pros and cons of natural ventilation, simple mechanical ventilation systems, germicidal ultraviolet air disinfection, fit-tested respirators on health care workers and short-term use of masks on patients before treatment is initiated.

Nasir, Zaheer Ahmad & Ian Colbeck, 2010. Assessment of Bacterial and Fungal Aerosol in Different Residential Settings. *Water Air Soil Pollut* (2010) 211:367-377

The concentration and size distribution of bacterial and fungal aerosol was studied in 15 houses. The houses were categorized into three types, based on occupant density and number of rooms: single room in shared accommodation (type I), single bedroom flat in three storey buildings (type II) and two or three bedroomed houses (type III). Sampling was undertaken with an Anderson six-stage impactor during the summer of 2007 in the living rooms of all the residential settings. The maximum mean geometric concentration of bacterial (5,036 CFU/m<sup>3</sup>,  $\pm$  2.5, n=5) and fungal (2,124 CFU/m<sup>3</sup>,  $\pm$  1.38, n=5) aerosol were in housing type III. The minimum levels of indoor culturable bacteria (1,557 CFU/m<sup>3</sup>,  $\pm$ 1.5, n=5) and fungal (925 CFU/m<sup>3</sup>,  $\pm$ 2.9, n=5) spores were observed in housing type I. The differences in terms of total bacterial and fungal concentration were less obvious between housing types I and II as compared to type III. With reference to size distribution, the dominant stages for culturable bacteria in housing types I, II and III were stage 3 (3.3-4.7  $\mu$ m), stage 1 (7  $\mu$ m and above) and stage 5 (1.1-2.1  $\mu$ m), respectively. Whereas the maximum numbers of culturable fungal spores were recovered from stage 2 (4.7-7  $\mu$ m), in housing type I, and from stage 4 (2.1- 3.3  $\mu$ m) in both type II and III houses. The average geometric mean diameter of bacterial aerosol was largest in type I (4.7  $\mu$ m), followed by type II (3.89  $\mu$ m) and III (1.96  $\mu$ m). Similarly, for fungal spores, type I houses had the highest average mean geometric diameter (4.5  $\mu$ m), while in types II and III the mean geometric diameter was 3.57 and 3.92  $\mu$ m, respectively. The results indicate a wide variation in total concentration and size of bioaerosols among different residential settings. The observed differences in the size distributions and concentrations reflect their variable airborne behaviour and, as a result, different risks of respiratory exposure of the occupants to bioaerosols in various residential settings.

Nesti, Maria M. M. and Moisés Goldbaum, 2007. Infectious diseases and daycare and preschool education. *J Pediatr (Rio J)*. 2007;83(4):299-312

Objective: To describe the increased risk of acquiring infectious diseases associated with out-of-home childcare and the effectiveness of measures for the control and prevention of diseases transmission at daycare and preschool education centers. Sources: A review of literature in the MEDLINE, LILACS and Cochrane Library databases, found using the descriptors daycare, infection, infection control and infectious diseases and focusing on studies that have compared

the risk of infectious diseases for children cared for in and out of the home, related risk to the type of out-of-home care and assessed the effectiveness of preventative measures. Summary of the findings: Children cared for at daycare or in preschool education exhibit a two to three times greater risk of acquiring infections, which impacts both on individual health and on the dissemination of diseases through the community. Among other factors, the risk is associated with the characteristics of daycare centers, and simple preventative measures are effective for reducing transmission of diseases. Recommended measures include: appropriate hand washing after exposure; employment of standard precautions; standardized routines for changing and disposal of used diapers, location and cleanliness of changing area, cleaning and disinfection of contaminated areas; use of disposable tissues for blowing noses; separate workers and area for handling foods; notification of infectious diseases; training of workers and guidance for parents. Conclusions: In the face of growing utilization of daycare and preschool education and their association with increased risk of acquired infections, control measures are indispensable to the prevention and control of infectious diseases.

Nicas, Mark and Alan Hubbard, 2002. A Risk Analysis for Airborne Pathogens with Low Infectious Doses: Application to Respirator Selection Against *Coccidioides immitis* Spores. *Risk Analysis*, Vol. 22:6, pp. 1153-1163.

Probability models incorporating a deterministic versus stochastic infectious dose are described for estimating infection risk due to airborne pathogens that infect at low doses. Such pathogens can be occupational hazards or candidate agents for bioterrorism. Inputs include parameters for the infectious dose model, distribution parameters for ambient pathogen concentrations, the breathing rate, the duration of an exposure period, the anticipated number of exposure periods, and, if a respirator device is used, distribution parameters for respirator penetration values. Application of the models is illustrated with a hypothetical scenario involving exposure to *Coccidioides immitis*, a fungus present in soil in areas of the southwestern United States. Inhaling *C. immitis* spores causes a respiratory tract infection and is a recognized occupational hazard in jobs involving soil dust exposure in endemic areas. An uncertainty analysis is applied to risk estimation in the context of selecting respiratory protection with a desired degree of efficacy.

Nicas, Mark, Nazaroff and Hubbard, 2005, Toward Understanding the Risk of Secondary Airborne Infection: Emission of Respirable Pathogens. *Journal of Occupational and Environmental Hygiene*, 2: 143-154.

Certain respiratory tract infections are transmitted through air. Coughing and sneezing by an infected person can emit pathogen-containing particles with diameters less than 10  $\mu\text{m}$  that can reach the alveolar region. Based on our analysis of the sparse literature on respiratory aerosols, we estimated that emitted particles quickly decrease in diameter due to water loss to one-half the initial values, and that in one cough the volume in particles with initial diameters less than 20  $\mu\text{m}$  is  $6 \times 10^{-8}$  mL. The pathogen emission rate from a source case depends on the frequency of expiratory events, the respirable particle volume, and the pathogen concentration in respiratory fluid. Viable airborne pathogens are removed by exhaust ventilation, particle settling, die-off, and air disinfection methods; each removal mechanism can be assigned a first-order rate constant. The pathogen concentration in well-mixed room air depends on the emission rate, the size distribution of respirable particles carrying pathogens, and the removal rate constants. The particle settling rate and the alveolar deposition fraction depend on particle size. Given these inputs plus a susceptible person's breathing rate and exposure duration to room air, an expected alveolar dose  $\mu$  is estimated. If the infectious dose is one organism, as appears to be true for tuberculosis, infection risk is estimated by the expression:  $R = 1 - \exp(-\mu)$ . Using published tuberculosis data concerning cough frequency, bacilli concentration in respiratory fluid, and die-off rate, we illustrate the model via a plausible scenario for a person visiting the room of a pulmonary tuberculosis case. We suggest that patients termed "superspreaders" or "dangerous disseminators" are those infrequently encountered persons with high values of cough and/or sneeze frequency, elevated pathogen concentration in respiratory fluid, and/or increased respirable aerosol volume per expiratory event such that their pathogen emission rate is much higher than average.

Nielsen, K. Fog 2003. Mycotoxin production by indoor molds. *Fungal Genetics and Biology*, Vol. 39, No. 2. (July 2003), pp. 103-117.

Fungal growth in buildings starts at a water activity ( $a_w$ ) near 0.8, but significant quantities of mycotoxins are not produced unless  $a_w$  reaches 0.95. *Stachybotrys* generates particularly high quantities of many chemically distinct metabolites in water-damaged buildings. These metabolites are carried by spores, and can be detected in air samples at high spore concentrations. Very little attention has been paid to major metabolites of *Stachybotrys* called spirocyclic



drimanones, and the precise structures of the most abundant of these compounds are unknown. Species of *Aspergillus* and *Penicillium* prevalent in the indoor environment produce relatively low concentrations of mycotoxins, with the exception of sterigmatocystins that can represent up to 1% of the biomass of *A. versicolor* at  $a_w$ 's close to 1. The worst-case scenario for homeowners is produced by consecutive episodes of water damage that promote fungal growth and mycotoxin synthesis, followed by drier conditions that facilitate the liberation of spores and hyphal fragments.

Nielsen, K.F., G. Holm, L.P. Uttrup, P.A. Nielsen, 2004. Mould growth on building materials under low water activities. Influence of humidity and temperature on fungal growth and secondary metabolism. *International Biodeterioration & Biodegradation* 54 (2004) 325 - 336.

The influence of relative humidity (RH) and temperature on growth and metabolism of eight microfungi on 21 different types of building material was investigated. The fungi were applied as a dry mixture to the materials, which were incubated at 5°C, 10°C, 20°C and 25°C at three humidity levels in the range 69-95% RH over 4-7 months. The lower limit for fungal growth on wood, wood composites and starch-containing materials was 78% RH at 20-25°C and increased to 90% RH at 5°C. An RH of 86% was necessary for growth on gypsum board. Ceramic materials supported growth at RH>90%, although 95% RH was needed to yield chemically detectable quantities of biomass. Almost exclusively only *Penicillium*, *Aspergillus* and *Eurotium* (contaminant) species grew on the materials. Production of secondary metabolites and mycotoxins decreased with humidity and the quantities of metabolites were insignificant compared with those produced at high RH (RH>95%), except in the case of *Eurotium*.

Nielsen, PV, 2009. Control of airborne infectious diseases in ventilated spaces. *J. R. Soc. Interface* 2009 6, S747-S755

We protect ourselves from airborne cross-infection in the indoor environment by supplying fresh air to a room by natural or mechanical ventilation. The air is distributed in the room according to different principles: mixing ventilation, displacement ventilation, etc. A large amount of air is supplied to the room to ensure a dilution of airborne infection. Analyses of the flow in the room show that there are a number of parameters that play an important role in minimizing airborne cross-infection. The air flow rate to the room must be high, and the air distribution pattern can be designed to have high ventilation effectiveness. Furthermore, personalized ventilation may reduce the risk of cross-infection, and in some cases, it can also reduce the source of infection. Personalized ventilation can especially be used in hospital wards, aircraft cabins and, in general, where people are in fixed positions.

Noakes, Catherine J. and P. Andrew Sleight, 2009. Mathematical models for assessing the role of airflow on the risk of airborne infection in hospital wards. *J. R. Soc. Interface* 2009 6, S791-S800

Understanding the risk of airborne transmission can provide important information for designing safe healthcare environments with an appropriate level of environmental control for mitigating risks. The most common approach for assessing risk is to use the Wells- Riley equation to relate infectious cases to human and environmental parameters. While it is a simple model that can yield valuable information, the model used as in its original presentation has a number of limitations. This paper reviews recent developments addressing some of the limitations including coupling with epidemic models to evaluate the wider impact of control measures on disease progression, linking with zonal ventilation or computational fluid dynamics simulations to deal with imperfect mixing in real environments and recent work on dose-response modelling to simulate the interaction between pathogens and the host. A stochastic version of the Wells-Riley model is presented that allows consideration of the effects of small populations relevant in healthcare settings and it is demonstrated how this can be linked to a simple zonal ventilation model to simulate the influence of proximity to an infector. The results show how neglecting the stochastic effects present in a real situation could underestimate the risk by 15 per cent or more and that the number and rate of new infections between connected spaces is strongly dependent on the airflow. Results also indicate the potential danger of using fully mixed models for future risk assessments, with quantia values derived from such cases less than half the actual source value.

Norbäck, Dan, Pawel Markowicz, Gui-Hong Cai, Zailina Hashim, Faridah Ali, Yi-Wu Zheng, Xu-Xin Lai, Michael Dho Spangfort, Lennart Larsson, Jamal Hisham Hashim, 2014. Endotoxin, Ergosterol, Fungal DNA and Allergens in Dust from Schools in Johor Bahru, Malaysia- Associations with Asthma and Respiratory Infections in Pupils. *PLoS ONE* 9(2): e88303. doi:10.1371/journal.pone.0088303

There are few studies on associations between respiratory health and allergens, fungal and bacterial compounds in schools in tropical countries. The aim was to study associations between respiratory symptoms in pupils and ethnicity, chemical microbial markers, allergens and fungal DNA in settled dust in schools in Malaysia. Totally 462 pupils (96%) from 8 randomly selected secondary schools in Johor Bahru, Malaysia, participated. Dust was vacuumed from 32 classrooms and analysed for levels of different types of endotoxin as 3-hydroxy fatty acids (3-OH), muramic acid, ergosterol, allergens and five fungal DNA sequences. Multiple logistic regression was applied. Totally 13.1% pupils reported doctor's diagnosed asthma, 10.3% wheeze and 21.1% pollen or pet allergy. Indian and Chinese children had less atopy and asthma than Malay. Carbon dioxide levels were low (380–690 ppm). No cat (Fel d1), dog (Can f 1) or horse allergens (Ecu cx) were detected. The levels of *Bloomia tropicalis* (Blo t), house dust mite allergens (Der p 1, Der f 1, Der m 1) and cockroach allergens (Per a 1 and Bla g 1) were low. There were positive associations between levels of *Aspergillus versicolor* DNA and daytime breathlessness, between C14 3-OH and respiratory infections and between ergosterol and doctors diagnosed asthma. There were negative (protective) associations between levels of C10 3-OH and wheeze, between C16 3-OH and day time and night time breathlessness, between cockroach allergens and doctors diagnosed asthma. Moreover there were negative associations between amount of fine dust, total endotoxin (LPS) and respiratory infections. In conclusion, endotoxin at school seems to be mainly protective for respiratory illness but different types of endotoxin could have different effects. Fungal contamination measured as ergosterol and *Aspergillus versicolor* DNA can be risk factors for respiratory illness. The ethnical differences for atopy and asthma deserve further attention.

Noris F, Siegel JA, Kinney KA. 2011. Evaluation of HVAC filters as a sampling mechanism for indoor microbial communities. *Atmos Environ* 45(2):338-46.

HVAC filters are in place for extended periods of time and can serve as integrated air samplers. This paper presents a comparison of bacterial and fungal concentrations and communities in HVAC filter dust and other sampling locations in occupied residences and in the unoccupied UTest House. A DNA-based, culture-independent approach was utilized to characterize the microbial communities. Microbial concentrations and communities in HVAC filter dust samples were not statistically different from those in high surface dust samples in occupied homes. Despite the general similarity in the communities, Proteobacteria were present in greater proportion in HVAC filter dust samples than in surface dust samples suggesting the air origin of this phylum. Gram-positive bacteria were present in greater proportion in occupied residences than in an unoccupied test house, confirming the potential association of this group with occupants. HVAC filter microbial communities were not different from those present in a composited month-long indoor air sample providing preliminary evidence that filters could be a viable option for long-term investigation of airborne biological contaminants. Research highlights.

Nunez, Maria, Mari S. Sivertsen, Johan Mattsson, 2012. Growth preferences on substrate, construction, and room location for indoor moulds and Actinomycetes. *Proceedings of Healthy Buildings 2012, Brisbane, Australia*

We describe the growth preferences of Actinomycetes and 13 common mould genera in moisture damaged buildings based on sampling and microscopic analyses of 11032 collections in Norway during the years 2001-2006. Sampling has systematically been carried out on nine types of building materials, six room locations, and six construction types. Our results indicate that *Ascotricha* and *Mycotrichum* are commonly found in insulated outer walls in basements, *Hyalodendron* grows almost exclusively on wood in cold attics, and *Chrysosporium* in cold basements and crawl spaces. *Aspergillus* and *Penicillium* have a wider ecology as genera, and studies must be carried out at species level.

Nunez, M., H. Hammer, 2014. Microbial specialists in below-grade foundation walls in Scandinavia. *Indoor Air 2014*

Below-grade foundation walls are often exposed to excessive moisture by water infiltration, condensation, leakage, or lack of ventilation. Microbial growth in these structures depends largely on environmental factors, elapsed time, and the type of building materials and construction setup. The ecological preferences of Actinomycetes (Actinobacteria) and the molds *Ascotricha chartarum*, *Myxotrichum chartarum* (Ascomycota), *Geomyces pannorum*, and *Monocillium* sp. (Hyphomycetes) have been addressed based on analyses of 1764 samples collected in below-grade spaces during the period of 2001–2012. Our results show a significant correlation between these taxa and moist foundation walls as ecological niches. Substrate preference was the strongest predictor of taxa distribution within the

wall, but the taxa's physiological needs, together with gradients of abiotic factors within the wall structure, also played a role. Our study describes for the first time how the wall environment affects microbial growth.

"Oberauner , Lisa, Christin Zachow, Stefan Lackner, Christoph Hogenauer, Karl-Heinz Smolle

& Gabriele Berg, 2013. The ignored diversity: complex bacterial communities in intensive care units revealed by 16S pyrosequencing. *SCIENTIFIC REPORTS* 3 : 1413, DOI: 0.1038/srep01413"

Indoor microbial communities play an important role in everyday human health, especially in the intensive care units (ICUs) of hospitals. We used amplicon pyrosequencing to study the ICU microbiome and were able to detect diverse sequences, in comparison to the currently used standard cultivation technique that only detected 2.5% of the total bacterial diversity. The phylogenetic spectrum combined species associated with the outside environment, taxa closely related to potential human pathogens, and beneficials as well as included 7 phyla and 76 genera. In addition, *Propionibacterium* spp., *Pseudomonas* spp., and *Burkholderia* spp. were identified as important sources of infections. Despite significantly different bacterial area profiles for floors, medical devices, and workplaces, similarities by network analyses and strains with identical molecular fingerprints were detected. This information will allow for new assessment of public health risks in ICUs, help create new sanitation protocols, and further our understanding of the development of hospital-acquired infections.

Ojima M, Toshima Y, Koya E, Ara K, Tokuda H, Kawai S, Kasuga F, Ueda N. 2002. Hygiene measures considering actual distributions of microorganisms in Japanese households. *J Appl Microbiol* 93(5):800-9

**Aims:** Effective household hygiene measures require that sources of bacterial contamination and the places to which contamination spreads be carefully identified. Therefore, a study was performed to examine the distribution of microorganisms throughout ordinary households in Japan, which has its own unique customs of daily life and food preparation. **Methods and Results:** Using the stamping method, samples were taken from 100 different places and items in each of 86 households. This study found kitchens/dining rooms to have the greatest level of microbial contamination and bathrooms, the next highest level. Toilets (water closets) were found to have an unexpectedly low level of bacterial contamination. The largest bacterial counts were found on items such as drain traps, dish-washing sponges, counter towels, sinks, dish-washing tubs, and bathroom sponges. **Conclusions:** It is necessary to carefully identify both the items that can become instruments for spreading bacterial contamination and the places that easily become subject to secondary contamination, and then to take timely and effective disinfection/sanitizing measures. **Significance and Impact of the Study:** The data gathered in this study will be very valuable for anticipating the pathways over which bacteria are transported and prioritizing disinfection targets, to make effective disinfection possible.

Oliveira, Manuela, Helena Ribeiro, Jose Luis Delgado and Ilda Abreu, 2009. Aeromycological profile of indoor and outdoor environments. *J. Environ. Monit.*, 2009, 11, 1360–1367

The aim of this work was to determine the differences between indoor and outdoor aeromycological composition. The aerobiological study was performed, from 15 January to 14 April 2008, using two volumetric spore traps, one placed indoors and another positioned outdoors on the roof of the Faculdade de Ciências building. A total of 23 000 spores were sampled outdoors and 15 500 spores were identified indoors. In both environments, the most abundant fungal spores were *Cladosporium*, *Aspergillus/Penicillium*, *Agaricus*, *Rusts*, *Agrocybe* and *Lepthosphaeria*. Moreover, *Alternaria*, *Botrytis*, *Coprinus*, *Fusarium* and *Ganoderma* spores were also detected in the outdoor air. The outdoor maximum (858 spores m<sup>-3</sup> day<sup>-1</sup>) was registered on the 9 February whereas the indoor peak (614 spores m<sup>-3</sup> day<sup>-1</sup>) was reached two days later. Qualitative similarities were found between the indoor and outdoor aeromycological content however quantitatively spore concentrations differed, suggesting the existence of airflows between the two environments due to ventilation, inefficient isolation or passive transport of spores. The majority of the selected fungal types were night sporulators, the exceptions were *Aspergillus/Penicillium* and *Cladosporium*, with daily maximum values during the morning and the afternoon, respectively. Several of the identified spores have been proved as causal agents of respiratory problems. Therefore, it is important to know the microbial composition of indoor air in order to take measures to improve air quality helping to reduce health problems related to respiratory allergic diseases in sensitized patients.

Ongwandee, M., S. S. Bettinger, G. C. Morrison, 2005. The influence of ammonia and carbon dioxide on the sorption of a basic organic pollutant to a mineral surface. *Indoor Air* 2005; 15: 408-419

Indoor surfaces have a sorptive capacity for organic pollutants which may be significantly influenced by other gases and the pH of the surface. In this research, we examine the influence of a common indoor gaseous acid, CO<sub>2</sub>, and base, NH<sub>3</sub>, on the adsorption of a volatile organic base, trimethylamine (TMA), to a mineral surface, zirconium silicate beads. Varying ammonia and CO<sub>2</sub> within concentration ranges of indoor relevance substantially influences the sorptive capacity of this mineral surface. Increasing the CO<sub>2</sub> mixing ratio to 1000 p.p.m. enhances surface capacity of TMA by 40-50%; increasing the NH<sub>3</sub> mixing ratio to 10 p.p.m. decreases the TMA surface capacity by ~5-80% depending on relative humidity. The phenomena of dissolution of TMA into bulk surface water and acid-base chemistry in the surface water do not adequately describe equilibrium adsorption on this surface. Instead, adsorption to the dry solid or to adsorbed water layers appears to dominate. Reduction in the equilibrium partition coefficient,  $k_e$ , in the presence of NH<sub>3</sub> is due to a competition between TMA and ammonia molecules for adsorption sites. Site competition appears to follow the Langmuir competitive model and most  $k_e$  values range from 0.003-0.045 m.

Ongwandee, M. and G. C. Morrison, 2008, Influence of Ammonia and Carbon Dioxide on the Sorption of a Basic Organic Pollutant to Carpet and Latex-Painted Gypsum Board, *Environ. Sci. Technol.* 2008, 42, 5415-5420

Sorptive interactions with indoor surfaces strongly influence indoor exposure to organic pollutants. Adsorption itself may be influenced by indoor levels of common indoor gases such as CO<sub>2</sub>, NH<sub>3</sub>, and H<sub>2</sub>O. We quantified sorption characteristics of trimethylamine (TMA) on carpet and painted wallboard, while challenging the surface with gas-phase CO<sub>2</sub>, NH<sub>3</sub> and H<sub>2</sub>O. We show that the capacity of the carpet to sorb TMA, doubles when the CO<sub>2</sub> mixing ratio is increased from 0 to 1000 ppm CO<sub>2</sub> at 90% relative humidity. In contrast, NH<sub>3</sub> decreases the surface capacity of both carpet and latex paint. Sorption of TMA to these indoor materials is primarily caused by interactions at one or more interfaces. Dissolution of TMA and aqueous acid-base chemistry appear to also contribute to the overall sorptive capacity of carpet at high relative humidity. The reduction in the distribution coefficient,  $k_e$ , in the presence of NH<sub>3</sub> is explained by competition between TMA and NH<sub>3</sub> molecules for sites on the substrates at low-to-medium relative humidity conditions.

Otter JA, Yezli S, French GL. 2011. The role played by contaminated surfaces in the transmission of nosocomial pathogens. *Infection Control and Hospital Epidemiology* 32(7):687-99

Studies in the 1970s and 1980s suggested that environmental surface contamination played a negligible role in the endemic transmission of healthcare-associated infections. However, recent studies have demonstrated that several major nosocomial pathogens are shed by patients and contaminate hospital surfaces at concentrations sufficient for transmission, survive for extended periods, persist despite attempts to disinfect or remove them, and can be transferred to the hands of healthcare workers. Evidence is accumulating that contaminated surfaces make an important contribution to the epidemic and endemic transmission of *Clostridium difficile*, vancomycin-resistant enterococci, methicillin-resistant *Staphylococcus aureus*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and norovirus and that improved environmental decontamination contributes to the control of outbreaks. Efforts to improve environmental hygiene should include enhancing the efficacy of cleaning and disinfection and reducing the shedding of pathogens. Further high-quality studies are needed to clarify the role played by surfaces in nosocomial transmission and to determine the effectiveness of different interventions in reducing associated infection rates.

