2nd Aerosols and Microbiology conference

9–11 June 2026

Leeds Marriott Hotel
Leeds, UK

INVITED AND OFFERED TALKS

iStock/ALIOUI Mohammed Elamine

#Aerosols2026

MICROBIOLOGY SOCIETY

Invited Speaker :

Epidemiology of respiratory virus transmission

Eunice Y. C. Shiu, Samuel M. S. Cheng, Polly P. L. Chung, Jessica Y. W. Liu, Gigi Y. Z. Liu, Alan M. C. Au, Natalie W. S. Yu, Tim K. L. Tsang, Dennis K. M. Ip, J. S. Malik Peiris, Benjamin J. Cowling, Nancy H. L. Leung

The University of Hong Kong, Hong Kong, Hong Kong

Abstract

In this talk, Dr. Leung aims to facilitate cross-disciplinary discussions and collaborations on studying and controlling airborne disease transmission by giving a broad overview on studying respiratory virus transmission through field and epidemiologic studies. She will introduce common epidemiologic concepts and methods in studying respiratory virus transmission in the population; the discussion on standardising airborne transmission route terminology; different levels of evidence in support of a transmission route, including technical hurdles in generating empirical evidence on airborne transmission and effectiveness of interventions; the challenges in assessing relative risk between transmission routes from field studies; and the clinical importance of understanding airborne transmission.

Decoding the air microbiome with nanopore sequencing and real-time metagenomics

Richard Leggett[1], Darren Heavens[1], Ned Peel[1], Jade van Wijk[1], Matt Clark[2]

[1]Earlham Institute, Norwich, United Kingdom. [2]Natural History Museum, London, United Kingdom

Abstract

Over the past decade, we have developed AirSeq, a whole-genome sequencing–based approach for characterising the air microbiome. AirSeq combines high-volume active air sampling (hundreds of litres per minute), amplification-free nanopore sequencing, and custom real-time bioinformatics implemented in MARTi (Metagenomic Analysis in Real-Time, Peel et al. 2025).

Initial applications focused on the early detection of airborne fungal pathogens in agricultural environments, including greenhouses and open fields, where AirSeq detected pathogen presence days to weeks before visible disease symptoms appeared on plants (Giolai et al. 2024). Subsequent work has expanded the approach to the surveillance of bacterial pathogens in cattle housing and in urban environments.

Alongside targeted pathogen detection, a major focus has been on characterising the background air microbiome. Between 2019 and 2021, we conducted air sampling at 13 sites across London, with most locations sampled in multiple seasons and one site sampled weekly for a full year. These data revealed a highly diverse assemblage of airborne flora and fauna, with pronounced and reproducible seasonal patterns. At one site – the wildlife garden at the Natural History Museum – we compared detected taxa with curated species inventories, highlighting gaps in available reference genomes that can constrain taxonomic classification.

More recently, we have extended this work to eight contrasting habitats across Norfolk and Suffolk, sampling each site seasonally over two years to investigate how habitat type shapes the background air microbiome. Together, these studies demonstrate the potential of whole-genome airborne metagenomics to link aerosol biology with ecosystem context, seasonality, and disease surveillance.

Can we create an infection resilient environment?

Catherine Noakes

University of Leeds, Leeds, United Kingdom

Abstract

The pandemic substantially raised awareness of the role the indoor environment plays in transmission of infection. While airborne transmission is now accepted as the dominant mode for COVID-19, there are substantial questions that remain around the specific mechanisms for pathogen transmission and just how effective different mitigation measures are.

Simple models such as the Wells-Riley approach are widely used to make the case for interventions such as ventilation, but transmission involves a complex chain of events that such models struggle to capture. From the emission of a pathogen into an environment, through transport mechanisms via air, surfaces and people within that environment, to exposure of a susceptible person, the process is determined by the spatial and transient interactions of physics, biology and chemistry as well as human behaviours. Measuring real-world infection outcomes is challenging, and even where it is possible, it is difficult to unpick the relative importance of different components.

Despite all of this complexity, policy makers and practitioners need evidence that can be easily translated into advice. This talk considers the processes involved in transmission, where we have evidence and where there are gaps. It considers the challenge of trading off simple advice with complex realities and explores how much we really can provide effective and practical protection from transmission in the built environment.

Clearing the air about vaccines and transmission of infectious pathogens

Adam Finn

University of Bristol, Bristol, United Kingdom

Abstract

Most people (including licensing authorities) consider vaccines as if they were drugs - simply: do they protect the recipient and/or cause side-effects? However, there is a growing appreciation that a key aspect of vaccine effectiveness is whether and how well they inhibit transmission of infections within populations. Vaccines and deployment strategies that focus on transmission are the most efficient and effective and can, in some cases, wipe out infectious pathogens altogether. This phenomenon is highly relevant to a large number of viral and bacterial infections that are only found in humans and which are transmitted from one person to another partly or entirely in droplets and aerosols generated in the upper respiratory tract (the nose and mouth) when we breathe, talk, sneeze, cough, shout and sing. In this talk I will discuss some of the approaches taken towards understanding how such infections transmit, explain ways in which vaccines can bring about indirect effects and provide examples of recent vaccine programmes designed primarily for their indirect effects.

Antibiotic resistance in bioaerosols: shedding a light on emissions, transport and fate

Caroline Duchaine

Université Laval, Quebec City, Canada

Abstract

A vast project, titled "Antimicrobial resistance genes (ARG) in bioaerosols in Canadian arctic, rural and urban environments: sources, profiles, transport, and fate" was funded by the 2019 Natural Sciences and Engineering Research Council of Canada (NSERC) Discovery Frontiers program. This project involving scientists from broad ranges of expertise (bioinformatics, bioaerosols, veterinary medicine, engineering, medical doctors, epidemiologists, modeling experts, and physiologists) has led to broad air sampling campaigns, providing rich information on various bioaerosol sources for antibiotic resistance genes both in natural and man-made environments. We have captured air samples from clouds, atmospheric particles, trans-Atlantic and Northern environments, hospitals, agricultural (pig, poultry, and fish) farming and manure spreading activities, and wastewater treatment. The project also explores alternative air sampling methods such as conifer needles, HVAC systems filters, and car air cabin filters that were used for a trans-Canada survey of circulating ARGs. A high-throughput PCR assay was also developed to increase analytical capacity. Findings. Our data will be used for dispersion modeling, risk assessment models, and in vivo ARG transfer. Data curation was secured through an extensive database and sample preservation system to ensure the sharing of information and material for future collaborations. This project is the first initiative to cover broad sources of bioaerosols and integrate the findings into models to better understand the role of air in the dispersion of ARG. The presentation will cover the methods, context and possibility of collaborations for future valorization of samples and data.

Atmospheric Incursions of Plant Pathogens: From Leaf Surfaces to Continental Transport

David G. Schmale

Virginia Tech University, Virginia, USA

Abstract

The atmospheric transport of plant pathogens unfolds across a continuum of scales, linking microscale release processes at leaf surfaces to long-distance movement across regions and continents. Together, these processes underpin atmospheric incursions, where pathogens cross borders unannounced and often undetected. At the smallest scale, dispersal begins with liberation from surfaces and escape through the laminar boundary layer. High-speed imaging reveals that raindrop impacts generate vortex-like flows that entrain leaf rust spores into the air, while jumping droplet condensation and cascading “billiard ball” interactions amplify spore release across leaf surfaces. At the farm scale, transport is governed by turbulent flow within the surface boundary layer, shaping dispersal across agricultural landscapes. Release–recapture studies show how fungal spores move from field-scale sources under natural conditions, while work on genetically engineered switchgrass demonstrates how pollen disperses beyond field boundaries, raising challenges for disease management and gene flow. At regional and continental scales, pathogens become entrained in the planetary boundary layer and free atmosphere, where structured airflows organize movement over hundreds to thousands of kilometers. These highways in the sky connect distant regions through coherent transport pathways, including atmospheric bridges linking Australia and New Zealand. Advances in sensing and sampling are enabling new insights into pathogen movement across scales. Integrating these observations with atmospheric transport models provides a pathway toward predictive frameworks capable of detecting, forecasting, and responding to biological threats before they arrive.

Bioaerosols as vital monitoring tool for One Health assessments of antimicrobial resistance

Paul George

Laval University, Quebec, Canada

Abstract

Global rates of antimicrobial resistant infections are rising, as are its associated mortality, morbidity, and economic impacts. Increasingly academic, governmental, and health stakeholders have worked to implement One Health approaches to attempt to monitor and control resistance. Despite this, major knowledge gaps surround the transport and prevalence of antimicrobial resistance in the environment. The roles of bioaerosols in the dispersal of antimicrobial resistance are important but have remained poorly characterised, especially outside of clinical settings. Many of these knowledge gaps related to limitations on bioaerosol collection and analyses.