Ownby, Dennis R., Edward L. Peterson, L. Keoki Williams, Edward M. Zoratti, Ganesa R. Wegienka, Kimberley J. Woodcroft, Christine L. M. Joseph and Christine C. Johnson, 2010. Variation of dust endotoxin concentrations by location and time within homes of young children. *Pediatr Allergy Immunol* 2010: 21: 533-540

Endotoxin may affect the development of allergic disease in childhood but little is known about endotoxin variation within homes. We sought to determine endotoxin concentration agreement within homes when five locations were each sampled twice 5 months apart. Endotoxin was measured using the recombinant Limulus factor C assay in dust samples from 585 homes of children enrolled in a prospective study and again in 335 homes 5 months later. The five locations sampled in each home were the child's bedroom floor, child's bed, mother's bedroom floor, mother's bed and living room floor. Concentrations of 4 allergens (Can f 1, Fel d 1, Der f 1 and Bla g 2) were also measured from the child's

bedroom floor. In pair-wise comparisons, endotoxin concentrations in all locations within each home were significantly different from all other locations ( $p < 0.001$ ) except for the child's and mother's bedroom floors ( $p = 0.272$ ). Spearman correlations between endotoxin concentrations from the different locations were all statistically significant ( $p < 0.05$ ) but of modest magnitude ( $r = 0.24-0.54$ ). Similarly, correlations at each site over the 5 month observation interval were statistically significant but modest ( $r = 0.17-0.44$ ). Pets and season of the year did not affect correlations, although correlations were lower if the floor was not carpeted. Endotoxin concentrations at all locations were minimally correlated with allergen concentrations in both negative and positive directions ( $r = -0.12$  to  $0.12$ ). We conclude that a single measurement of endotoxin from a home dust sample provides an imprecise estimate of dust endotoxin concentrations in other locations within the home and over a relatively short observation interval.

Pach D, Knoechel B, Luedtke R, Wruck K, Willich SN, Witt CM. 2010. Visiting a sauna: Does inhaling hot dry air reduce common cold symptoms? A randomised controlled trial. *Med J Aust* 193(11-12):730-4.

**Objective:** To compare the efficacy of applying hot dry air versus dry air at room temperature to the throat of patients with a newly acquired common cold using a symptom severity score. **Design, setting and participants:** A randomised single-blind controlled trial with a treatment duration of 3 days and a follow-up period of 4 days was conducted at a sauna in Berlin, Germany. Between November 2007 and March 2008 and between September 2008 and April 2009, 157 patients with symptoms of the common cold were randomly assigned to an intervention group ( $n = 80$ ) and a control group ( $n = 77$ ). **Interventions:** Participants in the intervention group inhaled hot dry air within a hot sauna, dressed in a winter coat, whereas participants in the control group inhaled dry air at room temperature within a hot sauna, also dressed in a winter coat. **Main outcome measures:** Area under the curve (AUC) summarising symptom severity over time (Days 2, 3, 5 and 7), symptom severity scores for individual days, intake of medication for the common cold and general ill feeling. **Results:** No significant difference between groups was observed for AUC representing symptom severity over time (intervention group mean, 31.2 [SEM, 1.8]; control group mean, 35.1 [SEM, 2.3]; group difference, -3.9 [95% CI, -9.7 to 1.9];  $P = 0.19$ ). However, significant differences between groups were found for medication use on Day 1 ( $P = 0.01$ ), symptom severity score on Day 2 ( $P = 0.04$ ), and participants' ratings of the effectiveness of the therapy on Day 7 ( $P = 0.03$ ). **Conclusion:** Inhaling hot air while in a sauna has no significant impact on overall symptom severity of the common cold.

Palmore TN, Henderson DK, Bonten MJ, Fishman NO, Lautenbach E, Gordon S, Harbarth S, Harris AD, Perencevich EN, Perl TM, et al. 2010. Enhancing patient safety by reducing healthcare-associated infections: The role of discovery and dissemination. *Infection Control and Hospital Epidemiology* 31(2):118-23

Healthcare associated infections (HAIs) take a major human toll on society and reduce public confidence in the healthcare system. The current convergence of scientific, public, and legislative interest in reducing rates of HAI can provide the necessary momentum to address and answer important questions in HAI research. This position paper outlines priorities for a national approach to HAIs: scrutinizing the science base, developing a prioritized research agenda, conducting studies that address the questions that have been identified, creating and deploying guidelines that are based on the outcomes of these studies, and then initiating new studies that assess the efficacy of the interventions

Pantelic, Jovan, Gin Nam Sze-To, Kwok Wai Tham, Christopher Y. H. Chao and Yong Chuan Mike Khoo, 2009. Personalized ventilation as a control measure for airborne transmissible disease spread. *J. R. Soc. Interface* 2009 6, S715-S726

The protective role of personalized ventilation (PV) against plausible airborne transmissible disease was investigated using cough droplets released from a 'coughing machine' simulating the human cough at different distances (1, 1.75 and 3 m) from the PV user. Particle image velocimetry was used to characterize and visualize the interaction between the cough-generated multiphase flow and PV-induced flow in the inhalation zone of the thermal breathing manikin. A dose-response model for unsteady imperfectly mixed environment was used to estimate the reduction in infection risk of two common diseases that can be transmitted by airborne mode. PV was able to both reduce the peak aerosol concentration levels and shorten the exposure time at all the examined injection distances. PV could reduce the infection risks of two diseases, influenza A and tuberculosis, by between 27 and 65 per cent. The protection offered by PV is less effective at a distance of 1.75 m than the other distances, as shown in the risk assessment results, as the PV-

generated flow was blown off by the cough-generated flow for the longest time. Results of this study demonstrate the ability of desktop PV to mitigate the infection risk of airborne transmissible disease.

Park, J.-H., K. Kreiss, J. M. Cox-Ganser, 2012. Rhinosinusitis and mold as risk factors for asthma symptoms in occupants of a water-damaged building. *Indoor Air* 2012; 22: 396-404

Mold exposure in damp buildings is associated with both nasal symptoms and asthma development, but the progression of building-related (BR) rhinosinusitis symptoms to asthma is unstudied. We examined the risk of developing BR-asthma symptoms in relation to prior BR-rhinosinusitis symptoms and microbial exposure among occupants of a damp building. We conducted four cross-sectional health and environmental surveys among occupants of a 20-story water-damaged office building. We defined BR-rhinosinusitis symptom (N = 131) and comparison (N = 361) groups from participants' first questionnaire responses. We compared the odds for the development of BR-asthma symptoms between these two groups over the subsequent surveys, using logistic regression models adjusted for demographics, smoking, building tenure, and first-survey exposures to fungi, endotoxin, and ergosterol. The BR-rhinosinusitis symptom group had higher odds for developing BR-asthma symptoms [odds ratio (OR) = 2.2; 95% confidence interval (CI) = 1.3-3.6] in any subsequent survey compared to those without BR-rhinosinusitis symptoms. The BR-rhinosinusitis symptom group with higher fungal exposure within the building had an OR of 7.4 (95% CI = 2.8-19.9) for developing BR-asthma symptoms, compared to the lower fungal exposure group without BR-rhinosinusitis symptoms. Our findings suggest that rhinosinusitis associated with occupancy of water-damaged buildings may be a sentinel for increased risk for asthma onset in such buildings.

Pasanen, A.-L., A. Korpi, J.-P. Kasanen, and P. Pasanen, 1998. CRITICAL ASPECTS ON THE SIGNIFICANCE OF MICROBIAL VOLATILE METABOLITES AS INDOOR AIR POLLUTANTS. *Environment International*, Vol. 24, No. 7, pp. 703-712

The effect of microbial growth in building materials on airborne levels of volatile organic compounds (VOCs) was demonstrated by theoretically calculating indoor air concentrations of selected VOCs for rooms with and without microbial contamination. The recommended indoor air level for individual VOCs was also estimated on the basis of their sensory irritation potency. Furthermore, the irritation potency for the mixtures of certain compounds (microbial volatile metabolites, MVOCs) at airborne concentrations measured in problem buildings was evaluated. The theoretical airborne concentrations of certain compounds, which are generally regarded as MVOCs, were estimated to be only about 1% higher in the biocontaminated rooms than in those with moist sterile materials. In fact, no individual VOCs indicated exclusively microbial contamination, but they could also be emitted even from sterile, moist constructions. Exposure to mixtures of the selected non-reactive VOCs at the theoretical airborne concentrations would not result in sensory irritation in humans, and, thus, microbial growth in constructions should not increase the probability of irritating symptoms considerably. The data on MVOC concentrations measured in some problem buildings also supported this idea. Irritation would be expected when the airborne concentrations of single non-reactive compounds approach a level of hundreds of  $\mu\text{g}/\text{m}^3$  or  $\text{mg}/\text{m}^3$

Pasanen A, Kasanen J, Rautiala S, Ikaheimo M, Rantamaki J, Kaariainen H, Kalliokoski P. 2000. Fungal growth and survival in building materials under fluctuating moisture and temperature conditions. *Int Biodeterior Biodegrad* 46(2):117-27.

Growth and viability of fungi on three building materials under moistening and drying conditions were investigated in the laboratory. The materials were taken from buildings under repair and no additional inoculation of fungi was used. The materials underwent four treatments (4-8 weeks of each): capillary absorption of water, drying in air at a relative humidity (RH) of 30%, condensation and finally drying at 50% RH. Moisture content (MC), equilibrium relative humidity (ERH), and concentrations of culturable fungi, actinomycetes and total spores were determined in the materials at 1- or 2-week intervals. The results showed that when water was absorbed by capillary action to the materials, fungal growth started fast and was abundant in the wood-based materials with MC above 20%. Such a limit value could not be defined for fungal contamination in the gypsum board because of complex behaviour of moisture between the gypsum bulk and paper covering. The condensation under the varying RH and temperature conditions caused only restrained fungal growth in the materials. The fast drying (RH 30%) seemed to decrease the viability of fungi but along with the experiment fungal flora was modified to tolerate fluctuating conditions and the drying at RH 50% had only a slight effect on the viability of fungi.

Pasanen A, Rautiala S, Kasanen J, Raunio P, Rantamaki J, Kalliokoski P. 2000. The relationship between measured moisture conditions and fungal concentrations in water-damaged building materials. *Indoor Air-International Journal of Indoor Air Quality and Climate* 10(2):111-20.

We determined the moisture levels, relative humidity (RH) or moisture content (MC) of materials, and concentrations of culturable fungi, actinomycetes and total spores as well as a composition of fungal flora in 122 building material samples collected from 18 moisture problem buildings. The purpose of this work was to clarify if there is any correlation between the moisture parameters and microbial levels or generic composition depending on the type of materials and the time passed after a water damage. The results showed an agreement between the concentrations of total spores and culturable fungi for the wood, wood-based and gypsum board samples ( $r > 0.47$ ). The concentrations of total spores and/or culturable fungi correlated with RH of materials particularly among the wood and insulation materials ( $r > 0.79$ ), but not usually with MC ( $r < 0.45$ ). For the samples collected from ongoing damage, there was a correlation between RH of materials and the concentrations of total spores and culturable fungi ( $r > 0.51$ ), while such a relationship could not be observed for the samples taken from dry damage. A wide range of fungal species were found in the samples from ongoing damage, whereas *Penicillia* and in some cases yeasts dominated the fungal flora in the dry samples. This study indicates that fungal contamination can be evaluated on the basis of moisture measurements of constructions in ongoing damage, but the measurements are not solely adequate for estimation of possible microbial growth in dry damage.

Peccia, Jordan, Werth, Holly M., Miller, Shelly and Hernandez,, Mark, 2007. 'Effects of Relative Humidity on the Ultraviolet Induced Inactivation of, Airborne Bacteria', *Aerosol Science and Technology*, 35:3, 728 - 740

Ultraviolet germicidal irradiation (UVGI) as an engineering, control against infectious bioaerosols necessitates a clear understanding, of environmental effects on inactivation rates. The response, of aerosolized *Serratia marcescens*, *Bacillus subtilis*, and *Mycobacterium parafortuitum* to, ultraviolet irradiation was assessed at, different relative humidity (RH) levels in a 0.8 m<sup>3</sup> completely-mixed, chamber. Bioaerosol response was characterized by physical factors, including median cell aerodynamic diameter and cell water, sorption capacity and by natural decay and UV-induced inactivation, rate as determined by direct microscopic counts and standard, plate counts. All organisms tested sorbed water from the atmosphere, at RH levels between 20% and 95% (up to 70% of dry, cell mass at 95%RH); however, no concomitant change in median, aerodynamic diameter in this same RH range was observed. Variations, in ultraviolet spherical irradiance were minor and not statistically, significant in the 20-95% RH range. Cell water sorption, and inactivation response was similar for each of the pure cultures, tested: when RH exceeded approximately 50%, sorption increased, markedly and a sharp concurrent drop in UV-induced inactivation, rate was observed.

Pegas PN, Alves CA, Evtugina MG, Nunes T, Cerqueira M, Franchi M, Pio CA, Almeida SM, Cabo Verde S, Freitas MC. 2011. Seasonal evaluation of outdoor/indoor air quality in primary schools in Lisbon. *Journal of Environmental Monitoring* 13(3):657-67.

The aim of this study was to evaluate the indoor (I) and outdoor (O) levels of NO<sub>2</sub>, speciated volatile organic compounds (VOCs) and carbonyls at fourteen primary schools in Lisbon (Portugal) during spring, autumn and winter. Three of these schools were also selected to be monitored for comfort parameters, such as temperature and relative humidity, carbon dioxide (CO<sub>2</sub>), carbon monoxide (CO), total VOCs, and both bacterial and fungal colony-forming units per cubic metre. The concentration of CO<sub>2</sub> and bioaerosols greatly exceeded the acceptable maximum values of 1800 mg m<sup>-3</sup> and 500 CFU m<sup>-3</sup>, respectively, in all seasons. Most of the assessed VOCs and carbonyls occurred at I/O ratios above unity in all seasons, thus showing the importance of indoor sources and building conditions in indoor air quality. However, it has been observed that higher indoor VOC concentrations occurred more often in the colder months, while carbonyl concentrations were higher in the warm months. In general, the I/O NO<sub>2</sub> ratios ranged between 0.35 and 1, never exceeding the unity. Some actions are suggested to improve the indoor air quality in Lisbon primary schools.

Peitzsch, Mirko, Michael Sulyok, Martin Taubel, Vinay Vishwanath, Esmeralda Krop, Alicia Borrás-Santos, Anne Hyvarinen, Aino Nevalainen, Rudolf Krska and Lennart Larsson, 2012. Microbial secondary metabolites in school buildings inspected for moisture damage in Finland, The Netherlands and Spain. *J. Environ. Monit.*, 14, 2044-2052, DOI: 10.1039/c2em30195d

Secondary metabolites produced by fungi and bacteria are among the potential agents that contribute to adverse health effects observed in occupants of buildings affected by moisture damage, dampness and associated microbial growth. However, few attempts have been made to assess the occurrence of these compounds in relation to moisture damage and dampness in buildings. This study conducted in the context of the HITEA project (Health Effects of Indoor Pollutants: Integrating microbial, toxicological and epidemiological approaches) aimed at providing systematic information on the prevalence of microbial secondary metabolites in a large number of school buildings in three European countries, considering both buildings with and without moisture damage and/or dampness observations. In order to address the multitude and diversity of secondary metabolites a large number of more than 180 analytes was targeted in settled dust and surface swab samples using liquid chromatography/mass spectrometry (LC/MS) based methodology. While 42%, 58% and 44% of all samples collected in Spanish, Dutch and Finnish schools, respectively, were positive for at least one of the metabolites analyzed, frequency of detection for the individual microbial secondary metabolites - with the exceptions of emodin, certain enniatins and physcion - was low, typically in the range of and below 10% of positive samples. In total, 30 different fungal and bacterial secondary metabolites were found in the samples. Some differences in the metabolite profiles were observed between countries and between index and reference school buildings. A major finding in this study was that settled dust derived from moisture damaged, damp schools contained larger numbers of microbial secondary metabolites at higher levels compared to respective dust samples from schools not affected by moisture damage and dampness. This observation was true for schools in each of the three countries, but became statistically significant only when combining schools from all countries and thus increasing the sample number in the statistical analyses.

"Pendleton, Jack N, Sean P Gorman and Brendan F Gilmore, 2013. Clinical relevance of the

ESKAPE pathogens. *Expert Rev. Anti Infect. Ther.* 11(3), 297–308 (2013)"

In recent years, the Infectious Diseases Society of America has highlighted a faction of antibiotic-resistant bacteria (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa* and *Enterobacter* spp.) – acronymically dubbed ‘the ESKAPE pathogens’ – capable of ‘escaping’ the biocidal action of antibiotics and mutually representing new paradigms in pathogenesis, transmission and resistance. This review aims to consolidate clinically relevant background information on the ESKAPE pathogens and provide a contemporary summary of bacterial resistance, alongside pertinent microbiological considerations necessary to face the mounting threat of antimicrobial resistance.

Percival, Steven L, Charlotte Emanuel, Keith F Cutting, David W Williams, 2011. Microbiology of the skin and the role of biofilms in infection. *Int Wound J* 2012; 9:14–32

The integrity of human skin is central to the prevention of infection. Acute and chronic wounds can develop when the integrity of skin as a barrier to infection is disrupted. As a multi-functional organ, skin possesses important biochemical and physical properties that influence its microbiology. These properties include a slightly acidic pH, a low moisture content, a high lipid content (which results in increased hydrophobicity) and the presence of antimicrobial peptides. Such factors have a role to play in preventing exogenous microbial colonisation and subsequent infection. In addition, the properties of skin both select for and enhance colonisation and biofilm formation by certain ‘beneficial’ micro-organisms. These beneficial micro-organisms can provide further protection against colonisation by potential pathogens, a process known as colonisation resistance. The aim of this paper is to summarise the microflora of skin and wounds, highlighting the role of certain micro-organisms and biofilms in associated infections.

Perdelli F, Cristina ML, Sartini M, Spagnolo AM, Dallera M, Ottria G, Lombardi R, Grimaldi M. 2006. Fungal contamination in hospital environments. *Infection Control and Hospital Epidemiology* 27(1):44-7

**Objectives.** To assess the degree of fungal contamination in hospital environments and to evaluate the ability of air conditioning systems to reduce such contamination. **Methods.** We monitored airborne microbial concentrations in various environments in 10 hospitals equipped with air conditioning. Sampling was performed with a portable Surface Air System impactor with replicate organism detection and counting plates containing a fungus-selective medium. The total fungal concentration was determined 72-120 hours after sampling. The genera most involved in infection were identified by macroscopic and microscopic observation. **Results.** The mean concentration of airborne fungi in the set of



environments examined was  $19 \pm 19$  colony-forming units (cfu) per cubic meter. Analysis of the fungal concentration in the different types of environments revealed different levels of contamination: the lowest mean values ( $12 \pm 14$  cfu/m<sup>3</sup>) were recorded in operating theaters, and the highest ( $45 \pm 37$  cfu/m<sup>3</sup>) were recorded in kitchens. Analyses revealed statistically significant differences between median values for the various environments. The fungal genus most commonly encountered was *Penicillium*, which, in kitchens, displayed the highest mean airborne concentration ( $1.2 \pm 2.4$  cfu/m<sup>3</sup>). The percentage (35%) of *Aspergillus* documented in the wards was higher than that in any of the other environments monitored. Conclusions. The fungal concentrations recorded in the present study are comparable to those recorded in other studies conducted in hospital environments and are considerably lower than those seen in other indoor environments that are not air conditioned. These findings demonstrate the effectiveness of air-handling systems in reducing fungal contamination.

Perez, Hernando R, Rachel Johnson, Patrick L. Gurian, Shawn G. Gibbs, Jennifer Taylor, and Igor Burstyn, 2011. Isolation of Airborne Oxacillin-Resistant *Staphylococcus aureus* from Culturable Air Samples of Urban Residences. *Journal of Occupational and Environmental Hygiene*, 8: 80-85.

Culturable single-stage impactor samples were collected onto nutrient agar in kitchen and bedroom areas of eight urban and four suburban residences in Philadelphia, Pennsylvania. *Staphylococcus aureus* colonies were identified by replica plating of the original impactor samples onto Chapman Stone medium followed by isolation of up to eight colonies for coagulase testing. Kirby-Bauer disk diffusion method was utilized to evaluate *S. aureus* resistance to both oxacillin and cefaclor. The median concentrations of total culturable bacteria observed in bedrooms and trash areas were 300 CFU/m<sup>3</sup> and 253 CFU/m<sup>3</sup>, respectively. Median culturable *Staphylococcus* spp. concentrations in bedrooms and trash areas were 142 CFU/m<sup>3</sup> and 204 CFU/m<sup>3</sup>, respectively. A total of 148 individual *S. aureus* colonies were isolated and tested for antibiotic resistance. Cefaclor resistance was encountered among only 6 of the 148 (4%) colonies. Nearly one-quarter of all *S. aureus* isolates tested displayed resistance ( $n = 30$ ) or intermediate resistance ( $n = 5$ ) to oxacillin. Twenty-six percent ( $n = 20$ ) of trash area isolates and 21% ( $n = 15$ ) of bedroom isolates displayed resistance or intermediate resistance to oxacillin. The median difference in percent resistance between trash and bedroom areas was 10% ( $p = 0.1$ ). Results suggest that there may be a systematic difference in bacterial populations between downtown and suburban residences. Storage of household waste and handling of food may contribute to presence of the organism in the air of residences.

Pessi, Anna-Mari, Jommi Suonketo, Matti Pentti, Mika Kurkilahti, Kaija Peltola, and Auli Rantio-Lehtimäki, 2002. Microbial Growth Inside Insulated External Walls as an Indoor Air Biocontamination Source. *Appl. Environ. Microbiol.* 2002, 68(2):963

The association between moisture-related microbial growth (mesophilic fungi and bacteria) within insulated exterior walls and microbial concentrations in the indoor air was studied. The studied apartment buildings with precast concrete external walls were situated in a subarctic zone. Actinomycetes in the insulation layer were found to have increased concentrations in the indoor air. The moisture content of the indoor air significantly affected all measurable airborne concentrations.

Peters, Junenette L.; Michael L. Mulienberg, Christine A. Rogers, Harriet A. Burge, and John D. Spengler, 2008. *Alternaria* measures in inner-city, low-income housing by immunoassay and culture-based analysis. *Ann Allergy Asthma Immunol.* 2008;100:364–369

Background: Sensitivity to *Alternaria* allergens has been associated with severe asthma and life-threatening exacerbations, and a high prevalence of *Alternaria* sensitivity has been reported among inner-city populations. Traditionally, epidemiologic studies have measured indoor *Alternaria* concentrations by cultural analyses; however, the number of viable spores may not be a good proxy for allergen levels. Furthermore, other genera share epitopes with *Alternaria* that may contribute to the allergenic effect. Objective: To compare measures of *Alternaria* antigen by enzyme-linked immunosorbent assay with measures of *Alternaria* and cross-reactive genera (*Ulocladium*, *Curvularia*, *Epicoccum*, and *Stemphylium*) by cultural analysis. Method: Antigen assays and cultural analyses were performed on vacuum-collected bed dust samples collected between June 18, 2002, and February 9, 2004, from 3 inner-city, low-income public housing developments. Results: *Alternaria* antigen was found in all bed dust samples regardless of season. However, culturable *Alternaria*, *Ulocladium*, *Curvularia*, *Epicoccum*, and *Stemphylium* were only found in 50%, 35%, 6%,

11%, and 0% of bed samples, respectively. No correlations were found between *Alternaria* antigen and culturable concentrations of *Alternaria* or of its cross-reactive genera except for marginal correlation with *Ulocladium* culturable concentrations. Conclusions: The results confirm that exposure to *Alternaria* antigens and allergens can occur even in the absence of culturable *Alternaria* or its cross-reactive genera, so further refinement and use of assays are essential for characterizing the distribution and determinants of indoor fungal allergen levels for sensitive populations.

Petrova, Olga E. and Karin Sauer, 2012. Sticky Situations: Key Components That Control Bacterial Surface Attachment. *J. Bacteriol.* 2012, 194(10):2413. DOI: 10.1128/JB.00003-12.

The formation of bacterial biofilms is initiated by cells transitioning from the free-swimming mode of growth to a surface. This review is aimed at highlighting the common themes that have emerged in recent research regarding the key components, signals, and cues that aid in the transition and those involved in establishing a more permanent surface association during initial attachment.

Pietarinen V, Rintala H, Hyvarinen A, Lignell U, Karkkainen P, Nevalainen A. 2008. Quantitative PCR analysis of fungi and bacteria in building materials and comparison to culture-based analysis. *J Environ Monit* 10(5):655-63.

Prolonged moisture on building materials can lead to microbial growth on them. Microbes can emit spores, metabolites and structural parts into the indoor air and thus, cause adverse health effects of people living and working in these buildings. So far, culture methods have been used for assessment of microbial contamination of building materials. In this work, we used quantitative PCR (qPCR) for the detection of selected fungal and bacterial groups in 184 building materials of different types and compared the results with culture-based analysis. Nine either commonly found species, genera or groups of fungi, or those considered as moisture damage indicators, and one bacterial genus, *Streptomyces*, were determined using qPCR. Fungi and mesophilic actinomycetes were also cultivated using standard media and conditions of the routine analysis. The bacterial genus *Streptomyces* and the fungal group *Penicillium/Aspergillus/Paecilomyces* were the most prevalent microbial groups in all building material types, followed by *Stachybotrys chartarum* and *Trichoderma viride/atroviride/koningii*. The highest prevalences, concentrations and species diversity was observed on wooden materials. In general, the results of the two methods did not correlate well, since concentrations of fungi and streptomycetes were higher and their occurrence more prevalent when determined by qPCR compared to culture-based results. However, with increasing concentrations, the correlation generally increased. The qPCR assay did not detect *Aspergillus versicolor* and *Acremonium strictum* as often as culture.

Pitkaranta, M., T. Meklin, A. Hyvarinen, L. Paulin, P. Auvinen, A. Nevalainen, and H. Rintala, 2008. Analysis of Fungal Flora in Indoor Dust by Ribosomal DNA Sequence Analysis, Quantitative PCR, and Culture. *Appl. Environ. Microbiol.* 2008, 74(1):233. DOI: 10.1128/AEM.00692-07

In recent years increasing attention has been given to the potential health effects of fungal exposure in indoor environments. We used large-scale sequencing of the fungal internal transcribed spacer region (ITS) of nuclear ribosomal DNA to describe the mycoflora of two office buildings over the four seasons. DNA sequencing was complemented by cultivation, ergosterol determination, and quantitative PCR analyses. Sequences of 1,339 clones were clustered into 394 nonredundant fungal operational taxonomical units containing sequences from 18 fungal subclasses. The observed flora differed markedly from that recovered by cultivation, the major differences being the near absence of several typical indoor mold genera such as *Penicillium* and *Aspergillus* spp. and a high prevalence of basidiomycetes in clone libraries. A total of 55% of the total diversity constituted of unidentifiable ITS sequences, some of which may represent novel fungal species. Dominant species were *Cladosporium cladosporioides* and *C. herbarum*, *Cryptococcus victoriae*, *Leptosphaerulina americana* and *L. chartarum*, *Aureobasidium pullulans*, *Thekopsora areolata*, *Phaeococcomyces nigricans*, *Macrophoma* sp., and several *Malassezia* species. Seasonal differences were observed for community composition, with ascomycetous molds and basidiomycetous yeasts predominating in the winter and spring and Agaricomycetidae basidiomycetes predominating in the fall. The comparison of methods suggested that the cloning, cultivation, and quantitative PCR methods complemented each other, generating a more comprehensive picture of fungal flora than any of the methods would give alone. The current restrictions of the methods are discussed.

Pitkäranta, Miia, Teija Meklin, Anne Hyvärinen, Aino Nevalainen, Lars Paulin, Petri Auvinen, Ulla Lignell and Helena Rintala, 2011. Molecular profiling of fungal communities in moisture damaged buildings before and after remediation - a comparison of culture-dependent and culture-independent methods. *BMC Microbiology* 2011, 11:235

Background: Indoor microbial contamination due to excess moisture is an important contributor to human illness in both residential and occupational settings. However, the census of microorganisms in the indoor environment is limited by the use of selective, culture-based detection techniques. By using clone library sequencing of full-length internal transcribed spacer region combined with quantitative polymerase chain reaction (qPCR) for 69 fungal species or assay groups and cultivation, we have been able to generate a more comprehensive description of the total indoor mycoflora. Using this suite of methods, we assessed the impact of moisture damage on the fungal community composition of settled dust and building material samples (n = 8 and 16, correspondingly). Waterdamaged buildings (n = 2) were examined pre- and post- remediation, and compared with undamaged reference buildings (n = 2). Results: Culture-dependent and independent methods were consistent in the dominant fungal taxa in dust, but sequencing revealed a five to ten times higher diversity at the genus level than culture or qPCR. Previously unknown, verified fungal phlotypes were detected in dust, accounting for 12% of all diversity. Fungal diversity, especially within classes Dothideomycetes and Agaricomycetes tended to be higher in the water damaged buildings. Fungal phlotypes detected in building materials were present in dust samples, but their proportion of total fungi was similar for damaged and reference buildings. The quantitative correlation between clone library phlotype frequencies and qPCR counts was moderate ( $r = 0.59$ ,  $p < 0.01$ ). Conclusions: We examined a small number of target buildings and found indications of elevated fungal diversity associated with water damage. Some of the fungi in dust were attributable to building growth, but more information on the material-associated communities is needed in order to understand the dynamics of microbial communities between building structures and dust. The sequencing-based method proved indispensable for describing the true fungal diversity in indoor environments. However, making conclusions concerning the effect of building conditions on building mycobiota using this methodology was complicated by the wide natural diversity in the dust samples, the incomplete knowledge of material-associated fungi and the semiquantitative nature of sequencing based methods

Posada J.A., J. Redrow, I. Celik, 2010. A mathematical model for predicting the viability of airborne viruses. *Journal of Virological Methods* 164 (2010) 88-95.

A mathematical model was developed to predict the viability of airborne viruses. The model uses water activity as the primary independent variable and an exponential decay function for the viability of the virus. This model was tested using published experimental data obtained by different investigators for influenza, Langkat and polio viruses. The aerosolized media were modelled as a binary solution of water and sodium chloride. The water activity is related directly to the solute concentration in the binary solution. The minimum viability usually occurred just above the efflorescence point, which is the relative humidity at which the solution crystallizes. The relationship between water activity and relative humidity is based on the Köhler theory, whereby the Kelvin term was taken into account. Physical explanations are provided on the variation of viral viability at different relative humidity levels. The predictions obtained by the proposed mathematical model compare well with most of the published experimental data

Poza M, Gayoso C, Gomez MJ, Rumbo-Feal S, Toma's M, et al. (2012) Exploring Bacterial Diversity in Hospital Environments by GS-FLX Titanium Pyrosequencing. *PLoS ONE* 7(8): e44105. doi:10.1371/journal.pone.0044105

Understanding microbial populations in hospital environments is crucial for improving human health. Hospital-acquired infections are an increasing problem in intensive care units (ICU). In this work we present an exploration of bacterial diversity at inanimate surfaces of the ICU wards of the University Hospital A Coruna (Spain), as an example of confined hospital environment subjected to selective pressure, taking the entrance hall of the hospital, an open and crowded environment, as reference. Surface swab samples were collected from both locations and recovered DNA used as template to amplify a hypervariable region of the bacterial 16S rRNA gene. Sequencing of the amplicons was performed at the Roche 454 Sequencing Center using GS-FLX Titanium procedures. Reads were pre-processed and clustered into OTUs (operational taxonomic units), which were further classified. A total of 16 canonical bacterial phyla were detected in both locations. Members of the phyla Firmicutes (mainly *Staphylococcus* and *Streptococcus*) and Actinobacteria (mainly *Micrococcaceae*, *Corynebacteriaceae* and *Brevibacteriaceae*) were over-represented in the ICU with respect to the Hall. The phylum Proteobacteria was also well represented in the ICU, mainly by members of the families *Enterobacteriaceae*, *Methylobacteriaceae* and *Sphingomonadaceae*. In the Hall sample, the phyla

Proteobacteria, Bacteroidetes, Deinococcus-Thermus and Cyanobacteria were over-represented with respect to the ICU. Over-representation of Proteobacteria was mainly due to the high abundance of Enterobacteriaceae members. The presented results demonstrate that bacterial diversity differs at the ICU and entrance hall locations. Reduced diversity detected at ICU, relative to the entrance hall, can be explained by its confined character and by the existence of antimicrobial selective pressure. This is the first study using deep sequencing techniques made in hospital wards showing substantial hospital microbial diversity.

Prasauskas, Tadas, Dainius Martuzevicius, Edvinas Krugly, Darius Ciuzas, Inga Stasiulaitiene, Ruta Sidaraviciute, Violeta Kauneliene, Lina Seduikyte, Andrius Jurelionis, Ulla Haverinen-Shaughnessy, 2014. Spatial and temporal variations of particulate matter concentrations in multifamily apartment buildings. *Building and Environment* 76 (2014) 10e17

We report a comprehensive assessment of PM concentrations and its variations in multifamily apartment buildings. Fifty apartments in ten multifamily buildings were investigated during heating seasons of 2011 and 2012 in Kaunas city, Lithuania. PM concentration and size distribution measurements were performed using the optical particle counters indoors and outdoors. Usually mean 24-h indoor PM concentrations were lower (median 7.8 mg/m<sup>3</sup> for PM<sub>2.5</sub>) than outdoor concentrations (median 16.9 mg/m<sup>3</sup> for PM<sub>2.5</sub>) of corresponding location, and I/O ratios of PM<sub>2.5</sub> were lower (0.70) than that of PM<sub>10</sub> (0.98). Night time levels, representing background indoor exposure to PM, were equal to 5.0 (PM<sub>2.5</sub>) and 6.7 mg/m<sup>3</sup> (PM<sub>10</sub>), respectively. Particle deposition rates were determined by regression fitting of the measured PM<sub>2.5</sub> concentration decay curves, with the median equal to 0.32 h<sup>-1</sup>. The data have been discussed aiming to characterize indoor PM sources and select the most representative indicator(s) for an assessment of the effects of energy saving refurbishment on indoor air quality. We found that a combination of several indicators allowed an adequate characterization of indoor PM sources and can be used in the subsequent assessment.

Removal of airborne particles in airborne infection isolation rooms is important for infection control of airborne diseases. Previous studies showed that the downward ventilation recommended by Centers for Disease Control and Prevention (CDC) could not produce the expected laminar flow for pushing down respiratory gaseous contaminants and removing them via floor-level exhausts. Instead, upper-level exhausts were more efficient in removing gaseous contaminants because of upward body plumes. The conventional wisdom in the current CDC-recommended design is that floor-level exhausts may efficiently remove large droplets/particles, but such a hypothesis has not been proven. We investigated the fate of respiratory particles in a full-scale six-bed isolation room with exhausts at different locations by both experimental and computational studies. Breathing thermal manikins were used to simulate patients, and both gaseous and large particles were used to simulate the expelled fine droplet nuclei and large droplets. Gaseous and fine particles were found to be removed more efficiently by ceiling-level exhausts than by floor-level exhausts. Large particles were mainly removed by deposition rather than by ventilation. Our results show that the existing isolation room ventilation design is not effective in removing both fine and large respiratory particles. An improved ventilation design is hence recommended.

Qian, Hua, Yuguo Li, W.H. Seto, Patricia Ching, W.H. Ching, H.Q. Sun, 2010b. Natural ventilation for reducing airborne infection in hospitals. *Building and Environment* 45 (2010) 559-565.

High ventilation rate is shown to be effective for reducing cross-infection risk of airborne diseases in hospitals and isolation rooms. Natural ventilation can deliver much higher ventilation rate than mechanical ventilation in an energy-efficient manner. This paper reports a field measurement of naturally ventilated hospital wards in Hong Kong and presents a possibility of using natural ventilation for infection control in hospital wards. Our measurements showed that natural ventilation could achieve high ventilation rates especially when both the windows and the doors were open in a ward. The highest ventilation rate recorded in our study was 69.0 ACH. The airflow pattern and the airflow direction were found to be unstable in some measurements with large openings. Mechanical fans were installed in a ward window to create a negative pressure difference. Measurements showed that the negative pressure difference was negligible with large openings but the overall airflow was controlled in the expected direction. When all the openings were closed and the exhaust fans were turned on, a reasonable negative pressure was created although the air temperature was uncontrolled. The high ventilation rate provided by natural ventilation can reduce cross-infection of airborne diseases, and thus it is recommended for consideration of use in appropriate hospital wards for infection

control. Our results also demonstrated a possibility of converting an existing ward using natural ventilation to a temporary isolation room through installing mechanical exhaust fans.

Qian, J., D. Hospodsky, N. Yamamoto, W. W. Nazaroff, J. Peccia, 2012. Size-resolved emission rates of airborne bacteria and fungi in an occupied classroom. *Indoor Air* 2012; 22: 339–351

The role of human occupancy as a source of indoor biological aerosols is poorly understood. Size-resolved concentrations of total and biological particles in indoor air were quantified in a classroom under occupied and vacant conditions. Per-occupant emission rates were estimated through a mass-balance modeling approach, and the microbial diversity of indoor and outdoor air during occupancy was determined via rDNA gene sequence analysis. Significant increases of total particle mass and bacterial genome concentrations were observed during the occupied period compared to the vacant case. These increases varied in magnitude with the particle size and ranged from 3 to 68 times for total mass, 12–2700 times for bacterial genomes, and 1.5–5.2 times for fungal genomes. Emission rates per person-hour because of occupancy were 31 mg,  $37 \times 10^6$  genome copies, and  $7.3 \times 10^6$  genome copies for total particle mass, bacteria, and fungi, respectively. Of the bacterial emissions, ~18% are from taxa that are closely associated with the human skin microbiome. This analysis provides size-resolved, per person-hour emission rates for these biological particles and illustrates the extent to which being in an occupied room results in exposure to bacteria that are associated with previous or current human occupants.

Quansah, Reginald, Maritta S. Jaakkola, Timo T. Hugg, Sirpa A. M. Heikkinen, Jouni J.K. Jaakkola, 2012. Residential Dampness and Molds and the Risk of Developing Asthma: A Systematic Review and Meta-Analysis. *PLoS ONE* 7(11): e47526. doi:10.1371/journal.pone.0047526

Recer GM. 2004. Long-term use of high-efficiency vacuum cleaners and residential airborne fungal-spore exposure. *Aerobiologia* 20(3-4):179-90.

Exposure to fungal allergens is an important contributor to allergic respiratory disease, but information on the efficacy of residential fungal allergen-avoidance in allergic-disease management is lacking. Using vacuum cleaners with high-efficiency exhaust filtration is one method recommended for reducing residential allergen exposure levels, but their use to reduce fungal-spore exposure levels has not been evaluated. To evaluate the effectiveness of high-efficiency vacuuming to control airborne fungal-spore levels, fungal bioaerosols were repeatedly assessed over the course of 10 months in homes randomly assigned to groups using either conventionally filtered (control) or high-efficiency-filtered vacuum cleaners for routine vacuum cleaning. Air samples were analyzed for three fungal-spore categories representing taxa with predominantly outdoor sources and one representing taxa that commonly have indoor sources. In a two-way analysis of variance, sampling period had a significant effect on mean levels of all fungal-spore categories. Vacuum cleaner type had a marginally significant effect on the indoor spore category, with one high-efficiency vacuum group mean (of three) significantly lower than one control mean. No effect was observed of vacuum cleaner type on outdoor spore categories. Including home-environment variables in analysis of covariance models strengthened the effect of the vacuum-type treatment on the indoor spore category, with no effect on the three outdoor spore categories. Decreased indoor spore levels vs. controls were only observed in high-efficiency vacuum groups during the last sampling period, at the end of the heating season. The results suggest that using a vacuum with high-efficiency filtered exhaust could have some modest effectiveness in controlling airborne fungal-spore exposure in homes when infiltration of outdoor air is very limited

Reis-Menezes, Adriana Araújo, Walderez Gambale, Mauro Cintra Giudice, 2011. A Survey of Fungal Contamination on Books in Public Libraries with Mechanical and Natural Ventilation. *Indoor Built Environ* 2011;000;000:1-7

Libraries are very propitious environments for the growth of fungi. The great concentration of organic material available for these microorganisms, and often with the lack of adequate ventilation or climate control, would favour this situation. This study was conducted in 2003 to determine the predominant genera of fungi in public libraries by a survey of fungi contaminating the upper surface of books, with and without air conditioning in the city of São Paulo, Brazil, in the winter and summer, during the respective periods with high and low levels of airborne fungi in that city. Six libraries

were chosen, located on the campus of the University of São Paulo, three of them with air conditioning and the other three with natural ventilation. In these six libraries, 31 genera of fungi were identified in total. The genera and frequency of contaminant fungi recovered differed significantly between the libraries with and without air conditioning and in the samples collected in the summer as opposed to the winter. *Cladosporium* was the most frequent in the libraries with and without air conditioning, and in the winter. *Aspergillus* was isolated more often in the summer.

Remold, Susanna K., Christopher K. Brown, Justin E. Farris, Thomas C. Hundley, Jessica A. Perpich & Megan E. Purdy, 2011. Differential Habitat Use and Niche Partitioning by *Pseudomonas* Species in Human Homes. *Microb Ecol* (2011) 62:505-517. DOI 10.1007/s00248-011-9844-5

Many species of *Pseudomonas* have the ability to use a variety of resources and habitats, and as a result *Pseudomonas* are often characterized as having broad fundamental niches. We questioned whether actual habitat use by *Pseudomonas* species is equally broad. To do this, we sampled extensively to describe the biogeography of *Pseudomonas* within the human home, which presents a wide variety of habitats for microbes that live in close proximity to humans but are not part of the human flora, and for microbes that are opportunistic pathogens, such as *Pseudomonas aeruginosa*. From 960 samples taken in 20 homes, we obtained 163 *Pseudomonas* isolates. The most prevalent based on identification using the Sepsitest BLAST analysis of 16S rRNA (<http://www.sepsitest-blast.de>) were *Pseudomonas monteilii* (42 isolates), *Pseudomonas plecoglossicida*, *Pseudomonas fulva*, and *P. aeruginosa* (approximately 25 each). Of these, all but *P. fulva* differed in recovery rates among evaluated habitat types (drains, soils, water, internal vertebrate sites, vertebrate skin, inanimate surfaces, and garbage/compost) and all four species also differed in recovery rates among subcategories of habitat types (e.g., types of soils or drains). We also found that at both levels of habitat resolution, each of these six most common species (the four above plus *Pseudomonas putida* and *Pseudomonas oryzae*) were over- or underrepresented in some habitats relative to their contributions to the total *Pseudomonas* collected across all habitats. This pattern is consistent with niche partitioning. These results suggest that, whereas *Pseudomonas* are often characterized as generalists with broad fundamental niches, these species in fact have more restricted realized niches. Furthermore, niche partitioning driven by competition among *Pseudomonas* species may be contributing to the observed variability in habitat use by *Pseudomonas* in this system.

Reponen, Tiina, Stephen Vesper, Linda Levin, Elisabet Johansson, Patrick Ryan, Jeffery Burkle, Sergey A. Grinshpun, Shu Zheng, David I. Bernstein, James Lockey, Manuel Villareal, Gurjit K. Khurana Hershey, and Grace LeMasters, 2011. High environmental relative moldiness index during infancy as a predictor of asthma at 7 years of age. *Ann Allergy Asthma Immunol*. 2011;107:120 -126.

Background: Mold exposures may contribute to the development of asthma, but previous studies have lacked a standardized approach to quantifying exposures. Objective: To determine whether mold exposures at the ages of 1 and/or 7 years were associated with asthma at the age of 7 years. Methods: This study followed up a high-risk birth cohort from infancy to 7 years of age. Mold was assessed by a DNA-based analysis for the 36 molds that make up the Environmental Relative Moldiness Index (ERMI) at the ages of 1 and 7 years. At the age of 7 years, children were evaluated for allergic sensitization and asthma based on symptom history, spirometry, exhaled nitric oxide, and airway reversibility. A questionnaire was administered to the parent regarding the child's asthma symptoms and other potential cofactors. Results: At the age of 7 years, 31 of 176 children (18%) were found to be asthmatic. Children living in a high ERMI value (5.2) home at 1 year of age had more than twice the risk of developing asthma than those in low ERMI value homes (1.5) (adjusted odds ratio [aOR], 2.6; 95% confidence interval [CI], 1.10-6.26). Of the other covariates, only parental asthma (aOR, 4.0; 95% CI, 1.69-9.62) and allergic sensitization to house dust mite (aOR, 4.1; 95% CI, 1.55-11.07) were risk factors for asthma development. In contrast, air-conditioning at home reduced the risk of asthma development (aOR, 0.3; 95% CI, 0.14-0.83). A high ERMI value at 7 years of age was not associated with asthma at 7 years of age. Conclusions: Early exposure to molds as measured by ERMI at 1 year of age, but not 7 years of age, significantly increased the risk for asthma at 7 years of age.

REYNOLDS, KELLY A., PAMELA M. WATT, STEPHANIE A. BOONE, & CHARLES P. GERBA, 2005. Occurrence of bacteria and biochemical markers on public Surfaces. *International Journal of Environmental Health Research* June 2005; 15(3): 225 - 234.

From 1999 - 2003, the hygiene of 1061 environmental surfaces from shopping, daycare, and office environments, personal items, and miscellaneous activities (i.e., gymnasiums, airports, movie theaters, restaurants, etc.), in four US cities, was monitored. Samples were analyzed for fecal and total coliform bacteria, protein, and biochemical markers. Biochemical markers, i.e., hemoglobin (blood marker), amylase (mucus, saliva, sweat, and urine marker), and urea (urine and sweat marker) were detected on 3% (26/801); 15% (120/801), and 6% (48/801) of the surfaces, respectively. Protein (general hygiene marker) levels 5200 mg/10 cm<sup>2</sup> were present on 26% (200/801) of the surfaces tested. Surfaces from children's playground equipment and daycare centers were the most frequently contaminated (biochemical markers on 36%; 15/42 and 46%; 25/54, respectively). Surfaces from the shopping, miscellaneous activities, and office environments were positive for biochemical markers with a frequency of 21% (69/333), 21% (66/308), and 11% (12/105), respectively). Sixty samples were analyzed for biochemical markers and bacteria. Total and fecal coliforms were detected on 20% (12/60) and 7% (4/60) of the surfaces, respectively. Half and one-third of the sites positive for biochemical markers were also positive for total and fecal coliforms, respectively. Artificial contamination of public surfaces with an invisible fluorescent tracer showed that contamination from outside surfaces was transferred to 86% (30/35) of exposed individual's hands and 82% (29/35) tracked the tracer to their home or personal belongings hours later. Results provide information on the relative hygiene of commonly encountered public surfaces and aid in the identification of priority environments where contaminant occurrence and risk of exposure may be greatest. Children's playground equipment is identified as a priority surface for additional research on the occurrence of and potential exposure to infectious disease causing agents

Rintala, Helena, Miia Pitkäranta, Mika Toivola, Lars Paulin and Aino Nevalainen, 2008. Diversity and seasonal dynamics of bacterial community in indoor environment. *BMC Microbiology* 2008, 8:56 doi:10.1186/1471-2180-8-56.