A major part of my early career research has been focused on assessing different bioaerosol collection techniques for monitoring antimicrobial resistance in environmental contexts. This work focused on using low-cost, passive air samplers, to monitor characterise the antimicrobial resistance gene profile ambient air as well as emissions from livestock buildings. This talk will describe the use of vehicle cabin air filters as to map and compare regional profiles antimicrobial resistance as well as the use of the phyllosphere sampling to monitor resistance in agricultural bioaerosols.

Finally, ongoing and planned work expanding these methods to other aspects of One Health will be presented. Monitoring fungal bioaerosols in diverse environments is being assessed to characterize the spread of antifungal resistance, disease emergence, and climate change impacts of biodiversity.

Offered Talk :

Investigation of novel methods to study the survival of foot-and-mouth disease virus in aerosols

Charlotte Reston[1,2], Eva Perez Martin[1], Simon Gubbins[1], Allen Haddrell[2], Jonathan Reid[2]

[1]The Pirbright Institute, Woking, United Kingdom. [2]University of Bristol, Bristol, United Kingdom

Abstract

While airborne transmission of viruses has long been a significant area of research, foot-and-mouth disease virus (FMDV) is relatively understudied in this regard. This is important as FMD has severe economic impacts; the 2001 outbreak cost the UK approximately £8 billion, in addition to the culling of 6.5 million animals. Although the primary mechanism of transmission is direct contact between infected cloven-hooved animals, a low probability but high consequence transmission mechanism is via aerosols. Aerosols can travel much further distances than larger droplets and therefore have the potential to circumvent quarantine zones, an important part of FMD control. This, combined with the fact that several outbreaks of FMD have likely resulted from aerosol transmission, demonstrates the importance of studying the conditions determining if infectivity is retained during aerosol transport.

This work studies FMDV survival in aerosols under a range of environmental conditions in high containment. Two complementary experimental methods were employed, 1) the use of microthreads, produced by winding natural spider silk onto frames and exposing them to FMDV in a controlled aerosol chamber; and 2) the CELEBS instrument (Controlled Electrodynamic Levitation and Extraction of Bioaerosols onto a Substrate), which allows individual virus-containing aerosols to be suspended under precisely controlled relative humidity or temperature. These methods will provide survival parameters for FMDV and allow strains to be compared. Results can determine if quarantine zones around infected farms are appropriate, account for the risk of aerosolised transmission, and ultimately better inform outbreak policy resulting in more effective control of FMD.

Airborne pathogen detection via MASC-On - a novel and innovative Technology

Pia Karbiener, Battist Utinger, Markus Kalberer

University of Basel, Basel, Switzerland

Abstract

In light of the COVID-19 pandemic, airborne bioaerosol like bacteria and viruses are a major concern for human health. Therefore, monitoring of the concentrations of these bioaerosols plays a vital role in understanding disease transmission. Rapid, automated, quantitative and specific bioaerosol monitoring would allow for continuous assessment of airborne virus and bacteria at hospitals and similar locations.

In this proof-of-concept study, we develop and characterise a continuous pathogenic bioaerosol sampler and detector. First, bioaerosols are transferred from air into a liquid phase; next, they are selectively captured and processed within a carrier system; and finally, they are separated and prepared for downstream analysis.

We have already successfully connected all three phases into one continuous, automated, and autonomous prototype for pathogenic bioaerosol monitoring. With a time resolution of 60 minutes (of which 15 are spent on sample acquisition) our instrument collects 99.5% of nebulized E. coli bacteria continuously. Our results were confirmed with agar plate analyses.

While other instruments for automated pathogen detection exist, these techniques lack either specificity, quantification, automation or time-resolution. This novel mix of methods attempts to combine all factors mentioned. Our next step is to optimize further and apply this method to airborne virus.

Assessing the placement of HEPA air cleaners in a multi-zone hospital ward to reduce infection risk using CONTAM modelling

Anushi Khandare[1], Alexander Edwards[2], Martin Lopez Garcia[1], Marco-Felipe King[1], Louise Fletcher[1], Andrew Carneige[3], Catherine Naokes[1]

[1]University of Leeds, Leeds, United Kingdom. [2]University of Bristol, Bristol, United Kingdom. [3]Air Sentry Limited, Wiltshire, United Kingdom

Abstract

The COVID-19 pandemic has emphasised the need for understanding the dynamics of airborne infections and good ventilation, particularly in a hospital. Air cleaners are an important advancement in mitigating against indoor air pollution and infection transmission, especially where increasing ventilation is challenging. This work investigates the impact of air cleaners on reducing the concentration of airborne pathogens in a multi-zone hospital ward using CONTAM modelling. The methodology and the ward design were based on prior work on ventilation by Edwards et.al [2023]. The model assumed HEPA-based air cleaners were strategically placed at different locations in the hospital ward zones. Simulations analysed fluctuations in pathogen concentration and occupant exposure over 7 days. Energy analysis was also carried out for three different flow rates of the air cleaner. The reduction in concentration was strongly influenced by the location of air cleaners relative to the pathogen source and the ventilation pattern along with spatial arrangement of each zone. As compared to the no-cleaner condition, a significant reduction in pathogen concentration was observed at the lowest airflow speed, and increasing the device's speed further enhanced the removal efficiency, leading to progressively lower pathogen concentrations. The model provides useful insights for designing multi-zone wards to minimize airborne transmission and improve safety for healthcare workers and patients. CONTAM is effective for exploring zonal flows and time fluctuations. However, validating the results with experimental data, and detailed analysis of airflow patterns using computational fluid dynamics to explore spatial variations will form the basis of future work.

Air pollution exposure enhances host-to-host transmission of *Streptococcus pneumoniae*

Daan Beentjes, Aras Kadioglu

University of Liverpool, Liverpool, United Kingdom

Abstract

BACKGROUND. Air pollution is considered a major risk factor for airway infections, with *Streptococcus pneumoniae* (the pneumococcus) causing most cases. Although epidemiological data strongly suggest an association between air pollution levels and the transmission of respiratory pathogens, direct causal evidence is lacking, and the underlying mechanisms remain poorly understood.

METHODS. To address this gap, we used a novel murine host-to-host transmission model to assess the impact of two prevalent sources of air pollution (Diesel exhaust particulates [DEP] and rail dust) on pneumococcal transmission and colonisation dynamics. In this model, mice were exposed daily to 15-30 µg of DEP or rail dust, representing typical daily human exposure in urban environments.

RESULTS. We demonstrate that air pollutants facilitate pneumococcal transmission in a dose- and type-dependent manner. Air pollution exposure increased host susceptibility to pneumococcal colonisation and significantly enhanced bacterial shedding from colonised hosts. Further investigation into the underlying mechanisms revealed that air pollutants induce inflammation and mucus production, leading to enhanced nasal secretion and bacterial release from the airways.

CONCLUSION. This study provides the first direct evidence that air pollution exposure drives host-to-host transmission of respiratory pathogens and identifies host factors that may be targeted to mitigate the impact of air pollution on respiratory infections.

A low burden broad-spectrum electrochemical pathogen sensor in a field trial

Richard de Campos[1], Amanda Weiler[2], Nathalie Turgeon[3], Caroline Ducharine[3], Nora Chan[2], Abebaw Jemere[1]

[1]National Research Council Canada – Quantum and Nanotechnologies Research Centre, Edmonton, Canada. [2]Defence Research and Development Canada – Suffield Research Centre, Medicine Hat, Canada. [3]Institut universitaire de cardiologie et de pneumologie de Quebec-Universite Laval, Laval, Canada

Abstract

Timely detection of harmful bioaerosols is critical for personnel protection and quick operational decisions. Conventional detection and identification methods are often slow, costly and impractical for onsite analysis, limiting early intervention and disease containment. This work integrates electrochemical impedance spectroscopy (EIS) with digital microfluidic (DMF) technology to enable rapid, multiplexed detection of pathogens using Toll-like receptor (TLR) proteins as biorecognition elements. This low-burden, portable broad-spectrum sensor could distinguish diverse airborne pathogens in near-real time without the need for *a priori* knowledge.

The integrated EIS-DMF detection platform consists of multiplexed electrodes functionalized with different TLRs to recognize specific, immutable pathogen-associated molecular patterns. Pathogen simulants were aerosolized in controlled and field conditions, collected using commercial and custom biosamplers, and analyzed on the DMF device. Impedance changes before and after sample exposure indicate the presence and types of pathogens, and the results were validated against quantitative PCR and lateral flow assay measurements.

The multiplexed and integrated EIS biosensor successfully detected and differentiated aerosolized pathogen simulants within 30 minutes. For example, TLR2/6 sensors responded distinctly to *Bacillus atrophaeus* spores, enabling qualitative comparison of biosampler performance. Additionally, bioaerosol sample analyses confirmed measurable signal changes above background levels, validating the sensor's capability for near-real-time, in-field detection and classification of airborne pathogens.