Background: We spend most of our lives in indoor environments and are exposed to microbes present in these environments. Hence, knowledge about this exposure is important for understanding how it impacts on human health. However, the bacterial flora in indoor environments has been only fragmentarily explored and mostly using culture methods. The application of molecular methods previously utilised in other environments has resulted in a substantial increase in our awareness of microbial diversity. Results: The composition and dynamics of indoor dust bacterial flora were investigated in two buildings over a period of one year. Four samples were taken in each building, corresponding to the four seasons, and 16S rDNA libraries were constructed. A total of 893 clones were analysed and 283 distinct operational taxonomic units (OTUs) detected among them using 97% sequence similarity as the criterion. All libraries were dominated by Gram-positive sequences, with the most abundant phylum being Firmicutes. Four OTUs having high similarity to *Corynebacterium*-, *Propionibacterium*-, *Streptococcus*- and *Staphylococcus* sequences were present in all samples. The most abundant of the Gram-negative OTUs were members of the family Sphingomonadaceae, followed by Oxalobacteraceae, Comamonadaceae, Neisseriaceae and Rhizobiaceae. The relative abundance of alpha- and betaproteobacteria increased slightly towards summer at the expense of firmicutes. The proportion of firmicutes and gammaproteobacteria of the total diversity was highest in winter and that of actinobacteria, alpha- and betaproteobacteria in spring or summer, whereas the diversity of bacteroidetes peaked in fall. A statistical comparison of the libraries revealed that the bacterial flora of the two buildings differed during all seasons except spring, but differences between seasons within one building were not that clear, indicating that differences between the buildings were greater than the differences between seasons. Conclusion: This work demonstrated that the bacterial flora of indoor dust is complex and dominated by Gram-positive species. The dominant phylotypes most probably originated from users of the building. Seasonal variation was observed as proportional changes of the phyla and at the species level. The microflora of the two buildings investigated differed statistically and differences between the buildings were more pronounced than differences between seasons.

Rohmann K, Tschernig T, Pabst R, Goldmann T, Droemann D. 2011. Innate immunity in the human lung: Pathogen recognition and lung disease RID E-5906-2010. *Cell Tissue Res* 343(1):167-74

As the human lung is exposed to a variety of microbial pathogens in the environment, a first line of defense is built up by pulmonary cells like bronchial/alveolar epithelial cells and alveolar macrophages. These cells express several pattern recognition receptors (PRRs) recognizing highly conserved microbial motifs and initiating the production of chemokines and pro- and anti-inflammatory cytokines acting as transmembrane or intracellular receptors. This might not only lead to acute but also to chronic inflammation which is discussed as an underlying mechanism in the pathogenesis of different lung diseases

Rook, Graham A.W. and John L. Stanford, 2008. Give us this day our daily germ. *Immunology Today*, Vol. 19 No. 3, pp. 113-116

Modern vaccinations, fear of germs and obsession with hygiene are depriving the immune system of the information input upon which it is dependent. This fails to maintain the correct cytokine balance and fine-tune T-cell regulation, and may lead to increased incidences of allergies and autoimmune diseases. If humans continue to deprive their immune systems of the input to which evolution has adapted it, it may be necessary to devise ways of replacing it artificially.

Rook, Graham A. W., 2009. Review series on helminths, immune modulation and the hygiene hypothesis: The broader implications of the hygiene hypothesis. *Immunology*, 126, 3-11, doi:10.1111/j.1365-2567.2008.03007.x

Man has moved rapidly from the hunter-gatherer environment to the living conditions of the rich industrialized countries. The hygiene hypothesis suggests that the resulting changed and reduced pattern of exposure to microorganisms has led to disordered regulation of the immune system, and hence to increases in certain inflammatory disorders. The concept began with the allergic disorders, but there are now good reasons for extending it to autoimmunity, inflammatory bowel disease, neuroinflammatory disorders, atherosclerosis, depression associated with raised inflammatory cytokines, and some cancers. This review discusses these possibilities in the context of Darwinian medicine, which uses knowledge of evolution to cast light on human diseases. The Darwinian approach enables one to correctly identify some of the organisms that are important for the 'Hygiene' or 'Old Friends' hypothesis, and to point to the potential exploitation of these organisms or their components in novel types of prophylaxis with applications in several branches of medicine.

Rosenthal, Mariana, Deborah Goldberg, Allison Aiello, Elaine Larson, Betsy Foxman, 2011. Skin microbiota: Microbial community structure and its potential association with health and disease. *Infection, Genetics and Evolution* 11 (2011) 839–848

Skin, the largest human organ, is a complex and dynamic ecosystem inhabited by a multitude of microorganisms. Host demographics and genetics, human behavior, local and regional environmental characteristics, and transmission events may all potentially drive human skin microbiota variability, resulting in an alteration of microbial community structure. This alteration may have important consequences regarding health and disease outcomes among individuals. More specifically, certain diversity patterns of human microbiota may be predictive or diagnostic of disease. The purpose of this review is to briefly describe the skin microbiota, outline the potential determining factors driving its variability, posit the likelihood of an association between the resulting microbial community structure on the skin with disease outcomes among individuals, and finally, to present some challenges and implications for studying the skin microbiota

Roth, R. and W. James, 1988. Microbial Ecology of the Skin. *Ann. Rev. Microbiol.* 42:441-64.

Normal human skin is colonized by large numbers of organisms that live harmlessly as commensals on its surface. Of the many different species of microorganisms found in nature, only a few species are found repeatedly on the skin of groups of individuals. This is surprising considering the large variety of organisms found in other areas such as the gastrointestinal tract. These frequently found organisms constitute the resident flora of the skin.

Roussel, S., Reboux, G., Millon, L., Parchas, M.-D., Boudih, S., Skana, F., Delaforge, M. and Rakotonirainy, M. S. (2012), Microbiological evaluation of ten French archives and link to occupational symptoms. *Indoor Air*, 22: 514-522. doi: 10.1111/j.1600-0668.2012.00781.x

Abstract Fungi that damage documents in archives may harm workers health, depending on which mold species are inhaled, the concentrations of fungal species inhaled, and individual factors. Our aim was to identify and quantify fungi in archives and to investigate possible links with the symptoms experienced by workers. Ten French archives were sampled using an air impactor and electrostatic dust collectors. Allergies and general symptoms felt by 144 workers were reported using a self-report questionnaire. Utilizing culture-based analysis methods along with qPCR, *Penicillium chrysogenum*, *Cladosporium sphaerospermum*, and *Aspergillus versicolor* were the three main fungi in air and dust in



terms of quantity and frequency. Median fungal concentrations in storage areas, ranged from 30 to 465 CFU/m<sup>3</sup>. People working in the most contaminated archives did not report more symptoms of allergy than others. However, workers in contact with moldy documents reported more headaches (odds ratio, 2.4; 95% confidence interval, 1.1-5.3), fatigue (OR, 2.9; 95% CI, 1.2-6.7), eye irritation (OR, 5.4; 95% CI, 1.9-14.9), throat irritation (OR, 2.4; 95% CI, 1.0-5.7), coughing (OR, 3.2; 95% CI, 1.2-8.4), and rhinorrhea (OR, 2.6; 95% CI, 1.0-6.4) than others. Other parameters such as dust levels and concentrations of metabolites and chemical substances should be considered as confounding factors in further investigations to isolate the role of molds.

Roy, C.J. and D.K. Milton, 2004. Airborne Transmission of Communicable Infection - The Elusive Pathway. *NEJM*, 350:17, pp. 1710-1712

What does it mean to describe an infection as airborne and what are the clinical implications? The concept of the air we breathe as a reservoir for disease-causing agents harkens back to the pre-Pasteur teachings of "miasmatic-induced disease" of Sir Edwin Chadwick. Modern germ theory largely rejects the vague concepts of airborne vapors as a cause of disease, and has focused on obvious transmission patterns of infectious agents from the source to a susceptible host. Observable mechanisms of transmission such as contaminated water, direct surface contact, and large droplet sprays, can all be validated as means of disease communicability. In addition, many of the aerosol-transmitted disease agents such as smallpox and measles have been effectively eliminated or controlled through aggressive preventive and primary care of the last century. As a result, the aerobiological basis of disease transmission has faded somewhat into the more obscure theoretical milieu. Only tuberculosis frequently defied directly observable transmission by close contact. Thanks largely to the work of William Wells and Richard Riley, we now know that tuberculosis is naturally transmitted only by the airborne route. But proof of airborne transmission was an arduous task, requiring continual exposure of a guinea pig colony to active tuberculosis cases in a clinical ward. Only after satisfying Koch's postulate by demonstrating disease agent transmission from the infected patient to a naive animal, was there recognition that tuberculosis was, in fact, an airborne-acquired disease. This article reviews the possible airborne transmission of acute respiratory system (SARS) at the Amoy Gardens apartment complex in Hong Kong. The SARS epidemic provides an opportunity for the critical reevaluation of the aerosol transmission of communicable respiratory diseases

Rudge, J. and R. Gilchrist, 2007. Measuring the health impact of temperatures in dwellings: Investigating excess winter morbidity and cold homes in the London Borough of Newham. *Energy and Buildings* 39 (2007) 847-858

Fossil fuel energy use in heating and cooling buildings is considered to be a major contributor to observed climate change effects, so there is an environmental imperative to reduce energy use in buildings. We should also improve buildings' energy efficiency on health grounds. Climate change is predicted to produce more frequent extreme weather events, while epidemiological evidence indicates relationships between ambient temperature and ill health. This points to the need for addressing both climate change itself and the way buildings mediate outdoor conditions, for the sake of vulnerable occupants. The UK government requires evidence in support of policy-making concerning energy use in buildings and consequences for health. This paper reviews epidemiological research to illustrate problems associated with measuring the direct health impact of indoor temperatures, for which evidence remains limited. Conventionally, temperature-related health effects are discussed in terms of seasonal excess deaths. The paper goes on to describe a population-based study in London that considers morbidity rather than mortality. A new methodology is developed that links the risk of cold homes with excess winter hospital episodes, demonstrating its potential for identifying small areas for priority action on improving domestic energy efficiency in terms of health as well as the environment.

Russell, ML, R Goth-Goldstein, MG Apte and WJ Fisk, 2002. METHOD FOR MEASURING THE SIZE DISTRIBUTION OF AIRBORNE RHINOVIRUS. *Proceedings: Indoor Air 2002*.

About 50% of viral-induced respiratory illnesses are caused by the human rhinovirus (HRV). Measurements of the concentrations and sizes of bioaerosols are critical for research on building characteristics, aerosol transport, and mitigation measures. We developed a quantitative reverse transcription-coupled polymerase chain reaction (RT-PCR) assay for HRV and verified that this assay detects HRV in nasal lavage samples. A quantitation standard was used to determine a detection limit of 5 fg of HRV RNA with a linear range over 1000-fold. To measure the size distribution of HRV aerosols, volunteers with a head cold spent two hours in a ventilated research chamber. Airborne particles from the

chamber were collected using an Andersen Six-Stage Cascade Impactor. Each stage of the impactor was analyzed by quantitative RT-PCR for HRV. For the first two volunteers with confirmed HRV infection, but with mild symptoms, we were unable to detect HRV on any stage of the impactor.

Sahakian, N., J.-H. Park, J. Cox-Ganser, 2009. Respiratory Morbidity and Medical Visits Associated with Dampness and Air-conditioning in Offices and Homes. *Indoor Air* 2009; 19: 58-67

We used data from 4345 adult US residents who were part of a 2004 national random mail survey to investigate associations between dampness and air-conditioning (AC) in homes and offices, and health outcomes, sick leave due to respiratory symptoms and medical visits during the past 12 months. We identified from this group 1396 office workers employed in professional, executive, administrative, managerial or administrative support occupations. Office workers reporting home dampness had an elevated prevalence of nasal symptoms [prevalence ratio (PR) = 1.4, P = 0.01] and constitutional symptoms (PR = 1.3, P = 0.01) in the previous year. Office workers reporting workplace dampness had an elevated prevalence of sick leave attributed to respiratory symptoms (PR = 1.3, P = 0.04) in the previous year. Office workers with home AC were more likely to have visited a medical specialist in the previous year (PR = 1.3, P = 0.02). We did not find any statistically significant associations between workplace AC and any of the health outcomes. We estimated an annual cost of US\$1.4 billion for excess respiratory-related sick leave among office workers with workplace dampness. Our study strengthens the evidence of a relationship between dampness and health effects, and highlights the resulting economic impact.

Said, Maria A., Trish M. Perl, and Cynthia L. Sears, 2008. Gastrointestinal Flu: Norovirus in Health Care and Long-Term Care Facilities. *HEALTHCARE EPIDEMIOLOGY*, November 1, pp. 1202 - 1208.

Noroviruses, recognized as the leading global cause of viral gastroenteritis and a major contributor to food-borne illness, present a growing challenge in health care and long-term care facilities. The virus spreads easily and by multiple routes. A visitor to a ward might initiate an outbreak by person-to-person contact, vomiting staff members or patients can disseminate the virus by airborne means, and contaminated surfaces, such as doorknobs and computer keyboards, can sustain an epidemic. In addition, although self-limited in healthy hosts, the virus can cause increased morbidity in more-vulnerable people. The GII.4 strain of the virus now dominates in multiple recent worldwide epidemics as well as in health care and long-term care facilities. Much like the influenza virus, norovirus appears to evolve by antigenic drift and evading the immune system, causing waves of global epidemics. Previous attempts at controlling outbreaks, both in the community and in closed facilities, provide guidance about the vigilance and action required by the health care community to diminish the clinical impact of norovirus infection.

Saijo, Y., A. Kanazawa, A. Araki, K. Morimoto, K. Nakayama, T. Takigawa, M. Tanaka, E. Shibata, T. Yoshimura, H. Chikara, R. Kishi. 2010. Relationships between mite allergen levels, mold concentrations, and sick building syndrome symptoms in newly built dwellings in Japan. *Indoor Air* 2011; 21: 253–263

This study investigated the possible relationships between exposures to mite allergen and airborne fungi with sick building syndrome (SBS) symptoms for residents living in newly built dwellings. We randomly sampled 5709 newly built dwellings in six prefectures from northern to southern Japan. A total of 1479 residents in 425 households participated in the study by completing questionnaire surveys and agreeing to environmental monitoring for mite allergen (Der 1), airborne fungi, aldehydes, and volatile organic compounds. Stepwise logistic regression analyses adjusted for confounders were used to obtain odds ratios (OR) of mite allergen and fungi for SBS symptoms. Der 1 had a significantly high OR for nose symptoms. *Rhodotorula* had a significantly high OR for any symptoms, and *Aspergillus* had significantly high OR for eye symptoms. However, the total colony-forming units had a significantly low OR for throat and respiratory symptoms. *Eurotium* had a significantly low OR for skin symptoms. In conclusion, dust-mite allergen levels and indoor airborne *Rhodotorula* and *Aspergillus* concentrations may result in SBS symptoms in newly built dwellings

Sakuragi, Yumiko and Roberto Kolter 2007. Quorum-Sensing Regulation of the Biofilm Matrix Genes (*pel*) of *Pseudomonas aeruginosa*. *J Bacteriology* 18: 5383-5386.

Quorum sensing (QS) has been previously shown to play an important role in the development of *Pseudomonas aeruginosa* biofilms (D. G. Davies et al., *Science* 280:295–298, 1998). Although QS regulation of swarming and DNA

release has been shown to play important roles in biofilm development, regulation of genes directly involved in biosynthesis of biofilm matrix has not been described. Here, transcription of the *pel* operon, essential for the production of a glucose-rich matrix exopolysaccharide, is shown to be greatly reduced in *lasI* and *rhII* mutants. Chemical complementation of the *lasI* mutant with 3-oxo-dodecanoyl homoserine lactone restores *pel* transcription to the wild-type level and biofilm formation ability. These findings thus connect QS signaling and transcription of genes responsible for biofilm matrix biosynthesis

Salares, Virginia R., Carol Ann Hinde J. David Miller, 2009. Analysis of Settled Dust in Homes and Fungal Glucan in Air Particulate Collected during HEPA Vacuuming. *Indoor Built Environ* 2009;18;6:485–491

Six occupied single-family dwellings in Ottawa, Canada were subjected to weekly or bi-weekly professional cleaning using a HEPA filter-equipped vacuum cleaner and following a strict cleaning protocol based on floor area and type of floor. Sieved weights of dust were collected from each cleaning. Statistically significant reductions of fine dust loading occurred only after four sequential cleanings. As dust loading of the floor was reduced, exposure to dust mite allergens, endotoxins, and fungal glucans in dust decreased. During the first cleaning (when loadings were highest), airborne particles were collected using a MOUDI sampler (0.18–18 mm size fractions). The fungal polysaccharide  $\beta$ -(1,3)-D-glucan was present in approximately equal proportions in each size fraction. This demonstrates that the majority of the fungal exposure was not to intact spores, but to fungal fragments much smaller than spores that have greater efficiency of deeper penetration into the lungs. This study also shows the importance of ensuring that cleaning interventions are effective before they can be related to health outcomes.

Sanchez-Silva, M. and David V. Rosowsky, 2008. Biodeterioration of Construction Materials: State of the Art and Future Challenges. *Journal of Materials in Civil Engineering*, Vol. 20, No. 5, 352-365.

Deterioration plays an important part in the life cycle of infrastructure systems. Among all causes of deterioration aging, chloride ingress, etc. the action of live organisms has shown to be critical in, for example, underground structures, sewage systems, and at-sea structures. This phenomenon is usually overlooked, in part, because in most cases live organisms accelerate other processes that may eventually lead to unacceptable structural performance or cause failure e.g., corrosion, cracking. By the direct or indirect action, it has been estimated that biodeterioration-related structural problems cost billions of dollars a year in infrastructure maintenance and repair. The paper shows that for all major civil engineering materials, in the long term and under the appropriate environmental conditions, biodeterioration may severely affect infrastructure components and their ability to perform as designed. This is particularly relevant given the large amount of existing infrastructure that has been exposed to aggressive environments for long periods of time. This paper presents an overview of the activity of live organisms on three widely used construction materials: wood, concrete, and metals. A description of the main organisms that affect each material and the associated biodeterioration mechanisms are described. In addition, this paper discusses the uncertainties associated with modeling biodeterioration and outlines the main areas for further research.

Schäfer, Jenny, Udo Jäckel, Peter Kämpfer, 2010. Analysis of Actinobacteria from mould-colonized water damaged building material. *Systematic and Applied Microbiology* 33: 260-268.

Mould-colonized water damaged building materials are frequently co-colonized by actinomycetes. Here, we report the results of the analyses of Actinobacteria on different wall materials from water damaged buildings obtained by both cultivation-dependent and cultivation-independent methods. Actinobacteria were detected in all but one of the investigated materials by both methods. The detected concentrations of Actinobacteria ranged between  $1.8 \times 10^4$  and  $7.6 \times 10^7$  CFU g<sup>-1</sup> of investigated material. A total of 265 isolates from 17 materials could be assigned to 31 different genera of the class Actinobacteria on the basis of 16S rRNA gene sequence analyses. On the basis of the cultivation-independent approach, 16S rRNA gene inserts of 800 clones (50%) were assigned to 47 different genera. Representatives of the genera *Streptomyces*, *Amycolatopsis*, *Nocardia*, *Saccharopolyspora*, *Promicromonospora*, and *Pseudonocardia* were found most frequently. The results derived from both methods indicated a high abundance and variety of Actinobacteria in water damaged buildings. Four bioaerosol samples were investigated by the cultivation-based approach in order to compare the communities of Actinobacteria in building material and associated air samples. A comparison of the detected genera of bioaerosol samples with those directly obtained from material samples resulted

in a congruent finding of 9 of the overall 35 detected genera (25%), whereas four genera were only detected in bioaerosol samples.

Schmidt, Michael G., Hubert H. Attaway, Silva Terzieva, Anna Marshall, Lisa L. Steed, Deborah Salzberg, Hameed A. Hamoodi, Jamil A. Khan, Charles E. Feigley, Harold T. Michels, 2012. Characterization and Control of the Microbial Community Affiliated with Copper or Aluminum Heat Exchangers of HVAC Systems. *Curr Microbiol* (2012) 65:141–149

Microbial growth in heating ventilation and airconditioning (HVAC) systems with the subsequent contamination of indoor air is of increasing concern. Microbes and the subsequent biofilms grow easily within heat exchangers. A comparative study where heat exchangers fabricated from antimicrobial copper were evaluated for their ability to limit microbial growth was conducted using a full-scale HVAC system under conditions of normal flow rates using single-pass outside air. Resident bacterial and fungal populations were quantitatively assessed by removing triplicate sets of coupons from each exchanger commencing the fourth week after their installation for the next 30 weeks. The intrinsic biofilm associated with each coupon was extracted and characterized using selective and differential media. The predominant organisms isolated from aluminum exchangers were species of *Methylobacterium* of which at least three colony morphologies and 11 distinct PFGE patterns we found; of the few bacteria isolated from the copper exchangers, the majority were species of *Bacillus*. The concentrations and type of bacteria recovered from the control, aluminum, exchangers were found to be dependent on the type of plating media used and were 11,411–47,257 CFU cm<sup>-2</sup> per coupon surface. The concentration of fungi was found to average 378 CFU cm<sup>-2</sup>. Significantly lower concentrations of bacteria, 3 CFU cm<sup>-2</sup>, and fungi, 1 CFU cm<sup>-2</sup>, were recovered from copper exchangers regardless of the plating media used. Commonly used aluminum heat exchangers developed stable, mixed, bacterial/fungal biofilms in excess of 47,000 organisms per cm<sup>2</sup> within 4 weeks of operation, whereas the antimicrobial properties of metallic copper were able to limit the microbial load affiliated with the copper heat exchangers to levels 99.97 % lower during the same time period.

Scott, Elizabeth, Susan Duty, and Karen McCue, 2009. A critical evaluation of methicillin-resistant *Staphylococcus aureus* and other bacteria of medical interest on commonly touched household surfaces in relation to household demographics. *Am J Infect Control* 2009;37:447-53

Background: We sought to characterize and quantify bacteria of medical interest on commonly touched household surfaces and to evaluate predictors such as employment, day care attendance, and presence of infants and pets. Methods: A convenience sample of 35 homes was recruited from the metro-Boston area, and 32 surfaces were sampled in kitchens, bathrooms, and living areas. Results: Highest bacterial counts were associated with wet sites including hand/skin contact surfaces such as the tub, kitchen sink, and faucet handles. Surfaces were found to be contaminated with the bacteria of medical interest including species of *Enterobacteriaceae*, *Pseudomonas*, methicillin-sensitive *Staphylococcus aureus* (MSSA), and methicillin-resistant *Staphylococcus aureus* (MRSA). Conclusion: A number of hand/skin contact surfaces were found to be frequently contaminated with one or more of the bacteria of medical interest. The presence of a cat in the home was found to be a strong predictor for the isolation of MRSA. This study provides further insight about microorganisms of medical interest on surfaces in American homes and the impact of factors that can influence bacterial contamination. The study may indicate that cleaning in private homes should be directed to the areas pinpointed by the Study as very rich in bacteria of potential medical importance.

Scott, James, 2012. An evolving architecture: The past, present & future of indoor microbiology. Keynote address at the IAQA 15th Annual Meeting and Indoor Air Expo, Las Vegas, NV March 5-7, 2012

In this presentation I will discuss the microbiology of the built environment, its history, current state of knowledge and its future with specific reference to the limitations of sampling and analytical methods. In turn, I'll outline how these factors have influenced our knowledge of the microbiology of the built environment as a determinant of health.

Shaman, Jeffrey and Melvin Kohn, 2009. Absolute humidity modulates influenza survival, transmission, and seasonality. *PNAS*, early edition.

Influenza A incidence peaks during winter in temperate regions. The basis for this pronounced seasonality is not understood, nor is it well documented how influenza A transmission principally occurs. Previous studies indicate that

relative humidity (RH) affects both influenza virus transmission (IVT) and influenza virus survival (IVS). Here, we reanalyze these data to explore the effects of absolute humidity on IVT and IVS. We find that absolute humidity (AH) constrains both transmission efficiency and IVS much more significantly than RH. In the studies presented, 50% of IVT variability and 90% of IVS variability are explained by AH, whereas, respectively, only 12% and 36% are explained by RH. In temperate regions, both outdoor and indoor AH possess a strong seasonal cycle that minimizes in winter. This seasonal cycle is consistent with a wintertime increase in IVS and IVT and may explain the seasonality of influenza. Thus, differences in AH provide a single, coherent, more physically sound explanation for the observed variability of IVS, IVT and influenza seasonality in temperate regions. This hypothesis can be further tested through future, additional laboratory, epidemiological and modeling studies.