These findings represent a significant advancement in portable, multiplexed biodetection technologies. This approach bridges the gap between laboratory-based diagnostics and field-deployable environmental monitoring tools, supporting rapid, broad-spectrum sensing platforms that strengthen public health preparedness, defence and security through early detection of emerging microbial threats.

Longitudinal Study of Respiratory Aerosol Emissions from Individuals and the Consequences for Understanding the Indoor Transmission of Respiratory Pathogens

Nan Zhou[1], Andrew J. Shrimpton[2], Natalie O'Hara[1], Anthony E. Pickering[2], Jonathan P. Reid[1]

[1]School of Chemistry, University of Bristol, Bristol, United Kingdom. [2]School of Physiology, Pharmacology & Neuroscience, Bristol, United Kingdom

Abstract

Background

Accurate measurement of respiratory aerosols is challenging because exhaled particle concentrations are extremely low and difficult to distinguish from indoor background aerosol. As measurements are often collected at a single time point, it remains unclear how individual emission rates vary over time and whether high emitters remain high over extended periods.

Methods

We developed a measurement approach to quantify respiratory aerosol emissions under non-ultra-clean indoor conditions. Exhaled particles were measured using an Aerodynamic Particle Sizer while participants wore a tightly sealed facemask connected to the instrument. Background aerosol was minimised by filtering inhaled air through five low-resistance filters and using air purifiers to reduce indoor particle concentrations. Participants completed a standardised sequence of breathing and speaking activities. Measurements were performed on Days 0, 1, 7, 14 and 28 (n = 43), with follow-up at Day 180 when available (n = 28).

Results

Individuals exhale consistent levels of aerosol over extended periods when breathing and speaking, although with large inter-individual variations. A subset of participants consistently emitted substantially more particles than others, up to 180 days in those with follow-up. Within the sampled age range, aerosol emissions showed a positive association with age across activities, whereas associations with height, weight and BMI were weaker.

Conclusion

Robust longitudinal respiratory aerosol measurements can be achieved outside ultra-clean environments using effective background filtration. Persistent high emitters over months highlight stable heterogeneity that should be considered in indoor exposure assessment and airborne transmission risk.

Quantifying and modeling surrogate bacteria inactivation in respiratory droplets

Taylor Medina[1], Beiping Luo[2], Thomas Peter[2], Tamar Kohn[1]

[1]Swiss Federal Institute of Technology Lausanne, Lausanne, Switzerland. [2]Swiss Federal Institute of Technology Zürich, Zürich, Switzerland

Abstract

Respiratory pathogens are transmitted through exhaled droplets and aerosols containing infectious respiratory particles (IRPs), where their persistence is shaped by rapid physicochemical transformations during drying. Although inactivation varies with microbial species, respiratory matrix composition, and environmental conditions, the underlying mechanisms remain poorly resolved. This study aims to quantify inactivation of surrogate bacterial pathogens, identify the dominant environmental and chemical drivers, and develop predictive relationships applicable to indoor air conditions.

To avoid high-level biosafety requirements, two bacterial surrogates were selected: *Escherichia coli* (gram-negative) and *Staphylococcus epidermidis* (gram-positive). Experiments were performed with 1 µL artificial saliva droplets equilibrated at controlled relative humidities (30%, 50%, 70%) and constant temperature. Inactivation was quantified using colony enumeration and digital PCR. Droplet evaporation behavior was characterized, and efflorescence time was determined by filming the drying droplets.

The Respiratory Aerosol Model (ReSAM) was used to simulate solute concentration dynamics and calculate changes in osmotic pressure and ionic strength during drying. For both *E. coli* and *S. epidermidis*, inactivation strongly correlated with increases in osmotic pressure (ΔΠ) at the point of droplet efflorescence, with the effect intensifying at lower relative humidity. Numerical fits relating inactivation to ΔΠ enabled prediction across additional RH conditions and different respiratory matrices.

These findings highlight distinct inactivation patterns between gram-negative and gram-positive bacteria and demonstrate the central role of droplet chemistry in determining airborne microbial persistence. The results contribute to improved assessment of transmission risks and the development of strategies to reduce exposure in indoor environments.

The effect of filter air sampling on DNA quality for microbial detection.

Simon Bate[1,2], Richard Thomas[1], Claire Lonsdale[1], Darryl Hill[2]

[1]Dstl, Salisbury, United Kingdom. [2]University of Bristol, Bristol, United Kingdom

Abstract

The detection of biological aerosol particles (bioaerosols) is relevant to many scientific fields. The mechanisms responsible for inactivating airborne microorganisms in the atmosphere may also impact their detection and measurement. This work aims to determine the effect of aerosol generation and filter air sampling on bacterial viable counts and DNA concentration and quality. Aerosols of *Escherichia coli* MRE162 and *Pseudomonas putida* NCTC10936 were generated into HEPA-filtered air, within a linear wind tunnel, for either 10 seconds or 20 minutes. Bioaerosols were sampled using glass-microfibre filters for either 10 minutes (short-term sampling) or 5 hours (long-term sampling). Relative humidity and temperature were monitored throughout. Bacteria were eluted from the filters and quantified using viable counts following overnight incubation. The remaining buffer was centrifuged to pellet the bacteria, and DNA was extracted following a standard DNA extraction protocol. DNA quality and concentration were determined using the TapeStation 4200 instrument and Qubit 4 reader. Although short-term air sampling had minimal effect on the viable counts of *E. coli*, it led to a significant reduction in *P. putida* counts. Sampling for extended periods, however, led to a significant reduction in viable counts for both bacterial species. The duration of air sampling had minimal impact on DNA concentration, however, the degree of DNA fragmentation significantly increased after 10 minutes of air sampling. Future work will determine the impact of filter air sampling on Polymerase Chain Reaction and third-generation sequencing techniques. This information will inform bioaerosol detection practices for human, animal and plant health and biodefence.

Impact of relative humidity, ozone, and simulated sunlight on the stability of infectious bioaerosols

Elizabeth Klug[1], Danielle Rivera[1], Daniel Ackerman[1,2], Ashley Ravnholdt[1], Kevin Crown[1,2], Gabriel Lucero[2], Ningjin Xu[3], Don Collins[3]

[1]University of Nebraska Medical Center (UNMC), Omaha, USA. [2]National Strategic Research Institute (NSRI), Omaha, USA. [3]University of California, Riverside, Riverside, USA

Abstract

Viral diseases that are transmitted as aerosols pose a significant risk to the public. These viral diseases may be transmitted from person-to-person, such as SARS-CoV-2, or as environmentally generated aerosols, like hantaviruses.

The threat a virus may pose as an aerosol depends on several factors, including its stability as an aerosol. Bioaerosol stability is generally studied as the decay of aerosol properties in response to environmental conditions. Many of these studies have been accomplished using the Goldberg rotating drum. However, use of the rotating drum comes with significant drawbacks, such as a failure to capture the loss of initial pathogen infectivity and a small sample volume. The Biological Aerosol Reaction Chamber (Bio-ARC) is an alternative approach that uses a flow-through system to rapidly expose large numbers of biological particles to controlled environmental conditions and determine the sensitivity and mechanisms of aging through analysis of the collected samples. Using this system, we investigated the stability of two viruses that represent two distinct types of aerosol transmission and may differ in how they respond to environmental insult: Sin Nombre Virus (SNV) and SARS-CoV-2. Both pathogens are enveloped and consist of similar protein structures. The major difference is the mode of transmission. SNV transmission occurs through the inhalation of mouse excreta in the environment, and SARS-CoV-2 transmission occurs through inhalation of infectious respiratory fluids. Using the Bio-ARC, we report the first aerostability experiments with SNV, as well as the sensitivity of SARS-CoV-2 when exposed to ozone, simulated sunlight, and elevated relative humidity.

Assessment of the role of handwash basins in the airborne transmission of multi-drug-resistant organisms in clinical and non-clinical settings

Sudheer Salana[1], Amin Shirkhani[1], Bhavarth Shukla[2], Chang-Yu Wu[1], Adriana Jimenez[2]

[1]University of Miami, Coral Gables, USA. [2]University of Miami, Miami, USA

Abstract

Background: Healthcare-associated infections remain a major public health challenge, with multidrug-resistant organisms (MDROs) accounting for a substantial proportion of cases. Although transmission is traditionally attributed to contact with contaminated surfaces and medical devices, increasing evidence indicates that hospital plumbing systems, particularly handwash basins, may serve as overlooked reservoirs and potential sources of airborne dissemination. Despite this emerging concern, the contribution of handwash basins to bioaerosol generation under real-world conditions remains poorly characterized. To address this gap, we conducted aerosol and surface sampling in five inpatient hospital rooms and three public restrooms.

Methods: Aerosols were collected under two conditions: with the faucet turned off, and turned on, using a single-stage Andersen Cascade Impactor and a BioSpot-VIVAS sampler. Swab samples were also collected from handwash basin drains. All samples were cultured on selective and non-selective agar media, and isolates were identified using MALDI-TOF mass spectrometry, with a focus on carbapenem-resistant bacteria and *Candida* species.

Results: In inpatient rooms, we detected at least seven MDRO in aerosol samples, including carbapenem-resistant gram-negative bacteria, with significant overlap between swab and aerosol samples supporting splash-mediated aerosolization. Microbial recovery differed substantially between the two sampling methods, demonstrating the limitation of relying on a single aerosol sampling method to characterize airborne microbiota.

Conclusion: Our findings indicate that faucet operation in handwash basins can generate aerosols containing MDROs in both clinical and non-clinical settings. Overall, these results identify handwash basins as a potential source contributing to airborne transmission of MDRO, warranting consideration in infection prevention.

Assessing stability of supercharged proteins in single levitated microdroplets

Viola Fieglein, Michael Jacobs

Texas State University, San Marcos, USA

Abstract

Biomolecule stability in aerosols has been widely studied in recent years due to their unique interactions at the air-water interface; however, we still lack a fundamental understanding of the molecular mechanisms that drive their behavior in microdroplets. It is well understood that proteins adsorb at the air-water interface, but the effect of the interface on their stability remains unclear. Supercharged proteins have become of interest due to their increased stability, which can change protein properties without changing protein function. Here, we describe our recent work examining the dynamics of a supercharged model protein, green fluorescent protein (GFP), in levitated microdroplets. Microdroplets are levitated within a quadrupole electrodynamic trap (QET), and the folded state of GFP is assessed *in situ* by monitoring changes in fluorescence intensity over time. Our results show a correlation between the net charge on a protein and its stability within levitated droplets. Furthermore, we observe that supercharged proteins are less stable in smaller droplets and in droplets with large ionic strengths. These results demonstrate that interactions with the large, exposed surface areas can impact biomolecule stability in microdroplets, even for species with weak surface affinities. By gaining an understanding of how proteins interact with the air-water interface, we can apply this knowledge to a variety of biomolecules. Ultimately, we can use this work to get a fundamental understanding of how biomolecules behave at the interface and tease out surface-mediated interactions from other driving forces.

Respirable NTM from showers: persistence, viability and the role of ventilation

Laura Steege[1,2], Simon Clark[1], Simon Waddell[2], Ginny Moore[1]

[1]UK Health Security Agency, Salisbury, United Kingdom. [2]Brighton and Sussex Medical School, Brighton, United Kingdom

Abstract

Non-tuberculous mycobacteria (NTM) are waterborne opportunistic pathogens that can cause serious infections in individuals with lung conditions and/or compromised immunity. This study investigated NTM aerosolisation from showers, assessed potential mitigations, and evaluated NTM aerostability – factors influencing inhalation exposure risk.

Two naturally NTM-colonised showers with identical showerheads were studied in an unventilated room and a highly ventilated room (14-15 air changes/hour) in a model hospital ward. Air samples were collected 170-185cm from showerheads, with and without a shower curtain, during 5-minute shower runs, using six-stage Andersen and slit-to-agar samplers. NTM were cultured then identified by MALDI-ToF. Aerostability was assessed by nebulising NTM suspensions, capturing aerosols on spider-silk microthreads, and quantifying viability by culture over 96 hours at 20°C and 40% or 60%RH.

NTM from shower aerosols were significantly higher in the unventilated room (~$1.3x10^4$ cfu/m^3) than the highly ventilated room (~$5.6x10^3$ cfu/m^3), with no significant effect of shower curtain use. Most NTM-containing aerosols (72.9-80.1%) were ≤2.1µm, capable of reaching terminal bronchi and/or alveoli. Ventilation reduced NTM-containing aerosols ≤2.1µm and cleared NTM 15-30 minutes post-shower, whereas without ventilation NTM persisted 220 minutes. NTM exhibited high aerostability. *M. chimaera* showed no significant decline over 96 hours. *M. chelonae* declined by 24-48 hours but remained viable at 96 hours, with significantly greater recovery at 60% than 40%RH.

Showers generated high concentrations of respirable NTM-containing aerosols capable of deep lung deposition. Aerosolised NTM persist and remain viable, highlighting ventilation as a key mitigation for NTM exposure risk.

Effects of pH-altering gaseous species on aerosol pH during engineered inactivation of viral aerosols

Zhenyu Ma, Hunter Richards, Herek Clack

University of Michigan, Ann Arbor, USA

Abstract

The infectivity of pathogenic aerosols is a critical factor for aerosol transmission of airborne pathogens and diseases. Among the key variables that could cause changes in viral aerosol infectivity, aerosol pH is recognized for its effects on the natural infectivity decay rate of various viral aerosols. (Longest, 2024)

However, how pH can potentially affect the efficiency of an engineered inactivation process is less examined. Studies have shown that the effectiveness of disinfection is affected by the liquid substrate pH for viral aerosols deposited on respirators. (Rockey, 2020) It is plausible that viral aerosol pH could also affect engineered inactivation methods, such as non-thermal plasma (NTP) exposure, whose well-documented virucidal effects rely on the highly oxidative species it produces.

We have demonstrated that the presence of gaseous ammonia and hydrogen sulfide can negatively affect the NTP inactivation efficiency of viral aerosols. (Ma, 2024) This study aims to further investigate the role of trace gaseous air contaminants with aerosol-pH-altering potential, in addition to their previously discussed roles in the redox chemistry. Preliminary results indicate exposure to NTP produces a statistically significant change in pH of the media used to collect virus-containing aerosols. By comparing the pH of collected aerosols in the presence of different gaseous species with and without NTP exposure, the role of pH-altering gases can be better understood. Besides, examining and cross-comparing the NTP inactivation efficiency in response to changes in the aqueous pH of viral aerosols could provide additional insights into the role of pH in engineering inactivation processes.

Quantifying airborne microbe inactivation rates by far-UVC, one droplet at a time.

Robert Alexander, Allen Haddrell, Xia Yi, Kennedy Peek, Tristan Cogan, Jamie Mann, Darryl Hill, Adam Finn, Andrew Davidson, Jonathan Reid

University of Bristol, Bristol, United Kingdom

Abstract

Far-UVC radiation is highly effective at inactivating microorganisms while exhibiting minimal penetration into human skin and eyes. This reduced tissue interaction lowers the risk of damage, allowing higher exposure limits and enabling safe disinfection of occupied spaces.

However, there is no standard technique to quantify far-UVC inactivation rates of airborne microorganisms across a range of conditions and distances. This results in limited engineering solutions that would maximize inactivation.

To address this, the University of Bristol has recently developed the QELEBS-UV (Quadrupole Electrodynamic Levitation and Extraction of Bioaerosol onto a Substrate). Microbe laden aerosol are levitated within an electrodynamic trap under controlled environment conditions (relative humidity, gas phase composition). The aerosol are irradiated with Far-UVC from a 222 nm KrCl excimer lamp for a set time, and after irradiation treatment, extracted from the trap for downstream viability analysis.

Here, we describe the far-UVC inactivation of Group A *Streptococcus pyogenes* (GAS) and Influenza A (PR8) in respiratory fluid surrogates. Specifically, the effect of far-UVC in relation to particle composition, particle size (10 to 5 microns) and relative humidity (20% to 90%). A unique aspect of this study is the initiation of far-UVC exposure at different stages of the aerosol lifetime and a comparison with non-irradiated samples, enabling investigation of how aerosol aging influences far-UVC disinfection efficacy.

These results identify the effects induced by far-UVC on pathogen-laden single particles and will establish how far-UVC installations need to be designed to effectively suppress airborne transmission and promote indoor air quality of the built environment.

Streptococcus: an Aerobiologist's Best Friend.

Henry Oswin, Robert Groth, Lidia Morawska

Queensland University of Technology, Brisbane, Australia

Abstract

Background

The bacterial genera *Streptococcus* is often studied within the context of its more pathogenic members. However, the abundance of *Streptococci* within respiratory fluids, and general absence from the environment means that it serves as an ideal marker for airborne respiratory particles, and therefore airborne transmission risk.

Methods

Strep selective agar was placed into an Andersen Impactor, allowing for air to be sampled onto the plates, and the colonies counted to quantify the sampled *Streptococci*. The generation of *Streptococci* by vocalisation, both directly from healthy volunteers and within controlled 'meetings' was measured.

Results

Streptococci were generated by vocalisation at an average rate of 7 CFU per minute. Two peaks in the particle size transporting the bacteria were observed, one in the first and one split between the fourth and fifth stages of the impactor, corresponding to particles >7 µm and particles 1-3 µm in diameter. Varying the type of vocal activity identified the larger particles as originating from the oral cavity and the smaller particles from the larynx. Within the controlled meetings, *Streptococcus* was readily detected within the meeting room air, with increased vocalisation increasing the sampled CFU. The Strep selective agar appeared specific to organisms originating within the respiratory tract, with no colonies growing on the agar when it was exposed to skin, dust, or air sampled from unoccupied spaces.