Shelton et al 2002, Profiles of Airborne Fungi in Buildings and Outdoor Environments in the United States, Applied And Environmental Microbiology, Apr. 2002, p. 1743-1753

We examined 12,026 fungal air samples (9,619 indoor samples and 2,407 outdoor samples) from 1,717 buildings located across the United States; these samples were collected during indoor air quality investigations performed from 1996 to 1998. For all buildings, both indoor and outdoor air samples were collected with an Andersen N6 sampler. The culturable airborne fungal concentrations in indoor air were lower than those in outdoor air. The fungal levels were highest in the fall and summer and lowest in the winter and spring. Geographically, the highest fungal levels were found in the Southwest, Far West, and Southeast. The most common culturable airborne fungi, both indoors and outdoors and in all seasons and regions, were *Cladosporium*, *Penicillium*, nonsporulating fungi, and *Aspergillus*. *Stachybotrys chartarum* was identified in the indoor air in 6% of the buildings studied and in the outdoor air of 1% of the buildings studied. This study provides industrial hygienists, allergists, and other public health practitioners with comparative information on common culturable airborne fungi in the United States. This is the largest study of airborne indoor and outdoor fungal species and concentrations conducted with a standardized protocol to date.

Simmons, Robert B., Laura J. Rose, Sidney A. Crow, Donald G. Ahearn, 1999. The Occurrence and Persistence of Mixed Biofilms in Automobile Air Conditioning Systems. CURRENT MICROBIOLOGY Vol. 39 (1999), pp. 141-145

Abstract. Twelve automobile air conditioner systems from six manufacturers and three countries, selected mostly because of complaints of unpleasant odors in the passenger compartment, were examined for microbial growth by direct microscopy and enrichment culture. Mixed populations of fungi and bacteria (with occasional protozoa) were observed in biofilms in at least some of the components from all used units. The aluminum heat exchanger fins from ten evaporators demonstrated bacterial biofilms that yielded *Methylobacterium mesophilicum*. *Penicillium viridicatum* colonized components from four units. These bacteria and fungi were recoverable repeatedly from these units during 'dry' storage of up to 27 months. This report associates a bacterial-fungal community with disagreeable air quality in some automobiles.

Simoni, M., I. Annesi-Maesano, T. Sigsgaard, D. Norback, G. Wieslander, W. Nystad, M. Cancianie, P. Sestini and G. Viegi, 2010. School air quality related to dry cough, rhinitis and nasal patency in children. Eur Respir J 2010; 35: 742-749.

Controls for indoor air quality (IAQ) in schools are not usually performed throughout Europe. The aim of this study was to assess the effects of IAQ on respiratory health of schoolchildren living in Norway, Sweden, Denmark, France and Italy. In the cross-sectional European Union-funded HESE (Health Effects of School Environment) Study, particulate matter with a 50% cut-off aerodynamic diameter of 10  $\mu\text{m}$  (PM<sub>10</sub>) and CO<sub>2</sub> levels in a day of normal activity (full classroom) were related to wheezing, dry cough at night and rhinitis in 654 children (10 yrs) and to acoustic rhinometry in 193 children. Schoolchildren exposed to PM<sub>10</sub> > 50  $\mu\text{g m}^{-3}$  and CO<sub>2</sub> >1,000 ppm (standards for good IAQ) were 78% and 66%, respectively. All disorders were more prevalent in children from poorly ventilated classrooms. Schoolchildren exposed to CO<sub>2</sub> levels > 1,000 ppm showed a significantly higher risk for dry cough (OR 2.99, 95% CI 1.65-5.44) and rhinitis (OR 2.07, 95% CI 1.14-3.73). By two-level (child, classroom) hierarchical analyses, CO<sub>2</sub> was significantly associated with dry cough (OR 1.06, 95% CI 1.00-1.13 per 100 ppm increment) and rhinitis (OR 1.06, 95% CI 1.00- 1.11). Nasal patency was significantly lower in schoolchildren exposed to PM<sub>10</sub> > 50  $\mu\text{g m}^{-3}$  than in those exposed to lower levels. A poor IAQ is frequent in European classrooms; it is related to respiratory disturbances and affects nasal patency.

Sinclair, J.D., Psota-Kelty, L.A., Weschler, C.J. and Shields, H.C., 1990. Measurement and Modeling of Airborne Concentrations and Indoor Surface Accumulation Rates of Ionic Substances at Neenah, Wisconsin. *Atmospheric Environment*, Vol. 24A, No. 3, pp. 627-638.

The objective of this continuing investigation of indoor/outdoor/surface relationships has been to develop an accurate method for predicting and subsequently managing the accumulation rates and ultimately the effects of corrosive substances on electronic equipment surfaces in field and manufacturing environments. We previously reported indoor/outdoor ratios and deposition velocities for Cl<sup>-</sup>, SO<sub>4</sub><sup>2-</sup>, Na<sup>+</sup>, NH<sub>4</sub><sup>+</sup>, K<sup>+</sup>, Mg<sup>2+</sup> and Ca<sup>2+</sup> associated with fine and coarse particles at telephone company switching equipment locations in Wichita (Kansas), Lubbock (Texas) and Newark (New Jersey). Using the results from these studies, a methodology was developed for predicting the average indoor surface accumulation rates of ionic substances from their outdoor concentrations. In this paper we report new results for a site at Neenah, Wisconsin. At this site detailed data on the operational status of the air handling equipment were also obtained through a permanent monitoring system. These data and the data on ionic species have been used in a mass balance model that calculates indoor concentrations from outdoor concentrations. Coupling this mass balance model with the measured deposition velocities substantially improves the earlier methodology for predicting surface accumulation rates from outdoor concentrations and enables decision makers to evaluate the effects of various manipulations in critical air handling system operating variables. Informed decisions can now be made when striking a balance between energy use and indoor air quality or equipment reliability.

Sloan, Chantel, Ph.D., Martin L. Moore, Ph.D., Tina Hartert, M.D., M.P.H., 2010. Impact of Pollution, Climate, and Sociodemographic Factors on Spatiotemporal Dynamics of Seasonal Respiratory Viruses. *CTS*, VOLUME 40 ISSUE 1, pp. 48-54.

Seasonal viruses present a major cause of morbidity and mortality in temperate climates. Through major pandemics and smaller annual epidemics, viruses such as influenza, respiratory syncytial virus (RSV) and human rhinovirus (HRV) result in lost school and work days for most that are infected and more serious complications for the immunocompromised. The reasons for these viruses showing strict seasonality include but are not limited to the influence of cold weather and humidity on virus particles, human physiology, and human behavior. The relative importance of each is dependent on what geographic scale is being explored as well as the individual region and time period. Theoretical mathematics has also revealed that climatic changes are likely not the only reasons for strong seasonal cycles, but these are also based in periodic resonance with the natural cycles of immunity and antigenic variance, as well as nationwide synchrony through transportation networks. Investigations of seasonality will aid in understanding disease transmission, and thereby effective prevention strategies. The authors present a review of the literature on seasonal viruses, their annual diffusion through populations, and factors that reduce or enhance their seasonal spread. They also offer suggestions for targeted interventions to reduce the disease burden from seasonal viruses. *Clin Trans Sci* 2011; Volume 4: 48-54

Smilanick, J. L., M. F. Mansour, D. A. Margosan, and F. Mlikota Gabler, 2005. Influence of pH and NaHCO<sub>3</sub> on Effectiveness of Imazalil to Inhibit Germination of *Penicillium digitatum* and to Control Postharvest Green Mold on Citrus Fruit. *Plant Dis.* 89:640-648.

In vitro, spores of *Penicillium digitatum* germinated without inhibition between pH 4 and 7, but were inhibited at higher pH. Estimated concentrations of imazalil (IMZ) in potato-dextrose broth-Tris that caused 50% reduction in the germination of spores (ED<sub>50</sub>) of an IMZ-sensitive isolate M6R at pH 4, 5, 6, and 7 were 0.16, 0.11, 0.015, and 0.006 µg/ml, respectively. ED<sub>50</sub> IMZ concentrations of an IMZ-resistant isolate D201 at pH 4, 5, 6, and 7 were 5.9, 1.4, 0.26, and 0.07 µg/ml, respectively. The natural pH within 2-mm-deep wounds on lemon was 5.6 to 5.1 and decreased with fruit age. IMZ effectiveness to control green mold and its residues increased with pH. The pH in wounds on lemon fruit 24 h after immersion in 1, 2, or 3% NaHCO<sub>3</sub> increased from pH 5.3 to 6.0, 6.3, and 6.7, respectively. NaHCO<sub>3</sub> dramatically improved IMZ performance. Green mold incidence among lemon fruit inoculated with M6R and treated 24 h later with IMZ at 10 µg/ml, 1% NaHCO<sub>3</sub>, or their combination was 92, 55, and 22%, respectively. Green mold among lemon fruit inoculated with D201 and treated 24 h later with water, IMZ at 500 µg/ml, 3% NaHCO<sub>3</sub>, or their combination was 96.3, 63.0, 44.4, and 6.5%, respectively. NaHCO<sub>3</sub> did not influence IMZ fruit residue levels.

Snitkin, Evan S., Adrian M. Zelazny, Pamela J. Thomas, Frida Stock, NISC Comparative Sequencing Program, David K. Henderson, Tara N. Palmore, and Julia A. Segre, 2012. Tracking a Hospital Outbreak of Carbapenem-Resistant *Klebsiella pneumoniae* with Whole-Genome Sequencing. *Sci Transl Med*, Vol 4 Issue 148, pp. 1-9

The Gram-negative bacteria *Klebsiella pneumoniae* is a major cause of nosocomial infections, primarily among immunocompromised patients. The emergence of strains resistant to carbapenems has left few treatment options, making infection containment critical. In 2011, the U.S. National Institutes of Health Clinical Center experienced an outbreak of carbapenem-resistant *K. pneumoniae* that affected 18 patients, 11 of whom died. Whole-genome sequencing was performed on *K. pneumoniae* isolates to gain insight into why the outbreak progressed despite early implementation of infection control procedures. Integrated genomic and epidemiological analysis traced the outbreak to three independent transmissions from a single patient who was discharged 3 weeks before the next case became clinically apparent. Additional genomic comparisons provided evidence for unexpected transmission routes, with subsequent mining of epidemiological data pointing to possible explanations for these transmissions. Our analysis demonstrates that integration of genomic and epidemiological data can yield actionable insights and facilitate the control of nosocomial transmission.

Song, Se Jin, Christian Lauber, Elizabeth K Costello, Catherine A Lozupone, Gregory Humphrey, Donna Berg-Lyons, J Gregory Caporaso, Dan Knights, Jose C Clemente, Sara Nakielny, Jeffrey I Gordon, Noah Fierer, Rob Knight, 2013. Cohabiting family members share microbiota with one another and with their dogs. *eLife* 2013;2:e00458. DOI: 10.7554/eLife.00458

Human-associated microbial communities vary across individuals: possible contributing factors include (genetic) relatedness, diet, and age. However, our surroundings, including individuals with whom we interact, also likely shape our microbial communities. To quantify this microbial exchange, we surveyed fecal, oral, and skin microbiota from 60 families (spousal units with children, dogs, both, or neither). Household members, particularly couples, shared more of their microbiota than individuals from different households, with stronger effects of co-habitation on skin than oral or fecal microbiota. Dog ownership significantly increased the shared skin microbiota in cohabiting adults, and dog-owning adults shared more 'skin' microbiota with their own dogs than with other dogs. Although the degree to which these shared microbes have a true niche on the human body, vs transient detection after direct contact, is unknown, these results suggest that direct and frequent contact with our cohabitants may significantly shape the composition of our microbial communities.

Sordillo JE, Alwis UK, Hoffman E, Gold DR, Milton DK, 2010 Home Characteristics as Predictors of Bacterial and Fungal Microbial Biomarkers in House Dust. *Environ Health Perspect* 119(2): doi:10.1289/ehp.1002004

Background: Measurement of fungal and bacterial biomarkers can be costly, but it is not clear whether home characteristics can be used as a proxy of these markers, particularly if the purpose is to differentiate specific classes of biologic exposures that have similar sources but may have different effects on allergic disease risk. Objective: We evaluated home characteristics as predictors of multiple microbial biomarkers, with a focus on common and unique determinants and with attention to the extent of their explanatory ability. Methods: In 376 Boston-area homes enrolled in a cohort study of home exposures and childhood asthma, we assessed the relationship between home characteristics gathered by questionnaire and measured gram-negative bacteria (GNB) (endotoxin and C10:0, C12:0, and C14:0 3-hydroxy fatty acids), gram-positive bacteria (GPB) (N-acetyl muramic acid), and fungal biomarkers [ergosterol and (1→6) branched, (1→3)-β-D-glucan ] in bed and family room dust. Results: Home characteristics related to dampness were significant predictors of all microbial exposures; water damage or visible mold/mildew in the home was associated with a 20-66% increase in GNB levels. Report of cleaning the bedroom at least once a week was associated with reduced GNB, GPB, and fungi. Presence of dogs or cats predicted increases in home bacteria or fungi. The proportion of variance in microbial biomarkers explained by home characteristics ranged from 4.2% to 19.0%. Conclusions: Despite their associations with multiple microbial flora, home characteristics only partially explain the variability in microbial biomarker levels and cannot substitute for specific microbial measurements in studies concerned with distinguishing effects of specific classes of microbes.

Sousa V, Almeida N, Meireles I, de Brito J. 2011. Anomalies in wall renders: Overview of the main causes of degradation. *International Journal of Architectural Heritage* 5(2):198-218.

The assessment of historical buildings is usually focused on: 1) structural features related to brick or stone walls, wooden floors and other structural elements, or 2) highly valued decorative features, such as frescoes, stuccos, and facade details. During the last quarter of the 20th century, some "secondary" elements also started to receive their share of attention from researchers and practitioners. Wall renders are one of the most important of such elements because of their role as a sacrificial protective layer and the numerous problems that were encountered in the past as a result of incompatibility issues in rehabilitation works. This article discusses the main causes of the deterioration of wall renders, with emphasis on lime-based renders; these renders thoroughly reviewed and their relative weight in the overall degradation is addressed.

Stanley NJ, Kuehn TH, Kim SW, Raynor PC, Anantharaman S, Ramakrishnan MA, Goyal SM. 2008. Background culturable bacteria aerosol in two large public buildings using HVAC filters as long term, passive, high-volume air samplers. *Journal of Environmental Monitoring* 10(4):474-81.

Background culturable bacteria aerosols were collected and identified in two large public buildings located in Minneapolis, Minnesota and Seattle, Washington over a period of 5 months and 3 months, respectively. The installed particulate air filters in the ventilation systems were used as the aerosol sampling devices at each location. Both pre and final filters were collected from four air handling units at each site to determine the influence of location within the building, time of year, geographical location and difference between indoor and outdoor air. Sections of each loaded filter were eluted with 10 ml of phosphate buffered saline (PBS). The resulting solutions were cultured on blood agar plates and incubated for 24 h at 36 °C. Various types of growth media were then used for subculturing, followed by categorization using a BioLog MicroStation (Biolog, Hayward, CA, USA) and manual observation. Environmental parameters were gathered near each filter by the embedded on-site environmental monitoring systems to determine the effect of temperature, humidity and air flow. Thirty nine different species of bacteria were identified, 17 found only in Minneapolis and 5 only in Seattle. The hardy spore-forming genus *Bacillus* was the most commonly identified and showed the highest concentrations. A significant decrease in the number of species and their concentration occurred in the Minneapolis air handling unit supplying 100% outdoor air in winter, however no significant correlations between bacteria concentration and environmental parameters were found.

Stilianakis , Nikolaos I. and Yannis Drossinos, 2010. Dynamics of infectious disease transmission by inhalable respiratory droplets. *J. R. Soc. Interface* (2010) 7, 1355–1366

Transmission of respiratory infectious diseases in humans, for instance influenza, occurs by several modes. Respiratory droplets provide a vector of transmission of an infectious pathogen that may contribute to different transmission modes. An epidemiological model incorporating the dynamics of inhalable respiratory droplets is developed to assess their relevance in the infectious process. Inhalable respiratory droplets are divided into respirable droplets, with droplet diameter less than 10 µm, and inspirable droplets, with diameter in the range 10–100 µm: both droplet classes may be inhaled or settle. Droplet dynamics is determined by their physical properties (size), whereas population dynamics is determined by, among other parameters, the pathogen infectivity and the host contact rates. Three model influenza epidemic scenarios, mediated by different airborne or settled droplet classes, are analysed. The scenarios are distinguished by the characteristic times associated with breathing at contact and with hand-to-face contact. The scenarios suggest that airborne transmission, mediated by respirable droplets, provides the dominant transmission mode in middle and long-term epidemics, whereas inspirable droplets, be they airborne or settled, characterize short-term epidemics with high attack rates. The model neglects close-contact transmission by droplet sprays (direct projection onto facial mucous membranes), retaining close-contact transmission by inspirable droplets.

Sze-To, Gin Nam, Yang Yang, Joseph K. C. Kwan, Samuel C. T. Yu, and Christopher Y. H. Chao, 2014. Effects of Surface Material, Ventilation, and Human Behavior on Indirect Contact Transmission Risk of Respiratory Infection. *Risk Analysis*, Vol. 34, No. 5., pp. 818-830

Infectious particles can be deposited on surfaces. Susceptible persons who contacted these contaminated surfaces may transfer the pathogens to their mucous membranes via hands, leading to a risk of respiratory infection. The exposure and infection risk contributed by this transmission route depend on indoor surface material, ventilation, and human behavior. In this study, quantitative infection risk assessments were used to compare the significances of these factors. The risks of three pathogens, influenza A virus, respiratory syncytial virus (RSV), and rhinovirus, in an



aircraft cabin and in a hospital ward were assessed. Results showed that reducing the contact rate is relatively more effective than increasing the ventilation rate to lower the infection risk. Nonfabric surface materials were found to be much more favorable in the indirect contact transmission for RSV and rhinovirus than fabric surface materials. In the cases considered in this study, halving the ventilation rate and doubling the hand contact rate to surfaces and the hand contact rate to mucous membranes would increase the risk by 3.7–16.2%, 34.4–94.2%, and 24.1–117.7%, respectively. Contacting contaminated nonfabric surfaces may pose an indirect contact risk up to three orders of magnitude higher than that of contacting contaminated fabric surfaces. These findings provide more consideration for infection control and building environmental design.

Tamerius, James, Martha I. Nelson, Steven Z. Zhou, Cécile Viboud, Mark A. Miller, and Wladimir J. Alonso, 2011. Global Influenza Seasonality: Reconciling Patterns across Temperate and Tropical Regions. *Environmental Health Perspectives*, volume 119, number 4, 439-445

**Background:** Despite the significant disease burden of the influenza virus in humans, our understanding of the basis for its pronounced seasonality remains incomplete. Past observations that influenza epidemics occur in the winter across temperate climates, combined with insufficient knowledge about the epidemiology of influenza in the tropics, led to the perception that cool and dry conditions were a necessary, and possibly sufficient, driver of influenza epidemics. Recent reports of substantial levels of influenza virus activity and well-defined seasonality in tropical regions, where warm and humid conditions often persist year-round, have rendered previous hypotheses insufficient for explaining global patterns of influenza. **Objective:** In this review, we examined the scientific evidence for the seasonal mechanisms that potentially explain the complex seasonal patterns of influenza disease activity observed globally. **Methods:** In this review we assessed the strength of a range of hypotheses that attempt to explain observations of influenza seasonality across different latitudes and how they relate to each other. We reviewed studies describing population-scale observations, mathematical models, and ecological, laboratory, and clinical experiments pertaining to influenza seasonality. The literature review includes studies that directly mention the topic of influenza seasonality, as well as other topics we believed to be relevant. We also developed an analytical framework that highlights the complex interactions among environmental stimuli, mediating mechanisms, and the seasonal timing of influenza epidemics and identify critical areas for further research. **Conclusions:** The central questions in influenza seasonality remain unresolved. Future research is particularly needed in tropical localities, where our understanding of seasonality remains poor, and will require a combination of experimental and observational studies. Further understanding of the environmental factors that drive influenza circulation also may be useful to predict how dynamics will be affected at regional levels by global climate change.

Tang, Julian W., 2009a The effect of environmental parameters on the survival of airborne infectious agents. *J. R. Soc. Interface* 2009 6, S737-S746 first published online 22 September 2009

The successful transmission of infection via the airborne route relies on several factors, including the survival of the airborne pathogen in the environment as it travels between susceptible hosts. This review summarizes the various environmental factors (particularly temperature and relative humidity) that may affect the airborne survival of viruses, bacteria and fungi, with the aim of highlighting specific aspects of environmental control that may eventually enhance the aerosol or airborne infection control of infectious disease transmission within hospitals.

Tang, Julian W., Thomas J. Liebner, Brent A. Craven and Gary S. Settles, 2009b. A schlieren optical study of the human cough with and without wearing masks for aerosol infection control. *J. R. Soc. Interface* 2009 6, S727-S736

Various infectious agents are known to be transmitted naturally via respiratory aerosols produced by infected patients. Such aerosols may be produced during normal activities by breathing, talking, coughing and sneezing. The schlieren optical method, previously applied mostly in engineering and physics, can be effectively used here to visualize airflows around human subjects in such indoor situations, non-intrusively and without the need for either tracer gas or airborne particles. It accomplishes this by rendering visible the optical phase gradients owing to real-time changes in air temperature. In this study, schlieren video records are obtained of human volunteers coughing with and without wearing standard surgical and N95 masks. The object is to characterize the exhaled airflows and evaluate the effect of these commonly used masks on the fluid-dynamic mechanisms that spread infection by coughing. Further, a high-speed schlieren video of a single cough is analysed by a computerized method of tracking individual turbulent eddies,

demonstrating the non-intrusive velocimetry of the expelled airflow. Results show that human coughing projects a rapid turbulent jet into the surrounding air, but that wearing a surgical or N95 mask thwarts this natural mechanism of transmitting airborne infection, either by blocking the formation of the jet (N95 mask), or by redirecting it in a less harmful direction (surgical mask).

Tang, J.W. C.J. Noakes, P.V. Nielsen, I. Eames, A. Nicolle, Y. Li, G.S. Settles, 2011. Observing and quantifying airflows in the infection control of aerosol- and airborne-transmitted diseases: an overview of approaches. *Journal of Hospital Infection* 77 (2011) 213-222

With concerns about the potential for the aerosol and airborne transmission of infectious agents, particularly influenza, more attention is being focused on the effectiveness of infection control procedures to prevent hospital-acquired infections by this route. More recently a number of different techniques have been applied to examine the temporal-spatial information about the airflow patterns and the movement of related, suspended material within this air in a hospital setting. Closer collaboration with engineers has allowed clinical micro-biologists, virologists and infection control teams to assess the effectiveness of hospital isolation and ventilation facilities. The characteristics of human respiratory activities have also been investigated using some familiar engineering techniques. Such studies aim to enhance the effectiveness of such preventive measures and have included experiments with human-like mannequins using various tracer gas/particle techniques, real human volunteers with real-time non-invasive Schlieren imaging, numerical modelling using computational fluid dynamics, and small scale physical analogues with water. This article outlines each of these techniques in a non-technical manner, suitable for a clinical readership without specialist airflow or engineering knowledge.

Taubel M, Rintala H, Pitkaranta M, Paulin L, Laitinen S, Pekkanen J, Hyvarinen A, Nevalainen A. 2009. The occupant as a source of house dust bacteria. *J Allergy Clin Immunol* 124(4):834-40.