Conclusion

Quantification of airborne *Streptococci* provides a simple, broadly applicable tool by which numerous aerobiological research questions regarding the factors influencing airborne infection risk can be explored.

Pre-existing immunity shapes influenza A virus replication and airborne shedding kinetics in ferrets.

Fabien Filaire, Maarten Wilbrink, Willemijn Rijnink, Ilona Tosheva, Bianca van Kekem, Dennis de Meulder, Theo Bestebroer, Kain Saygan, Suzanne Mijnhardt, Mathilde Richard, Ron Fouchier, Rory de Vries, Sander Herfst

ErasmusMC, Rotterdam, Netherlands

Abstract

Although influenza vaccination reduces disease severity, it has limited impact on airborne transmission. Understanding how pre-existing immunity shapes viral replication and airborne shedding is essential to identify host factors that influence transmission.

We investigated how homologous and heterologous pre-existing immunity influences influenza A virus shedding kinetics in the ferret model. Using a state-of-the-art air-sampling setup, we quantified infectious airborne viruses expelled by ferrets with defined immune backgrounds. Prior immunity was established through vaccination (H1N1, H3N2, H1N2, or H3N1) or infection (H1N1 or H3N2) followed by challenge infection with H1N1. Air samples were collected alongside daily nasal and throat swabs, clinical assessments, and immunological assays (serology and T-cell analyses).

Ferrets homologously re-challenged following H1N1 infection had no detectable infectious virus in air samples and swabs, consistent with the pre-challenge immune response. Among the remaining groups, the total amount of airborne virus expelled did not differ significantly. Nasal viral replication—known to correlate with airborne transmission—was reduced following prior H3N2 infection and, to a lesser extent, following homologous vaccination, whereas heterologous vaccination had minimal impact. Ferret T-cell analysis revealed H1- and NP-specific responses only after challenge, highlighting that vaccination alone did not prime detectable cellular immunity.

Pre-existing immunity was found to differentially impact influenza A virus replication and airborne shedding. Natural infection, which more effectively induces mucosal immunity, restricted upper respiratory replication and reduced shedding, unlike parental immunization. This work identifies host immune history as a key determinant of influenza A virus transmission and informs strategies to limit influenza virus spread.

Stability of Airborne Rhinovirus in different levels of Relative Humidity

Zhaleh Pourjam alavijeh[1], Mandy Menzel[2], Marcus Liljenberg[3], Sviataslau Sasinovich[4], Patrik Medstrand[4], Lena Uller[5], Malin Alsved[1], Kennedy Peek[6,7]

[1]Department of design science, Division of Ergonomics and Aerosol Technology, Lund University,, Lund, Sweden. [2]Department of experimental medical science, Lund University, Lund, Sweden. [3]Department of design science, Division of Ergonomics and Aerosol Technology, Lund University, Lund, Sweden. [4]Department of translational medicine, Lund University, Lund, Sweden. [5]Department of experimental medical science, Lund, Sweden. [6]School of Cellular and Molecular Medicine, University of Bristol, Bristol, United Kingdom. [7]Bristol Veterinary School, University of Bristol, Bristol, United Kingdom

Abstract

Introduction: Human rhinovirus (HRV) is the primary cause of acute respiratory infections, but research on the likely transmission pathway via aerosols remains limited. Here we investigate how relative humidity (RH) influence rhinovirus infectivity in aerosol phase, which is essential for developing effective mitigation strategies.

Method: Rhinovirus was aerosolized using a nebulizer into a flow tube with controlled humidity. Samples were collected after 8 s with a BioSpot, while particle size distributions were measured using an Aerodynamic Particle Sizer and a Scanning Mobility Particle Sizer. Viral genome and infectivity were quantified using qPCR and most probable number (MPN) methods, respectively. Finally, infectivity was normalized to viral gene concentration and total collected aerosol mass.

Results: Rhinovirus showed highest infectivity at 10% RH (6×10^{-5} MPN/copy number), followed by 90% RH (1.41×10^{-5} MPN/copy number), and lowest at 30% RH (8.44×10^{-6} MPN/copy number). Normalizing infectivity to total collected aerosol mass followed a similar pattern, consistent with assumption that viral genomes are generally correlated with aerosols mass. However, no significant differences across RH levels were observed for infectivity normalized by genome copy number ($p = 0.10$) or aerosol mass ($p = 0.20$). Within each RH group, aerosol concentration varied by ≤8% across 12 runs.

Conclusions: So far, no statistical difference was found at the different RH levels, but more replicates are about to be included in the analysis. In addition, a comparison with influenza A is ongoing, which may show differences in RH stability for non-enveloped and enveloped viruses**.**

Bioaerosol Studies to Optimize Efficacy Test Methods for Air Treatment Technologies

Katherine Ratliff

U.S. Environmental Protection Agency, Durham, NC, USA

Abstract

In recent years, there has been an increasing emphasis on air cleaning and treatment technologies that could be used to reduce infectious aerosol concentrations in occupied spaces, including traditional (e.g., filtration, 254 nm ultraviolet) and emerging (far-UVC, chemical treatments) methods. Although there has been a recent push to develop standardized test methods to evaluate the efficacy of these technologies against bioaerosols, they have largely been evaluated using disparate methods, making it difficult to compare results across studies. To address this challenge, the U.S. Environmental Protection Agency has been conducting systematic bioaerosol testing with a wide variety of technologies to understand how changes to test methodology impact performance against bioaerosols. Experiments have been conducted in chambers up to 85 m^3 using surrogates for airborne pathogens, primarily the bacteriophage MS2. Results have demonstrated that relatively simple changes to test methodology, including changing the aerosolization media (or even simulated saliva recipe used) can have a significant impact on efficacy results. Similarly, changing the chamber size or material composition can influence performance. These findings are not only critical for facilitating comparisons across technologies but are key to developing and optimizing reliable and repeatable efficacy test methods. As new public-health based indoor air quality standards and targets for reducing disease transmission emerge (e.g., ASHRAE Standard 241), improving the applicability of these test methods to real-world applications and settings is increasingly important. This presentation will also highlight fundamental knowledge gaps that remain in this field and bridge several disciplines.

Autochthonous Theta (Θ): A Refractory Index of Airborne Disease Transmissibility

Chad Roy

Tulane University School of Medicine, New Orleans, USA

Abstract

Airborne transmission of infectious agents is governed by a complex interplay of biological, environmental, and behavioral parameters that remain poorly unified by existing epidemiologic models. Here *theta* (Θ) is proposed, a hybridized, logarithmic, refractory index designed to dynamically characterize the airborne transmissibility of pathogens across the lifespan of an outbreak spanning from initial autochthonous emergence through epidemic acceleration and eventual resolution. Θ integrates empirical, real-time, and assumed data streams to quantify the probability of disease transmission between an infectious and a susceptible host via aerosol. The notional equation components supporting Θ accounts for *source contribution* including particle size distribution, exhaled breath aerosol production, and biologic load probability; *environmental airborne transport* including humidity, temperature, UV, particle dynamics, and pathogen resilience; and *host response* encompassing susceptibility, behavioral modifiers, immunization status, and mutational adaptation. Θ is adaptable to incomplete data, incorporates evolutionary mutation rate and bioterrorism contingencies, and is scalable across pathogens, environments, and user participation levels. The utility of Θ is demonstrated in modeled outbreaks of H5 influenza, SARS-CoV-2 variants, and airborne bacterial agents, showing its utility in capturing the trajectory of transmissibility over time. As a refractory index, Θ resists oversimplification while remaining interpretable to public health systems. Its integration into aspirational WiFi-anchored hyperlocal sensing networks, and users provisioning volunteer data from mobile devices offers real-time, location-specific insights into transmission risk, opening a new frontier for algorithm-enabled epidemic intelligence. Neural network-based models harness data sets to provide a swarm of recursively updated Θ estimates rather than a recalcitrant point transmission estimates.

Including farm particulate information in the dispersion modelling of foot and mouth disease virus

Katie Brown[1], William Thurston[1], Gemma Halloran[1], Emma Brown[2], Claire Colenutt[2], Simon Gubbins[2]

[1]Met Office, Exeter, United Kingdom. [2]The Pirbright Institute, Pirbright, United Kingdom

Abstract

Foot and mouth disease (FMD) is a highly contagious viral disease infecting livestock including cattle, pigs and sheep. Of the different spread mechanisms of the virus, airborne spread is the hardest to control in the event of an outbreak. To aid policy makers to decide on the order in which to test holdings around an infected premise, dispersion models are used to predict the airborne spread of the virus.

The atmospheric dispersion model, NAME, has been adapted to predict the airborne spread of the foot and mouth disease virus (FMDV). To best represent the spread of the virus, the properties of the material the virus is carried on needs to be understood. FMDV is thought to be dispersed on particulate matter when travelling long distances from a holding.

In order to model the particulates being emitted from a holding, The Pirbright Institute took measurements of the particulate matter at six holdings across England. We have used these measurements to add in three different sized bins of aerosol particles to the NAME model. This also allowed different deposition schemes within NAME to be tested. Using aerosol sizes, and particle size dependent deposition schemes in the dispersion model increases the air concentration of virus across different weather conditions.

Aerosol sampling performance of bacterial and viral simulants using an ESP-EWOD system

Amanda Weiler[1,2], Nathalie Turgeon[3], Lanka Weerasiri[4], Loïc Coudron[4], Ian Johnston[4], Matthew Schwengler[1], Timothy Foat[5,4], Caroline Duchaine[2,3], Nora Chan[1,2]

[1]Department of National Defence, Defence Research and Development Canada (DRDC) Suffield Research Centre, Medicine Hat, Canada. [2]Université Laval, Québec, Canada. [3]Centre de Researche de l'Institut Universitaire de Cardiologie et de Pneumologie de Québec, Québec, Canada. [4]University of Hertfordshire, Hatfield, United Kingdom. [5]Defence Science and Technology Laboratory, Salisbury, United Kingdom

Abstract

The Electrostatic Precipitation (ESP) collection and Electrowetting-on-dielectric (EWOD) elution system was designed as a bioaerosol sampling system for rapid field deployment. This work establishes its performance with bacterial and viral simulants relative to two commercial sampling systems.

Three bacterial simulants (Bacillus atrophaeus spores, Pantoea agglomerans, and Escherichia coli) and two viral simulants (bacteriophages MS2 and Phi6) were aerosolised in an aerosol chamber. The simulants were sampled by an ESP, SKC BioSampler®, and a 37 mm filter cassette with 0.8 µm polycarbonate filters for 20 minutes.

The ESP-EWOD system produced average sample concentration higher than the BioSampler® by factor of 21, 580 and 667 and the filter cassette by factor of 57, 1308 and 7619, for Bacillus atrophaeus spores, MS2 and Phi6, respectively, when measured by culture-based methods (CFU or PFU/mL). The ESP-EWOD unit performed poorly with Gram-negative bacteria, yielding no culturable bacteria. The viability loss may be due to the adverse effects of corona discharge generated by the ESP collector. Despite this, quantitative polymerase chain reaction results showed improved sample concentration (genome copies/mL) across all the microorganisms investigated. In particular, the average sample concentrations of Pantoea agglomerans, Escherichia coli, and MS2 were 775 and 2234 times higher than those with BioSampler® and filter cassette, respectively. The ESP-EWOD unit's ability to concentrate samples stems from its use of a low elution volume of 3 µL.

The low-burden ESP-EWOD system demonstrated the ability to generate highly concentrated samples of bacterial and viral simulants compared to the BioSampler® and filter cassette.

Assessing spatiotemporal trends in environmental influenza virus contamination during human infection in a tightly controlled indoor setting

Karin Brett, Sterling Knight, Zachariah Broemmel, Byron Hauser, Elizabeth Petzold, Christopher Woods, Nicole C. Rockey

Duke University, Durham, USA

Abstract

Influenza viruses impart a significant human health burden, with estimates of around one billion infections and nearly 650,000 deaths globally each year. Successful influenza virus transmission is dependent on several factors, including host shedding dynamics and environmental aspects of the transmission setting, among others. Yet we lack an understanding of how environmental loads vary by host, setting, and time into an infection. Here, we use a controlled human infection model to assess environmental influenza virus contamination over the course of an infection. In this model, participants are inoculated with a contemporary strain of influenza A virus (A/Arkansas/08/2020 (recH1N1)) and closely monitored over an eight-day isolation period, allowing for daily collection of environmental samples from rooms. By working in this tightly controlled yet realistic setting, our results establish how environmental loads vary with host, viral, and environmental factors.

Our preliminary results indicate that low levels of viral RNA are detectable from multiple participants' rooms on days one, two, three and six following inoculation day in a range of environmental samples, including on surfaces and in aerosols. The highest viral RNA concentration (0.8 gene copies/ air) was detected from an air purifier filter from a double-occupied room of two highly symptomatic participants. Ongoing work includes infectious virus quantification in samples positive for viral RNA to associate infectious and genomic environmental virus loads. Ultimately, this research will allow us to translate environmental monitoring findings into accurate exposure risks and identify when mitigation strategies should be employed to reduce transmission in indoor settings.

Exhaled viruses and particles during acute upper respiratory infection

MARCUS LILJENBERG[1], ZHALEH POURJAM ALAVIJEH[1], CARL JOHAN FRAENKEL[2,3], PATRIK MEDSTRAND[4], MALIN ALSVED[1], JAKOB LÖNDAHL[1]

[1]Division of Ergonomics and Aerosol Technology, Department of Design Sciences, Lund University, Lund, Sweden. [2]Department of Infection Control, Region Skåne, Lund, Sweden. [3]Division of Infection Medicine, Department of Clinical Sciences, Lund University, Lund, Sweden. [4]Department of Translational Medicine, Clinical Virology, Lund University, Lund, Sweden

Abstract

Background

Respiratory virus infection affects millions of humans every year, having a large economic and societal impact. The current study aims to investigate the particle size distribution, concentration, and viral RNA of exhaled aerosols from approximately 150 participants.

Methods

Subjects with recent onset of respiratory infection breathed, vocalized, and coughed into a funnel collection setup feeding the exhaled aerosols to instruments for collecting particles and measuring CO_2, H_2O, and dry particle size and concentration (0.3-20 µm). Collected particles were analysed by qPCR for virus gene detection. After the subject recovered from the infection, the experiments were repeated. An infectivity assay of exhaled samples is planned for spring 2026.

Results

At time of writing, 17 subjects performed the first visit while infected, and 12 subjects also did the healthy return visit. Preliminary data on particle concentration during early virus infection of the 2 first subjects indicate very low particle emissions during breathing, 500-5000 particles/L during vocalization, and 2000-4000 particles/L while coughing. Of 11 analysed nasopharynx samples, 64% had a rhinovirus/enterovirus infection, and 57% of those exhaled detectable levels of rhinovirus/enterovirus RNA.

Conclusion

During the COVID-19 pandemic we learned that aerosol transmission contributed to disease transmission of SARS-CoV-2, especially in the early phase. It is likely that other acute respiratory infections also can spread though aerosol transmission, which would have implications for infection prevention strategies throughout society. The outcomes from this study will contribute to a better understanding of acute respiratory infections' ability to spread via aerosol transmission.

A novel aerosol chamber provides insight into how droplet composition strongly shapes respiratory virus viability kinetics in the air

Suzanne Mijnhardt[1,2], Ilona Tosheva[1], Abilash Ravi[1], Dennis de Meulder[1], Tess Homan[3,2], Hanneke Gelderblom[4,2], Pieter Fraaij[1,5,2], Ron Fouchier[1,2], Sander Herfst[1,2]

[1]Department of Viroscience, Erasmus University Medical Center, Rotterdam, Netherlands. [2]Pandemic and Disaster Preparedness Center, Delft, Rotterdam, Netherlands. [3]Department of Mechanical Engineering, Eindhoven University of Technology, Eindhoven, Netherlands. [4]Department of Applied Physics, Eindhoven University of Technology, Eindhoven, Netherlands. [5]Department of paediatrics, Erasmus University Medical Center, Rotterdam, Netherlands

Abstract

Respiratory viruses pose a major public health burden and a significant pandemic risk. They can spread via (in)direct contact and through air, but airborne transmission is particularly difficult to study. Understanding how long respiratory viruses remain infectious in air, and which environmental factors affect their viability, is crucial for effective mitigation during future outbreaks and pandemics.

We present a novel, in-house developed aerosol chamber to artificially aerosolize viruses and assess their viability kinetics under various environmental conditions. First, Phase Doppler Anemometry confirmed that a physiologically relevant droplet size distribution was produced, with a mean droplet diameter of 3 µm and a range of 0.1-20 µm. Then, using the aerosol chamber, we assessed the viability of SARS-CoV-2, influenza A virus, RSV, HMPV, and hPIV3 in different matrices, including cell culture medium, respiratory mucus, and saliva. Our results show substantial differences in viral viability in air between the tested respiratory viruses and that this viability is strongly influenced by the matrices. Ongoing experiments aim to explore additional environmental factors, including relative humidity, to further elucidate the determinants of respiratory virus viability.

Our experimental aerosol chamber offers a valuable tool to systematically compare the viability kinetics of respiratory viruses and identify factors affecting viability in air. This systematic comparison of well-known respiratory viruses under varying conditions and droplet compositions provides a benchmark for evaluating newly emerging viruses with pandemic potential and ultimately enables predictions about the impact of airborne transmission for these viruses.