**Background** Markers for microbial groups are commonly measured in house dust samples to assess indoor exposure to microbes in studies on asthma and allergy. However, little is known about the sources of different microbes. A better understanding of the nature and origin of microbes present in the immediate environment of human beings is crucial if one wants to elucidate protective as well as adverse effects on human health. **Objective** To determine the extent to which the bacterial composition of mattress and floor dust reflects the presence of the human body in relation to other environmental sources. **Methods** House dust and skin surface swab samples of occupants in 4 homes were collected and analyzed for their bacterial content, using a culture-independent methodology. Bacterial sequences analyzed from the different house dusts and skin surface swabs represented random samples of bacteria present in a given sample. Highly similar sequences were grouped to assess biodiversity and to draw conclusions about the sources of bacteria. **Results** The bacterial flora in the house dust samples was found to be highly diverse and dominated by gram-positive bacteria. To a considerable extent, the presence of different bacterial groups was attributed to human sources. In the individuals' mattress dust samples, 69% to 88% of the bacterial sequences analyzed were associated with human origins. The respective percentages for the individual floor dusts ranged from 45% to 55%. **Conclusion** Our study indicates that human-derived bacteria account for a large part of the mainly gram-positive bacterial content in house dust.

Tellier, R., 2009. Aerosol transmission of influenza A virus: a review of new studies. *J. R. Soc. Interface* 2009 6, S783-S790.

Over the past few years, prompted by pandemic preparedness initiatives, the debate over the modes of transmission of influenza has been rekindled and several reviews have appeared. Arguments supporting an important role for aerosol transmission that were reviewed included prolonged survival of the virus in aerosol suspensions, demonstration of the low infectious dose required for aerosol transmission in human volunteers, and clinical and epidemiological observations were disentanglements of large droplets and aerosol transmission was possible. Since these reviews were published, several new studies have been done and generated new data. These include direct demonstration of the presence of influenza viruses in aerosolized droplets from the tidal breathing of infected persons and in the air of an emergency department; the establishment of the guinea pig model for influenza transmission, where it was shown that aerosol transmission is important and probably modulated by temperature and humidity; the demonstration of some genetic determinants of airborne transmission of influenza viruses as assessed using the ferret

model; and mathematical modelling studies that strongly support the aerosol route. These recent results and their implication for infection control of influenza are discussed in this review.

Tercelj, Marjeta, Barbara Salobir, Matevz Harlander, Ragnar Rylander, 2011. Fungal exposure in homes of patients with sarcoidosis - an environmental exposure study. *Environmental Health* 2011, 10:8.

Background: There is increasing evidence that exposure to moulds (fungi) may influence the development of sarcoidosis. To assess the influence of the environmental exposure, a study was undertaken to determine the exposure to fungi in homes of subjects with sarcoidosis. Methods: Subjects were patients with clinically established sarcoidosis recruited during the period September 2007 till June 2010. Of these 55 were newly diagnosed and currently under treatment for less than one year, 25 had been treated and had no recurrence and 27 had been treated but had recurrence of the disease. Controls were healthy subjects without any respiratory symptoms ( $n = 30$ ). Samples of air (about 2.5 m<sup>3</sup>) were taken in the bedroom of the subjects using a portable pump and cellulose ester filters. The filters were analysed for the content of the enzyme N-acetylhexosaminidase (NAHA) as a marker of fungal cell biomass, using a specific substrate and a fluorescent technique and expressed as NAHA units (U)/m<sup>3</sup>. Results: Compared to controls, subjects undergoing treatment of the disease (newly diagnosed or with recurrence) had significantly higher activities of NAHA in their homes than controls (33.6 and 39.9 vs 10.0 U/m<sup>3</sup>,  $p < 0.001$  and  $<0.001$ ). Among controls only 5 out of 30 subjects had levels of NAHA above the second quartile value (14 U/m<sup>3</sup>). In homes of subjects with newly diagnosed disease with treatment less than one year, values above 14 NAHA U/m<sup>3</sup> were found among 35 out of 55 and among those with recurrent disease among 18 out of 27. Conclusions: The higher activities of NAHA enzyme found in homes of subjects with active and recurrent sarcoidosis suggest that exposure to fungi is related to the risk of sarcoidosis. Further environmental studies to assess the importance of this exposure for subjects with sarcoidosis are warranted. The results suggest that remedial actions in homes with high levels of fungi may be justified.

Tham, K. W., M. S. Zuraimi, 2005. Size relationship between airborne viable bacteria and particles in a controlled indoor environment study. *Indoor Air* 2005; 15 (Suppl 9): 48-57

An attempt was made to determine the relationship between airborne viable bacteria (predominantly of human origin) and particle concentrations of different sizes in a controlled environmental chamber focusing on the effect of temperature setting. At temperature settings of 20° and 26° C, six subjects performed simulated office work for 2.5 h, and the particle and total bacteria concentrations at six aerodynamically corresponding size ranges were measured at 20-min intervals. The study revealed that the main contributor of viable bacteria was humans. Viable bacteria concentrations in the size range between 1 and 3 µm was higher at 20° C than at 26° C. Bacteria >7.5 µm showed good correlation with particles of similar minimum size, and it is postulated that this may be because of bacteria rafting on skin scales shed by the subjects. At sizes between 3 and 7.5 µm, the correlations indicated that bacteria exists as clumps, while at size ranges between 1.0 and 2 µm bacteria exists freely. At 26° C, bacteria of size >7.5 µm correlated with exhaled carbon dioxide indicating nasal carriers. Viability of bacteria was shown to be affected by thermal effects. The percentages of particles that were viable bacteria at the different sizes were all found to be very low (<1%).

Thomas, Yves, Guido Vogel, Werner Wunderli, Patricia Suter, Mark Witschi, Daniel Koch, Caroline Tapparel, and Laurent Kaiser, 2008. Survival of Influenza Virus on Banknotes. *APPLIED AND ENVIRONMENTAL MICROBIOLOGY*, May 2008, p. 3002-3007.

Successful control of a viral disease requires knowledge of the different vectors that could promote its transmission among hosts. We assessed the survival of human influenza viruses on banknotes given that billions of these notes are exchanged daily worldwide. Banknotes were experimentally contaminated with representative influenza virus subtypes at various concentrations, and survival was tested after different time periods. Influenza A viruses tested by cell culture survived up to 3 days when they were inoculated at high concentrations. The same inoculum in the presence of respiratory mucus showed a striking increase in survival time (up to 17 days). Similarly, B/Hong Kong/335/2001 virus was still infectious after 1 day when it was mixed with respiratory mucus. When nasopharyngeal secretions of naturally infected children were used, influenza virus survived for at least 48 h in one-third of the cases. The unexpected stability of influenza virus in this nonbiological environment suggests that unusual environmental contamination should be considered in the setting of pandemic preparedness

Thompson, K-A., A.M. Bennett, J.T. Walker, 2011. Aerosol survival of *Staphylococcus epidermidis*, 2011. *Journal of Hospital Infection* 78 (2011) 216-220.

Recent studies have suggested that aerosol dispersal might play a role in the dissemination of methicillin-resistant *Staphylococcus aureus* (MRSA). Relatively little has been published about the ability of staphylococci to survive in aerosols. This study measured the survival of *Staphylococcus epidermidis*, a surrogate for *S. aureus*, in aerosols and investigated the effect of relative humidity on survival. We used a Goldberg drum to assess survival at relative humidities of < 20%, 40-60%, 70-80% and > 90%. We controlled for the effects of aerosol dilution and physical decay by comparing the recovery of *S. epidermidis* with that of the aerosol-stable spores of *Bacillus atrophaeus*, using the ratio of their recovery rates to estimate biological degradation of *S. epidermidis* over time. At all relative humidities investigated 13% [95% confidence interval (CI): 10.1-16.2%] of the initial aerosol was recovered after 5 h (300 min). The mean percentage survival ratio (% *S. epidermidis*:% *B. atrophaeus*) after 5 h was 47% (95% CI: 33.5-60.5%). Overlapping 95% CIs of mean percentage survival ratios at each humidity level indicated that humidity did not have a significant effect on the survival in aerosol form of *S. epidermidis*. Additional experiments indicated that *S. epidermidis* was recoverable after five days at 76% humidity. The sizes of particles within the bacterial aerosol were well within the respirable range (< 2.1  $\mu\text{m}$ ). The survival of aerosolised *S. epidermidis* demonstrated in this study suggests that staphylococci have the potential for aerosol dissemination in hospitals.

Thorne, Peter S., Katarina Kulhankova, Ming Yin, Richard Cohn, Samuel J. Arbes, Jr., and Darryl C. Zeldin, 2005. Endotoxin Exposure Is a Risk Factor for Asthma. The National Survey of Endotoxin in United States Housing. *Am J Respir Crit Care Med* Vol 172. pp 1371-1377

Background: Although research has shown that early life exposure to household endotoxin protects against development of allergies, studies are less clear on the relationship between household endotoxin exposure and prevalence of wheezing and asthma. We assayed 2,552 house dust samples in a representative nationwide sample to explore relationships between endotoxin exposures and risk factors for asthma, asthma symptoms, and medication use. Methods: House dust was vacuum-sampled from five locations within homes and assayed for endotoxin. Health, demographic, and housing information was assessed through questionnaire and onsite evaluation of 2,456 residents of 831 homes selected to represent the demographics of the United States. Results: Endotoxin concentration (EU/mg) and load (EU/m<sup>2</sup>) were highly correlated ( $r = 0.73-0.79$ ). Geometric mean endotoxin concentrations were as follows (in EU/mg): bedroom floors, 35.3 (5th-95th percentile, 5.0-260); bedding, 18.7 (2.0-142); family room floors, 63.9 (11.5-331); sofas, 44.8 (6.4-240); and kitchen floors, 80.5 (9.8-512). Multivariate analysis demonstrated significant relationships between increasing endotoxin levels and diagnosed asthma, asthma symptoms in the past year, current use of asthma medications, and wheezing among residents of the homes. These relationships were strongest for bedroom floor and bedding dust and were observed in adults only. Modeling the joint effect of bedding and bedroom floor endotoxin on recent asthma symptoms yielded an adjusted odds ratio of 2.83 (95% confidence interval, 1.01-7.87). When stratified by allergy status, allergic subjects with higher endotoxin exposure were no more likely to have diagnosed asthma or asthma symptoms than nonallergic subjects. Conclusion: This study demonstrates that household endotoxin exposure is a significant risk factor for increased asthma prevalence

Thorne, Peter S., Richard D. Cohn, Deepak Mav, Samuel J. Arbes Jr., and Darryl C. Zeldin, 2009. Predictors of Endotoxin Levels in U.S. Housing. *Environ Health Perspect* 117:763-771 (2009). doi:10.1289/ehp.11759.

Background: The relationship of domestic endotoxin exposure to allergy and asthma has been widely investigated. However, few studies have evaluated predictors of household endotoxin, and none have done so for multiple locations within homes and on a national scale. Objectives: We assayed 2,552 house dust samples in a nationwide study to understand the predictors of household endotoxin in bedroom floors, family room floors, beds, kitchen floors, and family room sofas. Methods: Reservoir house dust from five locations within homes was assayed for endotoxin and demographic and housing information was assessed through questionnaire and onsite evaluation of 2,456 residents of 831 homes selected to represent national demographics. We performed repeated-measures analysis of variance (rANOVA) for 37 candidate variables to identify independent predictors of endotoxin. Meteorologic data were obtained for each primary sampling unit and tested as predictors of indoor endotoxin to determine if wetter or warmer microclimates were associated with higher endotoxin levels. Results: Weighted geometric mean endotoxin concentration ranged from 18.7 to 80.5 endotoxin units (EU)/mg for the five sampling locations, and endotoxin load ranged from 4,160 to 19,500 EU/m<sup>2</sup>. Bivariate analyses and rANOVA demonstrated that major predictors of endotoxin

concentration were sampling location in the home, census division, educational attainment, presence of children, current dog ownership, resident-described problems with cockroaches, food debris, cockroach stains, and evidence of smoking observed by field staff. Low household income entered the model if educational attainment was removed. Conclusion: Increased endotoxin in household reservoir dust is principally associated with poverty, people, pets, household cleanliness, and geography.

Thrasher JD and Crawley S. 2009. The biocontaminants and complexity of damp indoor spaces: More than what meets the eyes. *Toxicol Ind Health* 25(9-10):583-615.

Nine types of biocontaminants in damp indoor environments from microbial growth are discussed: (1) indicator molds; (2) Gram negative and positive bacteria; (3) microbial particulates; (4) mycotoxins; (5) volatile organic compounds, both microbial (MVOCs) and non-microbial (VOCs); (6) proteins; (7) galactomannans; (8) 1-3- $\beta$ -D-glucan (glucans) and (9) lipopolysaccharides (LPS - endotoxins). When mold species exceed those outdoors contamination is deduced. Gram negative bacterial endotoxins, LPS in indoor environments, synergize with mycotoxins. The gram positive *Bacillus* species, *Actinomycetes* (*Streptomyces*, *Nocardia* and *Mycobacterium*), produce exotoxins. The *Actinomycetes* are associated with hypersensitivity pneumonitis, lung and invasive infections. Mycobacterial mycobacterium infections not from *M. tuberculosis* are increasing in immunocompetent individuals. In animal models, LPS enhance the toxicity of roridin A, satratoxins G and aflatoxin B1 to damage the olfactory epithelium, tract and bulbs (roridin A, satratoxin G) and liver (aflatoxin B1). Aflatoxin B1 and probably trichothecenes are transported along the olfactory tract to the temporal lobe. Co-cultured *Streptomyces californicus* and *Stachybotrys chartarum* produce a cytotoxin similar to doxorubicin and actinomycin D (chemotherapeutic agents). Trichothecenes, aflatoxins, gliotoxin and other mycotoxins are found in dust, bulk samples, air and ventilation systems of infested buildings. Macrocyclic trichothecenes are present in airborne particles <2  $\mu$ m. Trichothecenes and stachylysin are present in the sera of individuals exposed to *S. chartarum* in contaminated indoor environments. Haemolysins are produced by *S. chartarum*, *Memnoniella echinata* and several species of *Aspergillus* and *Penicillium*. Galactomannans, glucans and LPS are upper and lower respiratory tract irritants. Gliotoxin, an immunosuppressive mycotoxin, was identified in the lung secretions and sera of cancer patients with aspergillosis produced by *A. fumigatus*, *A. terreus*, *A. niger* and *A. flavus*.

Tischer, Christina G. and Joachim Heinrich, 2013. Exposure assessment of residential mould, fungi and microbial components in relation to children's health: Achievements and challenges. *International Journal of Hygiene and Environmental Health* 216 (2013) 109– 114

Each day we are exposed to a complex mixture of microbial agents and components in indoor environments. A major part of this mixture derives from fungal and bacterial origin. The impact between those microbial agents in the home environment in relation to respiratory health in children is still a major issue in research. There is little known about the causal agents that provoke or arrest the development of allergic respiratory disorders in children. Identification is complicated by the biodiversity and variability of microbial components in indoor air as well as the lack of validated and standardized exposure assessment methods. In this review, we aim to consider all important aspects in terms of research which may encounter an epidemiological study. Apart from the need for standardized exposure assessment methods which consider cost, handling and effort, especially for the participants, we suggest that a combination of different analysis methods such as chemical and molecular methods may have the potential to best describe the microbial milieu in indoor environments at present. Further, the impact of mould and moisture remediation activities on health is still heavily under investigated, especially in larger prospective cohorts of children and should be a topic of future research. Moreover, the exposure to mould and microbial agents might be embedded in a broader spectrum of children's health such as behavior and cognitive development.

Torvinen, Eila, Teija Meklin, Pirjo Torkko, Sini Suomalainen, Marjut Reiman, Marja-Leena Katila, Lars Paulin, and Aino Nevalainen, 2006. Mycobacteria and Fungi in Moisture-Damaged Building Materials. *APPLIED AND ENVIRONMENTAL MICROBIOLOGY*, Oct. 2006, p. 6822-6824.

In contrast to the growth of fungi, the growth of mycobacteria in moisture-damaged building materials has rarely been studied. Environmental mycobacteria were isolated from 23% of samples of moisture-damaged materials (n = 88). The occurrence of mycobacteria increased with increasing concentrations of fungi. Mycobacteria may contribute to indoor exposure and associated adverse health effects

Tringe SG, Zhang T, Liu X, Yu Y, Lee WH, et al. (2008) The Airborne Metagenome in an Indoor Urban Environment. *PLoS ONE* 3(4): e1862. doi:10.1371/journal.pone.0001862

The indoor atmosphere is an ecological unit that impacts on public health. To investigate the composition of organisms in this space, we applied culture-independent approaches to microbes harvested from the air of two densely populated urban buildings, from which we analyzed 80 megabases genomic DNA sequence and 6000 16S rDNA clones. The air microbiota is primarily bacteria, including potential opportunistic pathogens commonly isolated from human-inhabited environments such as hospitals, but none of the data contain matches to virulent pathogens or bioterror agents. Comparison of air samples with each other and nearby environments suggested that the indoor air microbes are not random transients from surrounding outdoor environments, but rather originate from indoor niches. Sequence annotation by gene function revealed specific adaptive capabilities enriched in the air environment, including genes potentially involved in resistance to desiccation and oxidative damage. This baseline index of air microbiota will be valuable for improving designs of surveillance for natural or man-made release of virulent pathogens

TROUWBORST, T., SJOUKJE KUYPER, J. C. DE JONG AND A. D. PLANTINGA, 1974. Inactivation of some Bacterial and Animal Viruses by Exposure to Liquid-air Interfaces. *J. gen. Virol.* (1974), 24, 155-165

Surface inactivation of the bacteriophages T1, T3, T5, MS2, of EMC virus and Semliki Forest virus was studied, exposing the viruses to a large air/water interface by aeration or by rotating the fluid in a spherical flask. EMC virus in 1 M-NaCl was not sensitive to this treatment, phage T3 and T5 were only little affected, but the phages T1 and MS2 and Semliki Forest virus were rapidly inactivated by bubbling air or nitrogen gas through the suspension. In salt solutions at rest no inactivation of these viruses was observed. Inactivation by aeration was prevented by addition of peptone, by apolar carboxylic acids and by the surface active agent OED. If a large solution/glass interface is present, some loss of virus occurs by adsorption to the glass surface. Phenylalanine protected against adsorption to the glass surface, but protected less effectively against inactivation by aeration. The rate of surface inactivation was strongly dependent on the salt concentration in the medium. At low NaCl concentration (0.01 M) nearly no inactivation was found for phage T1 and MS2 and phage T3 was not sensitive to aeration in 1 M-NaCl but was rapidly inactivated in 2.6 M-NaCl. The rate of inactivation decreased with time of shaking and in the case of phage T1 a nearly completely resistant fraction of 10<sup>-4</sup> of the original particles remained. The resistance against surface inactivation was a non-heritable property. Resistance against thermal inactivation was not correlated with resistance to surface inactivation, suggesting that the mechanism of inactivation differs in these processes.

Tsai, F. C., J. M. Macher, 2005. Concentrations of airborne culturable bacteria in 100 large US office buildings from the BASE study. *Indoor Air* 2005; 15 (Suppl 9): 71–81

This paper presents summary statistics of airborne culturable bacteria from the US Environmental Protection Agency Building Assessment Survey and Evaluation (BASE) study. Air samples were collected with single-stage, multiple-hole, agar impactors in 100 large office buildings in 1994–1998 to obtain normative data on indoor environmental quality. Bacterial concentrations were compared by incubation temperature, location, season, and climate zone. Forty-one percent of the samples were below the 2- or 5-min detection limits (18 or 7 CFU/m<sup>3</sup>, respectively) but less than 1% were overgrown. Mesophilic bacteria (30 °C) accounted for >95% of culturable bacteria, both indoors and outdoors. Average concentrations were higher outdoors, except for Gram-positive cocci, which were the only group that were significantly higher indoors (39 vs. 24 CFU/m<sup>3</sup>), and Gram-negative cocci, for which both concentrations were low and the difference were not significant. Outdoor concentrations of culturable bacteria were somewhat higher in winter (194 vs. 165 CFU/m<sup>3</sup>), and the two dominant outdoor groups were unknown bacteria and Gram-positive rods. Conversely, indoor concentrations were significantly higher in summer (116 vs. 87 CFU/m<sup>3</sup>), consisting primarily of unknown bacteria and Gram-positive cocci. Bacterial concentrations were within the ranges reported in previous studies of non-problem buildings, and the extreme aggregated indoor concentrations (e.g. the 90th percentile, 175 CFU/m<sup>3</sup>) of these 100 representative buildings may serve as upper bounds to develop interpretation guidelines for office environments and similar non-manufacturing workplaces in various climate zones.

Tsai, Feng C., Janet M. Macher, Yun-Yi Hung, 2007. Biodiversity and concentrations of airborne fungi in large US office buildings from the BASE study. *Atmospheric Environment* 41 (2007) 5181-5191.

The Building Assessment Survey and Evaluation (BASE) study measured baseline concentrations of airborne fungi in 100 representative US office buildings in 1994-1998. Multiple samples for different sampling durations, sites, and times of the day were aggregated into building-wide indoor and outdoor average concentrations. Fungal concentrations were compared between locations (indoor vs. outdoor), sampling and analytical methods (culture vs. microscopy), and season (summer vs. winter). The arithmetic means (standard deviations) of the indoor/outdoor concentrations of culturable fungi and fungal spores were 100/680 (230/840) CFU<sub>m</sub>-3 and 270/6540 (1190/6780) spore m<sup>-3</sup>, respectively. Although fewer groups were observed indoors than outdoors, at lower average concentrations (except in two buildings), site-specific and building-wide indoor measurements had higher coefficients of variation. More groups were seen in summer, and aggregated concentrations tended to be higher than in winter except for culturable *Aureobasidium* spp. and *Botrytis* spp. outdoors and non-sporulating fungi in both locations. Rankings of the predominant fungi identified by both methods were similar, but overall indoor and outdoor spore concentrations were approximately 3 and 10 times higher, respectively, than concentrations of culturable fungi. In the 44 buildings with both measurements, the indoor and outdoor total culturable fungi to fungal spore ratios (total C/S ratios) were 1.27 and 0.25, with opposite seasonal patterns. The indoor C/S ratio was higher in summer than in winter (1.47 vs. 0.86; N = 29 and 15, respectively), but the outdoor ratio was lower in summer (0.19 vs. 0.36, respectively). Comparison of the number of different fungal groups and individual occurrence in buildings and samples indicated that the outdoor environment and summer season were more diverse, but the proportional contributions of the groups were very similar suggesting that the indoor and outdoor environments were related as were summer and winter seasons for each location. The extreme (e.g., 90th percentile) indoor concentrations (200 CFU m<sup>-3</sup> and 210 spore m<sup>-3</sup>) may provide reference values for non-complaint US office environments.

Tualdhar, Era, Wilma C. Hazeleger, Marion Koopmans, Marcel H. Zwietering, Rijkelt R. Beumer and Erwin Duizer, 2012. Residual viral and bacterial contamination of surfaces after cleaning and disinfection. *Appl Environ Microbiol.* 2012 Nov;78(21):7769-75

Environmental surfaces contaminated with pathogens can be sources of indirect transmission, and cleaning and disinfection are common interventions focused on reducing contamination levels. We determined the efficacy of cleaning and disinfection procedures for reducing contamination by noroviruses, rotavirus, poliovirus, parechovirus, adenovirus, influenza virus, *Staphylococcus aureus*, and *Salmonella enterica* from artificially contaminated stainless steel surfaces. After a single wipe with water, liquid soap, or 250-ppm free chlorine solution, the numbers of infective viruses and bacteria were reduced by 1 log<sub>10</sub> for poliovirus and close to 4 log<sub>10</sub> for influenza virus. There was no significant difference in residual contamination levels after wiping with water, liquid soap, or 250-ppm chlorine solution. When a single wipe with liquid soap was followed by a second wipe using 250- or 1,000-ppm chlorine, an extra 1- to 3-log<sub>10</sub> reduction was achieved, and except for rotavirus and norovirus genogroup I, no significant additional effect of 1,000 ppm compared to 250 ppm was found. A reduced correlation between reduction in PCR units (PCRU) and reduction in infectious particles suggests that at least part of the reduction achieved in the second step is due to inactivation instead of removal alone. We used data on infectious doses and transfer efficiencies to estimate a target level to which the residual contamination should be reduced and found that a single wipe with liquid soap followed by a wipe with 250-ppm free chlorine solution was sufficient to reduce the residual contamination to below the target level for most of the pathogens tested.