Environmental Detection of Plant Pests at Borders

Edward Haynes[1], Marco Benucci[1], Sarah Carroll[1], Chris Conyers[1], Bryden Fields[1], Angelika Kiepas[1], Lynn Laurenson[1], Roy Macarthur[1], John Walshaw[1], Sarah Eustace[2], Kong Wah Sing[2], Damien Hicks[3]

[1]Fera Science Ltd, York, United Kingdom. [2]Animal and Plant Health Agency, Manchester, United Kingdom. [3]Defra, Penrith, United Kingdom

Abstract

Early detection of plant pests and pathogens at points of entry is essential for preventing their establishment and spread. Environmental biosurveillance—widely used in human and animal health—may provide a new route for detecting plant-relevant taxa in border environments. This study piloted the feasibility of applying DNA-based environmental surveillance inside UK Border Control Posts (BCPs).

A total of 194 samples were collected across two BCPs (Port of Liverpool and Manchester Airport), including air samples, dust wipes, and sticky traps. DNA was extracted and analysed using metabarcoding (at 16S, ITS and COI loci), with a subset of samples (n=35) undergoing shotgun metagenomic sequencing. The resulting sequences underwent taxonomic classification, calculation of diversity metrics, and assessment of temporal signal using Sorensen dissimilarity index analysis.

All three sample types contained detectable DNA from diverse bacterial, fungal and invertebrate taxa. Community composition differed significantly between air, dust and sticky traps across all loci. Temporal analyses indicated that air and sticky trap samples could provide time-resolved information on environmental DNA at both sampling sites, but this varied across metabarcoding loci. Multiple detections were consistent with genera containing organisms of possible plant health relevance, although interpretation was limited by reference database quality.

This proof-of-concept study demonstrates that environmental DNA-based surveillance at BCPs is feasible and can capture taxonomically informative signals which may be relevant to plant health risk assessment. Further optimisation—particularly around sampling regimes, reference databases and interpretation frameworks—is needed before operational deployment.

Characterisation of seasonal trends in airborne fungal communities

Patrick McClean[1,2], Kevin King[1], Gail- Canning[1], Yong-ju Huang[2], Jon West[1]

[1]Rothamsted Research, Harpenden, United Kingdom. [2]University of Hertfordshire, Hatfield, United Kingdom

Abstract

Background: Outdoor air comprises a complex mixture of biological particles that are released in different seasons, weather and time of day. Understanding temporal changes in airborne fungal communities helps interpret their ecological roles and impact on crop health. Here, we describe sampling and metabarcoding approaches to characterise seasonal variation in airborne fungal communities at a rural agricultural site.

Methods: Rotorod spore traps collected weekly samples above wheat, oilseed rape, and bare fallow plots at 0.5 m and 2.5 m, or 1m heights above ground during spring and autumn over three years, alongside a 10m roof-level sampler. DNA was extracted from samples, the fungal ITS region was amplified by PCR and sequenced using an Oxford Nanopore MinION. Community structure and species richness was compared bioinformatically across crops, heights, fields, and seasons.

Results: Marked seasonal differences in airborne fungal community composition were observed. Autumn communities were characterised by a higher relative abundance of basidiomycetes and saprotrophic taxa, whereas spring communities contained a greater proportion of ascomycetes and plant-pathogens. Co-occurrence networks were visualised in R using igraph and ggraph, with nodes representing fungal genera and edges representing significant correlations. Network topology metrics were used to compare structural complexity and organisation between seasons.

Conclusions: Seasonal restructuring of the aerobiome can be characterised using community co-occurrence network approaches. Differences between small (24 m × 24 m) crop plots were relatively minor, indicating a strong background component of the airborne fungal community, highlighting important considerations for biodiversity monitoring and pathogen surveillance using air-sampling.

Towards Real-Time Identification of Pathogenic Bioaerosols

Joshua Santarpia[1], SCALE Biosensor Team[2]

[1]University of Nebraska Medical Center, Omaha, USA. [2]Various, Various, USA

Abstract

Automated identification of biological aerosols is a currently a multi-step process that involves the collection of particles from the environment, extraction of biological analytes from the collected material and subsequent analysis by either identifying proteins or nucleic acids (NA) associated with known agents of concern. Typically, these systems have been used to detect specific pathogens in order to provide warning of an attack with a biological weapon, and not to provide real-time data to improve public health. The limitations of the current approaches are severalfold. Aerosol is collected over long periods of time (typically hours, bioanalytes are extracted in batches and then tested using techniques like polymerase chain reaction (PCR) or immunoassays. This process requires both time and reagents. Optical bioaerosols systems were originally developed as a replacement for these systems, however, no optical technology is currently capable of confidently discriminating pathogens from non-pathogens, much less confidently identifying organisms at the species level, outside of the laboratory. In this effort we demonstrate a new paradigm for the identification of bioaerosols by continuously collecting, processes and biochemically analyzes bioaerosols moving traditional bio-identification technology closer to the time resolution of optical systems. In this work, we have integrated a multi-stage virtual impactor with a condensation growth tube collector to provide high volume air-to-liquid collection into 50-100 µL volume. The hydrosol is then continuously transferred, via microfluidics, for continuous nucleic acid extraction and electrochemical analysis, resulting in sample to initial detection times of only a few minutes.

Nationwide Bioaerosol Metagenomic Repository for Environmental Health Research

Kamil Khanipov[1], Katherine Araya[1], Sarah Alnemrat[1], Vivian Tat[1], Kostiantyn Botnar[1], Shanna Ratnesar-Shumate[2], Sean Kinahan[3], Riley Watson[1], Roman Petrov[1], Sajita Elaprolu[1], David Kimmel[3], Hema Narra[1], Christine Tomlinson[3], George Golovko[1]

[1]University of Texas Medical Branch at Galveston, Galveston, USA. [2]Johns Hopkins University Applied Physics Laboratory, Silver Springs, USA. [3]Department of Homeland Security Science and Technology Directorate, Washington, DC, USA

Abstract

Air remains the least characterized major environmental compartment despite recent studies showing that over 85% of indoor air samples contain detectable respiratory pathogens. We developed the largest dedicated bioaerosol metagenomic dataset to date: over 1,000 air samples from more than 140 locations across the continental United States, collected from December 2023 through October 2024 across all four seasons.

Using 3-micron fluoropore filters from high-volume environmental aerosol samplers, we developed standardized protocols optimized for Oxford Nanopore Technologies sequencing. DNA and RNA were extracted separately using ZymoBIOMICS kits. RNA was converted to cDNA, and both DNA and cDNA were prepared for sequencing on PromethION flow cells using Rapid PCR Barcoding kit. This approach enabled comprehensive metagenomic and metatranscriptomic characterization of airborne microbial communities. Sampling spanned indoor, outdoor, and transit environments, including special events such as the Boston Marathon and Mardi Gras.

This repository represents an unprecedented scale for air microbiome research, capturing comprehensive geographic and temporal variation across the continental United States. The resulting dataset established the first nationwide baseline of airborne microbial communities generated using nanopore sequencing, revealing distinct seasonal and geographic signatures in microbial composition.

All data have been made publicly accessible through the airmetagenomics.com dashboard, enabling interactive exploration of spatial and temporal patterns. Following the success of wastewater surveillance systems that provided one to four weeks of early warning before clinical case detection, this repository lays the foundation for analogous air-based environmental monitoring, empowering researchers to develop computational approaches that identify deviations with potential public health significance.

A cross-matrix approach to airborne microbiome, virome and antimicrobial resistance analysis

Rachel Samson P, Frederic Coulon, Zaheer Nasar, Francis Hassard

Cranfield University, Bedfordshire, United Kingdom

Abstract

Abstract

Background

Airborne microbial and viral assemblages originate from soil, water, wastewater systems, vegetation, and human-associated environments, creating a dynamic aerobiome that links surface ecosystems and built environments. These communities include bacteria, fungi, viruses and genetic material, and can transport cells and genes, including antimicrobial resistance determinants, across spatial scales via particulate matter and atmospheric transport. The airborne microbiome and virome, and their contribution to antimicrobial resistance (AMR) dissemination, remain poorly characterised due to low biomass, temporal and spatial variability in bioaerosol concentrations, and limited ability to interpret viral sequences without concurrent source-reference data.

Methods

We applied a cross-matrix, event-resolved sampling strategy combining real-time bioaerosol sensing with ultra-low-input nucleic-acid recovery to enable nanopore-based metagenomic, metaviromic, and AMR profiling. Sampling targeted engineered and agricultural emission settings, including wastewater treatment plants and poultry and dairy facilities, alongside urban and rural background sites, with reference sampling from water, wastewater, compost and soil. A Spectral Intensity Bioaerosol Sensor (SIBS) was co-located with a Coriolis µ sampler to record particle size and fluorescence while collecting biological material. Optical signals informed targeted collections during high-bioaerosol periods, with time-integrated sampling retained for comparison.

Results

Downstream readouts comprise nanopore metagenomes, metaviromes and AMR gene profiles. Bacteriophages are prioritised as indicators to link viral diversity with putative bacterial hosts and support interpretation beyond detection alone. Cross-matrix reference profiles support attribution of airborne signatures.