Ud-Dean, S.M. Minhaz, 2010. Structural explanation for the effect of humidity on persistence of airborne virus: Seasonality of influenza. *Journal of Theoretical Biology* 264(3) 822-829

Seasonal variation of infectious diseases is one of the oldest observations in epidemiology, most particularly for Influenza and other respiratory viral infections. The reason for this seasonality is poorly understood, despite the profound importance of these infections as communicable diseases capable of causing global epidemics. Environmental factors including relative humidity, vapor pressure and temperature are known to affect seasonal virus survival and transmission. Immunological status of the host and evolution of the virus have also been proposed to be the reason behind the cyclic recurrence. The molecular basis of these effects or their interplay with biological factors has not been reported before. Here a theoretical analysis shows that the structure of the viral envelope determines its persistence and transmission in various environmental conditions. Physico-chemical properties of the virus particles and their interaction with atmospheric processes along with the availability and susceptibility of hosts generates the conspicuous seasonality prevalent in the temperate zones and the apparent lack of it in the tropics. Additionally this model can

estimate virus transmission in different weather conditions. This model may help to determine the right actions effective in preventing outbreaks of the flu-like respiratory viruses.

Vacher, Sebastien, Catalina Hernandez, Claire Bartschi, Nathalie Poussereau, 2010. Impact of paint and wall-paper on mould growth on plasterboards and aluminum. *Building and Environment* 45 (2010) 916-921.

Biocide-free and biocide-treated plasterboards as well as aluminum plate as a reference material normally considered as being insensitive to mould growth have been used as substrate to check the influence of different common wall coverings, i.e. paints and wall papers, on fungal growth. The results described in this paper show that any non-biodegradable material (such as aluminum) can become a substrate to fungal infestation once painted or wall paper applied, depending on the type of paint or wall paper used. Moreover, a biodegradable material treated with a biocide (biocide-treated plasterboard) offers partial resistance to fungal growth at a biodegradable surface covering. The main conclusion of this study is that composition of the surface covering applied on building materials is as important as the substrate itself when considering the bioreceptivity of this material to potential fungal infestation. Accordingly, any discussion on the ability of a given building material to resist or not to fungal infestation must refer to the exact composition of the surface covering (paint, varnish, wall paper, etc). This has not often been the case in many of the previous studies published on the topic.

Van Lancker F, Adams A, Delmulle B, De Saeger S, Moretti A, Van Peteghem C, De Kimpe N. 2008. Use of headspace SPME-GC-MS for the analysis of the volatiles produced by indoor molds grown on different substrates. *Journal of Environmental Monitoring* 10(10):1127-33.

An automated headspace solid phase microextraction method followed by GC-MS analysis was used to evaluate and compare the in vitro production of microbial volatile organic compounds (MVOCs) on malt extract agar, plasterboard and wallpaper. Five fungal strains were isolated from the walls of waterdamaged houses and identified. In addition, four other common molds were studied. In general, MVOC production was the highest on malt extract agar. On this synthetic medium, molds typically produced 2-methylpropanol, 2-methylbutanol and 3-methylbutanol. On wallpaper, mainly 2-ethylhexanol, methyl 2-ethylhexanoate and compounds of the C8-complex such as 1-octene-3-ol, 3-octanone, 3-octanol and 1,3-octadiene were detected. The detection of 2-ethylhexanol and methyl 2-ethylhexanoate indicates an enhanced degradation of the substrate by most fungi. For growth on plasterboard, no typical metabolites were detected. Despite these metabolite differences on malt extract agar, wallpaper and plasterboard, some molds also produced specific compounds independently of the used substrate, such as trichodiene from *Fusarium sporotrichioides* and aristolochene from *Penicillium roqueforti*. Therefore, these metabolites can be used as markers for the identification and maybe also mycotoxin production of these molds. All five investigated *Penicillium* spp. in this study were able to produce two specific diterpenes, which were not produced by the other species studied. These two compounds, which remain unidentified until now, therefore seem specific for *Penicillium* spp. and are potentially interesting for the monitoring of this fungal genus. Further experiments will be performed with other *Penicillium* spp. to study the possibility that these two compounds are specific for this group of molds.

Vereecken, Evy and Staf Roels, 2012. Review of mould prediction models and their influence on mould risk evaluation. *Building and Environment* 51 (2012) 296-310

A reliable prediction of mould risk in buildings is important to ensure a healthy environment and to avoid social and economical damage. Whereas previously the temperature ratio was often used to minimize the mould risk, nowadays more advanced mould prediction models can be found (e.g. isopleth systems, biohygrothermal model, ESP-r mould prediction model, empirical VTT model). These models include the main influencing factors for mould growth: the surface temperature and relative humidity. However, they are based on either experiments or assumptions and some of them neglect a third important influencing factor: the exposure time. The current paper gives an overview of the different existing models and analyses the impact of the mould prediction model on the mould risk evaluation. To do so, the existing mould prediction models are used to predict the mould risk for different temperature and relative humidity courses. The mould risk, the time until mould growth starts and the mould intensity according to the existing prediction models are compared. Based on the obtained results, the influence of simplifications or shortcomings in the mould prediction models is discussed.



Vickery, K., A. Deva, A. Jacombs, J. Allan, P. Valente, I.B. Gosbell, 2011. Presence of biofilm containing viable multiresistant organisms despite terminal cleaning on clinical surfaces in an intensive care unit. *Journal of Hospital Infection* 80 (2012) 52-55

**Background:** Despite recent attention to surface cleaning and hand hygiene programmes, multiresistant organisms (MROs) continue to be isolated from the hospital environment. Biofilms, consisting of bacteria embedded in exopolymeric substances (EPS) are difficult to remove due to their increased resistance to detergents and disinfectants, and periodically release free-swimming planktonic bacteria back into the environment which may act as an infection source. **Aim:** To establish whether reservoirs of MROs exist in the environment as biofilms. **Methods:** Following terminal cleaning, equipment and furnishings were removed aseptically from an intensive care unit (ICU) and subjected to culture and scanning electron microscopy (SEM). Samples were placed in 5 mL of tryptone soya broth, sonicated for 5 min before plate culture on horse blood agar, Brilliance MRSA and Brilliance VRE agar plates. Samples for SEM were fixed in 3% glutaraldehyde and hexamethyldisilazane (HMDS) prior to sputter-coating with gold and examination in an electron microscope. **Findings:** Biofilm was demonstrated visually on the sterile supply bucket, the opaque plastic door, the venetian blind cord, and the sink rubber, whereas EPS alone was seen on the curtain. Viable bacteria were grown from three samples, including MRSA from the venetian blind cord and the curtain. **Conclusion:** Biofilm containing MROs persist on clinical surfaces from an ICU despite terminal cleaning, suggesting that current cleaning practices are inadequate to control biofilm development. The presence of MROs being protected within these biofilms may be the mechanism by which MROs persist within the hospital environment.

Viitanen H, Vinha J, Salminen K, Ojanen T, Peuhkuri R, Paajanen L, Lahdesmaki K. 2010. Moisture and bio-deterioration risk of building materials and structures. *Journal of Building Physics* 33(3):201-24.

There are several biological processes causing aging and damage to buildings. This is partly due to natural aging of materials and excessive moisture. The demands on durability, energy balance, and health of houses are continually rising. For mold development, the minimum (critical) ambient humidity requirement is shown to be between RH 80% and 95% depending on other factors like ambient temperature, exposure time, and the type and surface conditions of building materials. For decay development, the critical humidity is above RH95%. Mold typically affects the quality of the adjacent air space with volatile compounds and spores. The next stage of moisture-induced damage, the decay development, forms a serious risk for structural strength depending on moisture content, materials, temperature, and time. The worst decay damage cases in North Europe are found in the floors and lower parts of walls, where water accumulates due to different reasons. Modeling of mold growth and decay development based on humidity, temperature, exposure time, and material will give new tools for the evaluation of durability of different building materials and structures. The models make it possible to evaluate the risk and development of mold growth and to analyze the critical conditions needed for the start of biological growth. The model is also a tool to simulate the progress of mold and decay development under different conditions on the structure surfaces. This requires that the moisture capacity and moisture transport properties in the material and at the surface layer be taken into account in the simulations. In practice there are even more parameters affecting mold growth, e.g., thickness of the material layers combined with the local surface heat and mass transfer coefficients. Therefore, the outcome of the simulations and in situ observations of biological deterioration may not agree. In the present article, results on mold growth in different materials and wall assemblies will be shown and existing models on the risk of mold growth development will be evaluated. One of the results of a newly finished large Finnish research project 'modeling of mold growth' is an improved and extended mathematical model for mold growth. This model and more detailed research results will be published in other papers.

Vonberg, Ralf-Peter, Petra Gastmeier<sup>2</sup>, Björn Kenneweg<sup>3</sup>, Hinrich Holdack-Janssen, Dorit Sohr and Iris F Chaberny, 2010. The microbiological quality of air improves when using air conditioning systems in cars. *Infectious Diseases* 2010, 10:146

**Background:** Because of better comfort, air conditioning systems are a common feature in automobiles these days. However, its impact on the number of particles and microorganisms inside the vehicle - and by this its impact on the risk of an allergic reaction - is yet unknown. **Methods:** Over a time period of 30 months, the quality of air was investigated in three different types of cars (VW Passat, VW Polo FSI, Seat Alhambra) that were all equipped with an automatic air conditioning system. Operation modes using fresh air from outside the car as well as circulating air from inside the car were examined. The total number of microorganisms and the number of mold spores were measured by

impaction in a high flow air sampler. Particles of 0.5 to 5.0  $\mu\text{m}$  diameter were counted by a laser particle counter device. Results: Overall 32 occasions of sampling were performed. The concentration of microorganisms outside the cars was always higher than it was inside the cars. Few minutes after starting the air conditioning system the total number of microorganisms was reduced by 81.7%, the number of mold spores was reduced by 83.3%, and the number of particles was reduced by 87.8%. There were no significant differences neither between the types of cars nor between the types of operation mode of the air conditioning system (fresh air vs. circulating air). All parameters that were looked for in this study improved during utilization of the car's air conditioning system. Conclusions: We believe that the risk of an allergic reaction will be reduced during use also. Nevertheless, we recommend regular maintenance of the system and replacement of older filters after defined changing intervals.

Walsh, Rebecca L. and Andrew Camilli, 2011. *Streptococcus pneumoniae* Is Desiccation Tolerant and Infectious upon Rehydration. *mBio* 2(3): doi:10.1128/mBio.00092-11.

*Streptococcus pneumoniae* (pneumococcus) is a frequent colonizer of the nasopharynx and one of the leading causative agents of otitis media, pneumonia, and meningitis. The current literature asserts that *S. pneumoniae* is transmitted person to person via respiratory droplets; however, environmental surfaces (fomites) have been linked to the spread of other respiratory pathogens. Desiccation tolerance has been shown to be essential for long-term survival on dry surfaces. This study investigated the survival and infectivity of *S. pneumoniae* following desiccation under ambient conditions. We recovered viable bacteria after all desiccation periods tested, ranging from 1 h to 4 weeks. Experiments conducted under nutrient limitation indicate that desiccation is a condition separate from starvation. Desiccation of an acapsular mutant and 15 different clinical isolates shows that *S. pneumoniae* desiccation tolerance is independent of the polysaccharide capsule and is a species-wide phenomenon, respectively. Experiments demonstrating that nondesiccated and desiccated *S. pneumoniae* strains colonize the nasopharynx at comparable levels, combined with their ability to survive long-term desiccation, suggest that fomites may serve as alternate sources of pneumococcal infection.

Walther, Bruno A. and Paul W. Ewald, 2004. Pathogen survival in the external environment and the evolution of virulence. *Biol. Rev.* (2004), 79, pp. 849-869

Recent studies have provided evolutionary explanations for much of the variation in mortality among human infectious diseases. One gap in this knowledge concerns respiratory tract pathogens transmitted from person to person by direct contact or through environmental contamination. The sit-and-wait hypothesis predicts that virulence should be positively correlated with durability in the external environment because high durability reduces the dependence of transmission on host mobility. Reviewing the epidemiological and medical literature, we confirm this prediction for respiratory tract pathogens of humans. Our results clearly distinguish a high virulence high-survival group of variola (smallpox) virus, *Mycobacterium tuberculosis*, *Corynebacterium diphtheriae*, *Bordetella pertussis*, *Streptococcus pneumoniae*, and influenza virus (where all pathogens have a mean percent mortality  $\geq 0.01\%$  and mean survival time  $> 10$  days) from a low-virulence low-survival group containing ten other pathogens. The correlation between virulence and durability explains three to four times of magnitude of difference in mean percent mortality and mean survival time, using both across-species and phylogenetically controlled analyses. Our findings bear on several areas of active research and public health policy: (1) many pathogens used in the biological control of insects are potential sit-and-wait pathogens as they combine three attributes that are advantageous for pest control: high virulence, long durability after application, and host specificity; (2) emerging pathogens such as the 'hospital superbug' methicillin-resistant *Staphylococcus aureus* (MRSA) and potential bioweapons pathogens such as smallpox virus and anthrax that are particularly dangerous can be discerned by quantifying their durability; (3) hospital settings and the AIDS pandemic may provide footholds for emerging sit-and-wait pathogens; and (4) studies on food-borne and insect pathogens point to future research considering the potential evolutionary trade-offs and genetic linkages between virulence and durability.

Wang, Hong, Marc Edwards, Joseph O. Falkinham III and Amy Pruden, 2012. Molecular Survey of the Occurrence of *Legionella* spp., *Mycobacterium* spp., *Pseudomonas aeruginosa* and *Ameoba* Hosts in two Chloraminated Drinking Water Distribution Systems. *Appl. Environ. Microbiol.* 2012, 78(17):6285. DOI: 10.1128/AEM.01492-12.

The spread of opportunistic pathogens via public water systems is of growing concern. The purpose of this study was to identify patterns of occurrence among three opportunistic pathogens (*Legionella pneumophila*, *Mycobacterium*

avium, and *Pseudomonas aeruginosa*) relative to biotic and abiotic factors in two representative chloraminated drinking water distribution systems using culture-independent methods. Generally, a high occurrence of *Legionella* ( $\geq 69.0\%$ ) and mycobacteria (100%), lower occurrence of *L. pneumophila* ( $\leq 20\%$ ) and *M. avium* ( $\leq 33.3\%$ ), and rare detection of *Pseudomonas aeruginosa* ( $\leq 13.3\%$ ) were observed in both systems according to quantitative PCR. Also, *Hartmannella vermiformis* was more prevalent than *Acanthamoeba*, both of which are known hosts for opportunistic pathogen amplification, the latter itself containing pathogenic members. Three-minute flushing served to distinguish distribution system water from plumbing in buildings (i.e., premise plumbing water) and resulted in reduced numbers of copies of *Legionella*, mycobacteria, *H. vermiformis*, and 16S rRNA genes ( $P < 0.05$ ) while yielding distinct terminal restriction fragment polymorphism (T-RFLP) profiles of 16S rRNA genes. Within certain subgroups of samples, some positive correlations, including correlations of numbers of mycobacteria and total bacteria (16S rRNA genes), *H. vermiformis* and total bacteria, mycobacteria and *H. vermiformis*, and *Legionella* and *H. vermiformis*, were noted, emphasizing potential microbial ecological relationships. Overall, the results provide insight into factors that may aid in controlling opportunistic pathogen proliferation in real-world water systems.

Weber, TP and Stilianakis, NI, Inactivation of influenza A viruses in the environment and modes of transmission: A critical review. *Journal of Infection*. 2008; 57(5) 361-373.

**Objectives:** The relative importance of airborne, droplet and contact transmission of influenza A virus and the efficiency of control measures depends among other factors on the inactivation of viruses in different environmental media. **Methods:** We systematically review available information on the environmental inactivation of influenza A viruses and employ information on infectious dose and results from mathematical models to assess transmission modes. **Results:** Daily inactivation rate constants differ by several orders of magnitude: on inanimate surfaces and in aerosols daily inactivation rates are in the order of 1-102, on hands in the order of 103. Influenza virus can survive in aerosols for several hours, on hands for a few minutes. Nasal infectious dose of influenza A is several orders of magnitude larger than airborne infectious dose. **Conclusions:** The airborne route is a potentially important transmission pathway for influenza in indoor environments. The importance of droplet transmission has to be reassessed. Contact transmission can be limited by fast inactivation of influenza virus on hands and is more so than airborne transmission dependent on behavioral parameters. However, the potentially large inocula deposited in the environment through sneezing and the protective effect of nasal mucus on virus survival could make contact transmission a key transmission mode.

Wessén, Bengt and Janne Lager, 2008. The correlation of microbial and chemical contents of indoor air and perceived IAQ. *Proceedings of Indoor Air 2008*, 17-22 August 2008, Copenhagen, Denmark - Paper ID: 104.

In order to keep buildings from causing bad health to its users there is a need to control the indoor air quality (IAQ). By using a screening approach in analysing airborne particles and gases it was possible to distinguish 93% of buildings suffering from odour problems and 77% of buildings with pronounced SBS complaints. The screening method involved key compounds from microbial exposure, moisture produced chemicals, chemical emissions from building material, wood preservatives and exhaust from engines.

Wheeler AJ, Dobbin NA, Lyrette N, Wallace L, Foto M, Mallick R, Kearney J, Van Ryswyk K, Gilbert NL, Harrison I, et al. 2011. Residential indoor and outdoor coarse particles and associated endotoxin exposures. *Atmos Environ* 45(39):7064-71

There is a growing body of evidence demonstrating that coarse particles (PM<sub>10-2.5</sub>) have detrimental impacts upon health, especially for respiratory effects. There are limited data available for indoor residential exposures. Some data exist regarding the composition of this PM size fraction with emphasis on crustal elements and biological components. This study includes data from 146 homes sampled in Regina, Saskatchewan (SK) where 5-day integrated concurrent monitoring of indoor and outdoor coarse particles was conducted during the winter and summer of 2007. The coarse particle filters were subsequently analysed for endotoxin content to determine the contribution of this compound. Winter indoor geometric mean concentrations of coarse particles exceeded outdoor concentrations (3.73  $\mu\text{g m}^{-3}$  vs 2.49  $\mu\text{g m}^{-3}$ ; paired t-test  $p < 0.0001$ ); however the reverse was found in summer (4.34  $\mu\text{g m}^{-3}$  vs 8.82  $\mu\text{g m}^{-3}$ ; paired t-test  $p < 0.0001$ ). Linear regression indicated that winter predictors of indoor coarse particles were outdoor coarse particles, ventilation and presence of at least two or more occupants. During the summer, increased use of

central air conditioning was associated with reduced coarse particles, while smoking and the presence of two or more occupants resulted in increased coarse particles. Endotoxin concentrations (EU  $\mu\text{g-1}$ ) were lower indoors than outdoors in both seasons. Spatial variability of ambient coarse particles was assessed to determine the suitability of using a single monitoring station within a city to estimate exposure. The coefficients of variation between homes sampled simultaneously and the central monitoring station were calculated (median COV in summer = 15% and winter = 24%) and showed significant variability by week, especially during the summer months, suggesting a single site may be insufficient for characterizing exposure. Future studies should consider daily measurements per home to understand shorter term exposures and day to day variability of these pollutants.

Wickens, K. Wickens, J. Douwes, R. Siebers, P. Fitzharris, I. Wouters, G. Doekes, K. Mason, M. Hearfield, M. Cunningham, J. Crane, 2003. Determinants of endotoxin levels in carpets in New Zealand homes. *Indoor Air* 2003; 13: 128-135

Endotoxin in house dust has been shown to be associated with asthma severity. Little is known about the influence of housing characteristics on endotoxin distribution. Using standardized methods, dust was sampled from a 1m<sup>2</sup> site and the whole accessible carpet area in selected Wellington, New Zealand homes (n = 77). Endotoxin was measured using a *Limulus Amoebocyte Lysate* assay. Relative humidity and temperature were recorded using sensors placed in carpet bases. Questionnaires were used to collect information on housing characteristics. All analyses were performed for endotoxin units (EU)/mg and EU/m<sup>2</sup> for each site. Geometric mean endotoxin levels were 22.7 EU/mg [geometric standard deviation (GSD) = 2.4] or 30,544 EU/m<sup>2</sup> (GSD = 3.2) from the 1m<sup>2</sup> site, and 28.4 EU/mg (GSD = 3.4) or 5653 EU/m<sup>2</sup> (GSD = 6.4) from the whole room. After controlling for confounding, endotoxin was positively associated with dogs inside [geometric mean ratio (GMR): 0.9-2.0], total household occupants (GMR: 1.7-2.0, for 1 m<sup>2</sup> sample only), vacuum cleaners <1-year old (GMR: 2.3-2.7), reusing vacuum dust collection bags (GMR: 1.4-3.1), steamcleaning or shampooing the carpet (GMR: 1.4-2.2) and high relative humidity (GMR: 1.4-1.6). Lower endotoxin was associated with floor insulation (GMR: 0.4-0.8), and north-facing living rooms (GMR: 0.4-0.8). This study has identified home characteristics that could be modified to reduce endotoxin exposure.

Wiener-Well, Yonit, MD, Margalit Galuty, RN, MSc, Bernard Rudensky, PhD, Yechiel Schlesinger, MD, Denise Attias, BSc, and Amos M. Yinnon, 2011. Nursing and physician attire as possible source of nosocomial infections. *Am J Infect Control* 2011;39:555-9

Background: Uniforms worn by medical and nursing staff are not usually considered important in the transmission of microorganisms. We investigated the rate of potentially pathogenic bacteria present on uniforms worn by hospital staff, as well as the bacterial load of these microorganisms. Methods: Cultures were obtained from uniforms of nurses and physicians by pressing standard blood agar plates at the abdominal zone, sleeve ends, and pockets. Each participant completed a questionnaire. Results: A total of 238 samples were collected from 135 personnel, including 75 nurses (55%) and 60 physicians (45%). Of these, 79 (58%) claimed to change their uniform every day, and 104 (77%) defined the level of hygiene of their attire as fair to excellent. Potentially pathogenic bacteria were isolated from at least one site of the uniforms of 85 participants (63%) and were isolated from 119 samples (50%); 21 (14%) of the samples from nurses' gowns and 6 (6%) of the samples from physicians' gowns (P = NS) included antibiotic-resistant bacteria. Conclusion: Up to 60% of hospital staff's uniforms are colonized with potentially pathogenic bacteria, including drug-resistant organisms. It remains to be determined whether these bacteria can be transferred to patients and cause clinically relevant infection

Wilkins, Ken, Kjeld Larsen, Mirella Simkus, 2000. Volatile metabolites from mold growth on building materials and synthetic media. *Chemosphere* 41 (2000) 437-446

Mold species which were isolated from damp buildings were grown on sterile building materials and some synthetic media in order to study the microbial volatile organic compounds produced. Patterns of the microbial volatile organic compounds (MVOC) were very media dependent but media which favor terpene biosynthesis may give patterns unique enough for identification of dominant indoor molds.

Winther, B., K. McCue, K. Ashe, J. Rubino and J.O. Hendley, 2011. Rhinovirus Contamination of Surfaces in Homes of Adults With Natural Colds: Transfer of Virus to Fingertips During Normal Daily Activities. *Journal of Medical Virology* 83:906-909

Multiple surfaces contaminated with rhinovirus were detected in hotel rooms by reverse transcriptase-polymerase chain reaction (RT-PCR) following occupancy by a cold sufferer. Whether infectious rhinovirus contaminates surfaces in homes and is transferred from surfaces to fingertips through normal activities is not known. Nasal secretions from 30 subjects with new colds were tested for rhinovirus genome by RT-PCR; infectious rhinovirus was sought with tissue cultures. Each subject identified 10 sites in their home touched during the preceding 24 hr. Samples from sites were tested for rhinovirus by RT-PCR and cell culture. Later, each subject's mucus (stored at 70°C) was deposited on surfaces for testing transfer to fingertips through daily life activities such as flipping a light switch, touching the telephone keypad, and holding the telephone handset. Nasal secretions from 16/30 subjects were positive for rhinovirus by RT-PCR; 66 (41%) of 160 surfaces in homes were positive. Contaminated surfaces included doorknobs (6 positive/18 tested), refrigerator door handles (8/14), TV remote controls (5/10), and bathroom faucets (8/10). Five (19%) of 26 RT-PCR positive sites from culture positive subjects were positive in cell culture. Nasal mucus from six culture positive subjects was deposited on objects. Infectious rhinovirus was detected on 22% of fingertips following contact with objects contaminated for 1 hr; transfer dropped to 3% after 24 hr of contamination, and 0% after 48 hr. Infectious rhinovirus found on surfaces in homes of people with colds can be transferred to fingertips, but infectivity of virus in mucus declines by 24 hr after deposition.

Wolkoff, Peder and Søren K. Kjærgaard, 2007. The dichotomy of relative humidity on indoor air quality. *Environment International* 33 (2007) 850-857.

Dry and irritated mucous membranes of the eyes and airways are common symptoms reported in office-like environments. Earlier studies suggested that indoor pollutants were responsible. We have re-evaluated, by review of the literature, how low relative humidity (RH) may influence the immediately perceived indoor air quality (IAQ), including odour, and cause irritation symptoms (i.e. longer-term perceived IAQ). "Relative humidity" were searched in major databases, and combined with: air quality, cabin air, dry eyes, formaldehyde, inflammation, mucous membranes, offices, ozone, pungency, sensory irritation, particles, precorneal tear film, sick building syndrome, stuffy air, and VOCs. The impact of RH on the immediately and longer-term perceived IAQ by VOCs, ozone, and particles is complex, because both the thermodynamic condition and the emission characteristics of building materials are influenced. Epidemiological, clinical, and human exposure studies indicate that low RH plays a role in the increase of reporting eye irritation symptoms and alteration of the precorneal tear film. These effects may be exacerbated during visual display unit work. The recommendation that IAQ should be "dry and cool" may be useful for evaluation of the immediately perceived IAQ in material emission testing, but should be considered cautiously about the development of irritation symptoms in eyes and upper airways during a workday. Studies indicate that RH about 40% is better for the eyes and upper airways than levels below 30%. The optimal RH may differ for the eyes and the airways regarding desiccation of the mucous membranes.

Womack, Ann M., Brendan J. M. Bohannon and Jessica L. Green, 2010. Biodiversity and biogeography of the atmosphere. *Phil. Trans. R. Soc. B* (2010) 365, 3645-3653.

The variation of life has predominantly been studied on land and in water, but this focus is changing. There is a resurging interest in the distribution of life in the atmosphere and the processes that underlie patterns in this distribution. Here, we review our current state of knowledge about the biodiversity and biogeography of the atmosphere, with an emphasis on micro-organisms, the numerically dominant forms of aerial life. We present evidence to suggest that the atmosphere is a habitat for micro-organisms, and not purely a conduit for terrestrial and aquatic life. Building on a rich history of research in terrestrial and aquatic systems, we explore biodiversity patterns that are likely to play an important role in the emerging field of air biogeography. We discuss the possibility of a more unified understanding of the biosphere, one that links knowledge about biodiversity and biogeography in the lithosphere, hydrosphere and atmosphere.

Womilojua, Taiwo O., J. David Millera\*, Paul M. Mayerb, Jeffrey R. Brook, 2003. Methods to determine the biological composition of particulate matter collected from outdoor air. *Atmospheric Environment* 37 (2003) 4335-4344.

Associations between increased morbidity and exposure to ambient air particulates have been the subject of intense study. Few data exist on the presence of cells or cell materials of fungi, bacteria and pollen in fine particle samples (< 2.5 µm). Because it is not possible to recognize such fragments by conventional means, one approach is to

determine the presence of signature biochemicals. This paper reports the development of a method for the analysis of intact glycerophospholipids present in extracts of fungi and pollen common in outdoor air by normal-phase liquid chromatography/electrospray ionization tandem mass spectrometry. Using cluster analysis of the phospholipids found, both mycelia and spores of fungi and pollen common in outdoor air could be separated. Little variation was detected between single spore isolates of individual strains of such fungi isolated across North America. White Birch and ragweed pollen contained similar phospholipid patterns but different from the fungi. From literature data, both were different than Gram negative bacteria. Semi-hivolume fine particle samples were collected on glass fibre filters in three locations in and near Toronto, extracted and analyzed. The concentrations of phospholipids measured suggested that fungal cells and pollen were responsible for 12-22% of the organic carbon fraction or 4-11% of the total mass depending upon location. The qualitative and quantitative estimates obtained compared favourably to data from concurrent rotorod samples. This suggests that, with improved sensitivity, the analysis of a larger number of samples would provide useful data for epidemiological studies and on the nature of organic carbon in fine particulate samples.

Wong, Bonnie C. K., Nelson Lee, Yuguo Li, Paul K. S. Chan, Hong Qiu, Zhiwen Luo, Raymond W. M. Lai, Karry L. K. Ngai, David S. C. Hui, K. W. Choi, and Ignatius T. S. Yu, 2010. Possible Role of Aerosol Transmission in a Hospital Outbreak of Influenza. *CLINICAL INFECTIOUS DISEASES* 2010:51 (15 November), 1176-1183

**Background.** We examined the role of aerosol transmission of influenza in an acute ward setting. **Methods.** We investigated a seasonal influenza A outbreak that occurred in our general medical ward (with open bay ward layout) in 2008. Clinical and epidemiological information was collected in real time during the outbreak. Spatiotemporal analysis was performed to estimate the infection risk among patients. Airflow measurements were conducted, and concentrations of hypothetical virus-laden aerosols at different ward locations were estimated using computational fluid dynamics modeling. **Results.** Nine inpatients were infected with an identical strain of influenza A/H3N2 virus. With reference to the index patient's location, the attack rate was 20.0% and 22.2% in the "same" and "adjacent" bays, respectively, but 0% in the "distant" bay ( $P = .04$ ). Temporally, the risk of being infected was highest on the day when noninvasive ventilation was used in the index patient; multivariate logistic regression revealed an odds ratio of 14.9 (95% confidence interval, 1.7-131.3;  $P = .015$ ). A simultaneous, directional indoor airflow blown from the "same" bay toward the "adjacent" bay was found; it was inadvertently created by an unopposed air jet from a separate air purifier placed next to the index patient's bed. Computational fluid dynamics modeling revealed that the dispersal pattern of aerosols originated from the index patient coincided with the bed locations of affected patients. **Conclusions.** Our findings suggest a possible role of aerosol transmission of influenza in an acute ward setting. Source and engineering controls, such as avoiding aerosol generation and improving ventilation design, may warrant consideration to prevent nosocomial outbreaks.

Wooley JC, Godzik A, Friedberg I (2010) A Primer on Metagenomics. *PLoS Comput Biol* 6(2): e1000667. doi:10.1371/journal.pcbi.1000667

Metagenomics is a discipline that enables the genomic study of uncultured microorganisms. Faster, cheaper sequencing technologies and the ability to sequence uncultured microbes sampled directly from their habitats are expanding and transforming our view of the microbial world. Distilling meaningful information from the millions of new genomic sequences presents a serious challenge to bioinformaticians. In cultured microbes, the genomic data come from a single clone, making sequence assembly and annotation tractable. In metagenomics, the data come from heterogeneous microbial communities, sometimes containing more than 10,000 species, with the sequence data being noisy and partial. From sampling, to assembly, to gene calling and function prediction, bioinformatics faces new demands in interpreting voluminous, noisy, and often partial sequence data. Although metagenomics is a relative newcomer to science, the past few years have seen an explosion in computational methods applied to metagenomic-based research. It is therefore not within the scope of this article to provide an exhaustive review. Rather, we provide here a concise yet comprehensive introduction to the current computational requirements presented by metagenomics, and review the recent progress made. We also note whether there is software that implements any of the methods presented here, and briefly review its utility. Nevertheless, it would be useful if readers of this article would avail themselves of the comment section provided by this journal, and relate their own experiences. Finally, the last section of this article provides a few representative studies illustrating different facets of recent scientific discoveries made using metagenomics.

Wouters, INGE M., JEROEN DOUWES, GERT DOEKES, PETER S. THORNE, BERT BRUNEKREEF, AND DICK J. J. HEEDERIK, 2000. Increased Levels of Markers of Microbial Exposure in Homes with Indoor Storage of Organic Household Waste. *Appl. Environ. Microbiol.* 2000, 66(2):627

As part of environmental management policies in Europe, separate collection of organic household waste and nonorganic household waste has become increasingly common. As waste is often stored indoors, this policy might increase microbial exposure in the home environment. In this study we evaluated the association between indoor storage of organic waste and levels of microbial agents in house dust. The levels of bacterial endotoxins, mold  $\beta(1\rightarrow3)$ -glucans, and fungal extracellular polysaccharides (EPS) of *Aspergillus* and *Penicillium* species were determined in house dust extracts as markers of microbial exposure. House dust samples were collected in 99 homes in The Netherlands selected on the basis of whether separated organic waste was present in the house. In homes in which separated organic waste was stored indoors for 1 week or more the levels of endotoxin, EPS, and glucan were 3.2-, 7.6-, and 4.6-fold higher, respectively (all  $P < 0.05$ ), on both living room and kitchen floors than the levels in homes in which only nonorganic residual waste was stored indoors. Increased levels of endotoxin and EPS were observed, 2.6- and 2.1-fold ( $P < 0.1$ ), respectively, when separated organic waste was stored indoors for 1 week or less, whereas storage of nonseparated waste indoors had no effect on microbial agent levels ( $P > 0.2$ ). The presence of textile floor covering was another major determinant of microbial levels ( $P < 0.05$ ). Our results indicate that increased microbial contaminant levels in homes are associated with indoor storage of separated organic waste. These increased levels might increase the risk of bioaerosol-related respiratory symptoms in susceptible people.

Wu, P.-C., Y.-Y. Li, C.-M. Chiang, C.-Y. Huang, C.-C. Lee, F.-C. Li, H.-J. Su, 2005. Changing microbial concentrations are associated with ventilation performance in Taiwan's air-conditioned office buildings. *Indoor Air* 2005; 15: 19-26

Our study conducted serial environmental measurements in 12 large office buildings with two different ventilation designs to obtain airborne microbial concentrations in typical office buildings, and to examine the effects of occupant density, ventilation type and air exchange efficiency on indoor microbial concentrations. Duplicate samples of airborne fungi and bacteria, a total of 2477 measurements, were collected based on a scheme of conducting sampling three times a day for at least seven consecutive days at every study building. Air change rates (ACHs) were also estimated by tracer gas concentration decay method, and measured by continuous Multi-Gas monitor for each building. Most sampling sites were with total fungal and bacteria concentrations higher than 1000 CFU/m<sup>3</sup>, an often-quoted guideline in earlier research. Significantly higher concentrations of fungi and bacteria, as well as higher indoor/outdoor (I/O) ratios across most groups of airborne microbes, were identified in buildings with fan coil unit (FCU) system than those with air-handling unit (AHU) system (Student's t test,  $P < 0.0001$ ). Older buildings and higher air exchange rates were statistically associated with greater indoor bacteria levels in FCU ventilated buildings ( $R^2 = 0.452$ ); a pattern not found in AHU buildings. Increasing ACH seemed to be the determinant factor for rising indoor fungal and *Cladosporium* concentrations in those FCU buildings ( $R^2 = 0.346$ ;  $0.518$ ). Our data indicated that FCU ventilated buildings might have provided more outdoor matters into indoor environments through direct penetration of outdoor air. Results also demonstrated a quantitative association between rising numbers of occupants and increasing indoor levels of yeast in both FCU and AHU ventilated buildings. The regression model identified in this study may be considered a reference value for proposing an optimal ACH, while with adequate filtration of fresh air, as an effective strategy in lowering indoor microbial concentrations in air-conditioned buildings.

Xie, X., Y. Li, A. T. Y. Chwang, P. L. Ho, W. H. Seto, 2007. How far droplets can move in indoor environments - revisiting the Wells evaporation-falling curve. *Indoor Air* 2007; 17: 211-225

A large number of infectious diseases are believed to be transmitted between people via large droplets and by airborne routes. An understanding of evaporation and dispersion of droplets and droplet nuclei is not only significant for developing effective engineering control methods for infectious diseases but also for exploring the basic transmission mechanisms of the infectious diseases. How far droplets can move is related to how far droplet-borne diseases can transmit. A simple physical model is developed and used here to investigate the evaporation and movement of droplets expelled during respiratory activities; in particular, the well-known Wells evaporation-falling curve of droplets is revisited considering the effect of relative humidity, air speed, and respiratory jets. Our simple model considers the movement of exhaled air, as well as the evaporation and movement of a single droplet. Exhaled air is treated as a steady-state non-isothermal (warm) jet horizontally issuing into stagnant surrounding air. A droplet is assumed to evaporate and move in this non-isothermal jet. Calculations are performed for both pure water droplets and droplets of

sodium chloride (physiological saline) solution (0.9% w/v). We calculate the droplet lifetimes and how droplet size changes, as well as how far the droplets travel in different relative humidities. Our results indicate that a droplet's size predominately dictates its evaporation and movement after being expelled. The sizes of the largest droplets that would totally evaporate before falling 2 m away are determined under different conditions. The maximum horizontal distances that droplets can reach during different respiratory activities are also obtained. Our study is useful for developing effective prevention measures for controlling infectious diseases in hospitals and in the community at large.

Yamamoto, N., D. G. Shendell and J. Peccia, 2011. Assessing allergenic fungi in house dust by floor wipe sampling and quantitative PCR. *Indoor Air* doi:10.1111/j.1600-0668.2011.00732.x

In the present study, we modified an existing surface wipe sampling method for lead and other heavy metals to create a protocol to collect fungi in floor dust followed by real-time quantitative PCR (qPCR)-based detection. We desired minimal inconvenience for participants in residential indoor environmental quality and health studies. Accuracy, precision, and method detection limits (MDLs) were investigated. Overall, MDLs ranged from 0.6 to 25 cell/cm<sup>2</sup> on sampled floors. Overall measurement precisions expressed as the coefficient of variation because of sample processing and qPCR ranged 6-63%. Median and maximum fungal concentrations in house dust in study homes in Visalia, Tulare County, California, were 110 and 2500 cell/cm<sup>2</sup>, respectively, with universal fungal primers (allergenic and nonallergenic species). The field study indicated samplings in multiple seasons were necessary to characterize representative whole-year fungal concentrations in residential microenvironments. This was because significant temporal variations were observed within study homes. Combined field and laboratory results suggested this modified new wipe sampling method, in conjunction with growth-independent qPCR, shows potential to improve human exposure and health studies for fungal pathogens and allergens in dust in homes of susceptible, vulnerable population subgroups.

Yang L, Wong CM, Chan KP, Chau PYK, Ou CQ, Chan KH, Peiris JSM. 2009. Seasonal effects of influenza on mortality in a subtropical city RID E-5183-2011. *BMC Infect Dis* 9:133.

**Background** Influenza has been associated with a heavy burden of mortality. In tropical or subtropical regions where influenza viruses circulate in the community most of the year, it is possible that there are seasonal variations in the effects of influenza on mortality, because of periodic changes in environment and host factors as well as the frequent emergence of new antigenically drifted virus strains. In this paper we explored this seasonal effect of influenza. **Methods** A time-varying coefficient Poisson regression model was fitted to the weekly numbers of mortality of Hong Kong from 1996 to 2002. Excess risks associated with influenza were calculated to assess the seasonal effects of influenza. **Results** We demonstrated that the effects of influenza were higher in winter and late spring/early summer than other seasons. The two-peak pattern of seasonal effects of influenza was found for cardio-respiratory disease and sub-categories pneumonia and influenza, chronic obstructive pulmonary disease, cerebrovascular diseases and ischemic heart disease as well as for all-cause deaths. **Conclusion** The results provide insight into the possibility that seasonal factors may have impact on virulence of influenza besides their effects on virus transmission. The results warrant further studies into the mechanisms behind the seasonal effect of influenza.

Yang L, Chen PY, He JF, Chan KP, Ou CQ, Deng AP, Peiris JSM, Wong CM. 2011. Effect modification of environmental factors on influenza-associated mortality: A time-series study in two Chinese cities. *BMC Infect Dis* 11:342

**Background** Environmental factors have been associated with transmission and survival of influenza viruses but no studies have ever explored the role of environmental factors on severity of influenza infection. **Methods** We applied a Poisson regression model to the mortality data of two Chinese metropolitan cities located within the subtropical zone, to calculate the influenza associated excess mortality risks during the periods with different levels of temperature and humidity. **Results** The results showed that high absolute humidity (measured by vapor pressure) was significantly ( $p < 0.05$ ) associated with increased risks of all-cause and cardiorespiratory deaths, but not with increased risks of pneumonia and influenza deaths. The association between absolute humidity and mortality risks was found consistent among the two cities. An increasing pattern of influenza associated mortality risks was also found across the strata of low to high relative humidity, but the results were less consistent for temperature. **Conclusions** These findings highlight the need for people with chronic cardiovascular and respiratory diseases to take extra caution against influenza during hot and humid days in the subtropics and tropics.



Yang, Wan, Subbiah Elankumaran and Linsey C. Marr, 2011. Concentrations and size distributions of airborne influenza A viruses measured indoors at a health centre, a day-care centre and on aeroplanes. *J. R. Soc. Interface* 2011 8, doi: 10.1098/rsif.2010.0686

The relative importance of the aerosol transmission route for influenza remains contentious. To determine the potential for influenza to spread via the aerosol route, we measured the size distribution of airborne influenza A viruses. We collected size-segregated aerosol samples during the 2009–2010 flu season in a health centre, a day-care facility and onboard aeroplanes. Filter extracts were analysed using quantitative reverse transcriptase polymerase chain reaction. Half of the 16 samples were positive, and their total virus concentrations ranged from 5800 to 37 000 genome copies m<sup>-3</sup>. On average, 64 per cent of the viral genome copies were associated with fine particles smaller than 2.5 µm, which can remain suspended for hours. Modelling of virus concentrations indoors suggested a source strength of  $1.6 \pm 1.2 \times 10^5$  genome copies m<sup>-3</sup> air h<sup>-1</sup> and a deposition flux onto surfaces of  $13 \pm 7$  genome copies m<sup>-2</sup> h<sup>-1</sup> by Brownian motion. Over 1 hour, the inhalation dose was estimated to be  $30 \pm 18$  median tissue culture infectious dose (TCID<sub>50</sub>), adequate to induce infection. These results provide quantitative support for the idea that the aerosol route could be an important mode of influenza transmission.

Yang, Wan, and Linsey C. Marr, 2012. Mechanisms by Which Ambient Humidity May Affect Viruses in Aerosols. *Applied and Environmental Microbiology*, Volume 78 Number 19 p. 6781-6788

Many airborne viruses have been shown to be sensitive to ambient humidity, yet the mechanisms responsible for this phenomenon remain elusive. We review multiple hypotheses, including water activity, surface inactivation, and salt toxicity, that may account for the association between humidity and viability of viruses in aerosols. We assess the evidence and limitations for each hypothesis based on findings from virology, aerosol science, chemistry, and physics. In addition, we hypothesize that changes in pH within the aerosol that are induced by evaporation may trigger conformational changes of the surface glycoproteins of enveloped viruses and subsequently compromise their infectivity. This hypothesis may explain the differing responses of enveloped viruses to humidity. The precise mechanisms underlying the relationship remain largely unverified, and attaining a complete understanding of them will require an interdisciplinary approach.

Yang W, Elankumaran S, Marr LC (2012) Relationship between Humidity and Influenza A Viability in Droplets and Implications for Influenza's Seasonality. *PLoS ONE* 7(10): e46789. doi:10.1371/journal.pone.0046789

Humidity has been associated with influenza's seasonality, but the mechanisms underlying the relationship remain unclear. There is no consistent explanation for influenza's transmission patterns that applies to both temperate and tropical regions. This study aimed to determine the relationship between ambient humidity and viability of the influenza A virus (IAV) during transmission between hosts and to explain the mechanisms underlying it. We measured the viability of IAV in droplets consisting of various model media, chosen to isolate effects of salts and proteins found in respiratory fluid, and in human mucus, at relative humidities (RH) ranging from 17% to 100%. In all media and mucus, viability was highest when RH was either close to 100% or below ~50%. When RH decreased from 84% to 50%, the relationship between viability and RH depended on droplet composition: viability decreased in saline solutions, did not change significantly in solutions supplemented with proteins, and increased dramatically in mucus. Additionally, viral decay increased linearly with salt concentration in saline solutions but not when they were supplemented with proteins. There appear to be three regimes of IAV viability in droplets, defined by humidity: physiological conditions (~100% RH) with high viability, concentrated conditions (50% to near 100% RH) with lower viability depending on the composition of media, and dry conditions (<50% RH) with high viability. This paradigm could help resolve conflicting findings in the literature on the relationship between IAV viability in aerosols and humidity, and results in human mucus could help explain influenza's seasonality in different regions.

Yli-Piri, T., J. Kusnetsov, M.-R. Hirvonen, M. Seuri, A. Nevalainen, 2009. Survival of amoebae on building materials. *Indoor Air* 2009; 19: 113-121.

Moisture damage and concurrent microbial growth in buildings are associated with adverse health effects among the occupants. However, the causal agents for the symptoms are unclear although microbes are assumed to play a major role. Fungi and bacteria are not the only microbes inhabiting moist building materials; it was recently revealed that amoebae are also present. As amoebae have the potential to harbor many pathogens and to modulate the

characteristics of growing microbes, a better appreciation of the growth and survival of amoebae in moisture damage conditions will add to the understanding of their effects on health outcomes. In this study, we investigated the ability of amoebae to survive on six building materials. Furthermore, both aged and unused materials were tested. Amoebae survived on gypsum board and mineral wool for the whole 2 months experiment even without additional sustenance. When sustenance (heat-killed bacteria) was available, aged pine wood and birch wood also allowed their survival. In contrast, amoebae were quickly killed on fresh pine wood and they did not survive on concrete or linoleum. In conclusion, our data show that amoebae can persist on several common building materials once these materials become wet.

Zhang X, Zhao Z, Nordquist T, Larsson L, Sebastian A, Norback D. 2011. A longitudinal study of sick building syndrome among pupils in relation to microbial components in dust in schools in china. *Sci Total Environ* 409(24):5253-9.

There are few longitudinal studies on sick building syndrome (SBS), which include ocular, nasal, throat, and dermal symptoms, headache, and fatigue. We studied the associations between selected microbial components, fungal DNA, furry pet allergens, and incidence and remission of SBS symptoms in schools in Taiyuan, China. The study was based on a two-year prospective analysis in pupils (N=1143) in a random sample of schools in China. Settled dust in the classrooms was collected by vacuum cleaning and analyzed for lipopolysaccharide (LPS), muramic acid (MuA), and ergosterol (Erg). Airborne dust was collected in Petri dishes and analyzed for cat and dog allergens and fungal DNA. The relationship between the concentration of allergens and microbial compounds and new onset of SBS was analyzed by multi-level logistic regression. The prevalence of mucosal and general symptoms was 33% and 28%, respectively, at baseline, and increased during follow-up. At baseline, 27% reported at least one symptom that improved when away from school (school-related symptoms). New onset of mucosal symptoms was negatively associated with concentration of MuA, total LPS, and shorter lengths of 3-hydroxy fatty acids from LPS, C14, C16, and C18. Onset of general symptoms was negatively associated with C18 LPS. Onset of school-related symptoms was negatively associated with C16 LPS, but positively associated with total fungal DNA. In general, bacterial compounds (LPS and MuA) seem to protect against the development of mucosal and general symptoms, but fungal exposure measured as fungal DNA could increase the incidence of school-related symptoms.