Conclusion

This approach supports exposure-relevant surveillance across connected environmental matrices. It provides a practical basis for One Health interpretation of airborne microbial and viral signals.

Characterising Speech-Generated Aerosol Emission Using Commensal Bacterial Shedding and Multi-Modal Sampling

Patricia Barkoci[1], Nan Zhou[2], Nicola Yaxley[1], Jonathan Reid[2], Simon Clark[1], Ginny Moore[1]

[1]UKHSA, Salisbury, United Kingdom. [2]University of Bristol, Bristol, United Kingdom

Abstract

Background:
Inter-individual differences in respiratory aerosol emission influence pathogen transmission, yet working with respiratory pathogens is challenging. Upper-airway commensals may provide a surrogate marker. This study characterised bacterial recovery during speech using multiple air-sampling approaches, conducted alongside a parallel APS-based particle-emission study, informing planned comparison.

Methods:
Twenty-five participants read a standardised text three times inside a flexible-film isolator. Respiratory particles were collected using culture settle plates placed 10–50 cm from the participant and parallel molecular plates containing preservation medium. Active sampling used Andersen and slit-to-agar impactors, and a cyclone collecting into preservation medium. Large droplets were captured using water-sensitive paper. Culture plates were enumerated for respiratory commensals, and raw and log10-transformed counts analysed using Spearman and Pearson correlations. Molecular samples are undergoing qPCR targeting *Streptococcus mitis* group, *Neisseria* spp., Torque Teno Virus, and human 18S rRNA. Temperature, humidity, and CO_2 were recorded. APS particle counts were collected independently by a collaborating researcher.

Results:
Commensals were consistently recovered across culture-based samplers, with substantial between-participant variability. Moderate to strong correlations were observed between Andersen, slit sampler, and settle-plate counts, with some outliers. High- and low-emitter rankings have been generated for comparison with APS profiles. Molecular and droplet-image analyses are ongoing.

Conclusions:
Preliminary findings indicate that commensal bacterial emission during speech is measurable and broadly consistent across sampling platforms. Integration of size-resolved Andersen data with independently collected APS measurements will assess whether shedding reflects overall respiratory aerosol-emission behaviour.

Best Practices for Large-Scale Chamber Testing of In-Room Germicidal UV Systems

Ernest R. Blatchley III[1,2], J. Vivian Belenky[3], Holger Claus[4], Christopher T. DeGroot[5], Amin Hadizade[5], Waseem Hiwar[6], Catherine J. Noakes[6], Shohoria Afrin Shorno[1], Richard D. Williamson[7]

[1]Lyles School of Civil & Construction Engineering, Purdue University, West Lafayette, USA. [2]School of Sustainability Engineering and Environmental Engineering, Purdue University, West Lafayette, USA. [3]Center for Radiological Research, Columbia University Irving Medical Center, New York, USA. [4]4ALighting Consulting, CA, USA. [5]Department of Mechanical & Materials Engineering, Western University, Ontario, Canada. [6]School of Civil Engineering, University of Leeds, Leeds, United Kingdom. [7]Blueprint Biosecurity, Washington DC, USA

Abstract

The likelihood of additional disease outbreaks in the future highlights the need for effective strategies to reduce airborne disease transmission. In-room germicidal ultraviolet (GUV) systems are increasingly recognised as an effective intervention for reducing the spread of infectious diseases in indoor environments. Large-scale chamber testing plays a critical role in validating the performance of these systems under controlled conditions while remaining representative of real-world environments. However, at present, no unified standard exists for conducting such tests or for translating experimental results to real-world applications.

This review summaries existing standards for large-scale testing of in-room GUV systems and proposes best practices for experimental design, measurement, and data interpretation. Current protocols are evaluated with respect to chamber dimensions, environmental control, air mixing, ventilation, and safety considerations. We also summaries commonly used microbial and non-microbial challenge agents, as well as aerosol generation and sampling methods. The strengths and limitations of steady-state, static decay, and dynamic decay testing approaches are compared.

Key knowledge gaps are identified, notably the lack of standardised methods for quantifying UV inactivation kinetics of aerosolised microorganisms. The findings provide a framework to support more consistent evaluation, comparison, and design of GUV systems to improve indoor air quality and infection control.

An investigation of the physical and biological characteristics of dental aerosols generated during routine dental care in community dental clinics in Ireland.

Danielle McGeown[1], Michael B Prentice[2], Cormac Gahan[3], Stig Hellebust[4], Gareth Griffith[5], David O Connor[6], Mengfan Ding[7], Catherine Stanton[7], Paul Ross[7], Catherine Gallagher[8], Máiréad Harding[1]

[1]Oral Health Services Research Centre, University College Cork, Cork, Ireland. [2]School of Microbiology & Department of Pathology, University College Cork, Cork, Ireland. [3]School of Microbiology, University College Cork, Cork, Ireland. [4]School of Chemistry, University College Cork, Cork, Ireland. [5]Department of Life Sciences, Aberystwyth University, Aberystwyth, United Kingdom. [6]School of Chemical Sciences, Dublin City University., Dublin, Ireland. [7]APC Microbiome Ireland, University College Cork, Cork, Ireland. [8]Cork Dental University Hospital, University College Cork, Cork, Ireland

Abstract

Background/Aims :

Many dental procedures are considered aerosol-generating-procedures (AGPs), producing saliva-contaminated bioaerosol. The study aims were: (1) to characterize the size, concentration and biological content of particles, and (2) to characterise the microbiome of bioaerosols; generated during routine dental care in an Irish community dental surgery.

Methods :

An initial assessment of indoor air quality was carried out using the AirVisual Pro (IQAir) air monitor in seventeen dental surgeries. An average surgery was identified and sampled for 2-weeks during routine dental-care. Continuous real-time aerosol monitoring used a Waveband Integrated Bioaerosol Sensor (WIBS)-4 (Droplet Measurement Technologies), accompanied by a clinical care record. Environmental air sampling was conducted using: (1) a SKC Universal-Deluxe-MTX-pump (SKC Ltd) with filter assembly containing a sterile polyethersulfone membrane; and (2) an AberTrap Mk.3 device with two laser-cut, greased impactor paddles. Ten patients undergoing AGPs gave saliva samples and three air samples were taken: before, during and after the AGP, using a Coriolis®µ (Bertin Instruments) cyclonic sampler. Negative controls and field blanks were incorporated. Samples were processed using a DNeasy PowerSoil Pro Kit (Qiagen) and subject to 16S rRNA gene amplicon sequencing and analysis.

Results :

Particle counts from seventeen surgeries showed typical diurnal patterns in carbon dioxide and bioaerosols, correlated to room occupancy and AGPs. This was confirmed by WIBS measurements. Preliminary data from 16S rRNA-based analysis of microbial communities and correlations between physical and biological particle dynamics will be presented.

Conclusions:

The impact of clinical activity on diurnal particle dynamics in a dental surgery was determined.

Inhibition of tuberculosis transmission to guinea pigs (GPs) by direct far-UV-C222 ultra-violet irradiation.

Veronica Uekermannn[1], Ruvandhi Nathavitharana[2], Elsabe de Kock[3], Dawid Cordie[3], Paul Jensen[4], Tobias van Reenen[5], richard Vincent[6], Chad Roy[7], Edward Nardell[2], Michael Barer[8]

[1]University of Pretoria, Pretoria, South Africa. [2]Harvard, Boston, USA. [3]Retrasol, Pretoria, South Africa. [4]CDC, Atlanta, USA. [5]Council for Scientific and Industrial Research, Pretoria, South Africa. [6]Icahn School of Medicine, New York, USA. [7]Tulane University, New Orleans, USA. [8]University of Leicester, Leicester, United Kingdom

Abstract

In the Airborne Infection Research (AIR) facility near Pretoria we have conducted the first of a series of trials to determine the potential of UV_{222nm} to disinfect air in settings where transmission of airborne infection is considered a significant hazard.

Through rapid clinic review, including facemask sampling to assess infectiousness, we recruited 7 individuals newly diagnosed with pulmonary TB and prior to starting treatment (as agreed by local ethics) to reside at AIR where all ward extract air is passed to one of two guinea pig (GP) housing rooms. The patient rooms were illuminated with UV-C_{222nm} (3uW/cm^2 average fluence rate) on alternate days providing 90 GPs exposed to UV-treated air and 90 to control untreated air (one animal in the UV group died due to an unrelated cause). A total of 1040.54 person hours of GP exposure to extract air was recorded, with a slight excess (6.9%) for the control animals. Both control and UV-protected animals were skin tested for TB by standard tuberculin testing 6 weeks after study initiation. There was a striking and significant ($p<0.0001$) difference between the frequency of TST reactions with almost complete absence of reactivity (indicating infection) in the group exposed to UV-treated air. Although no participants either reported or were observed to show adverse effects attributable to UV-exposure, we now plan to determine the efficacy of lower UV irradiation levels in similar studies to minimise human exposure and optimise cost-benefit aspects of this approach to air disinfection.

From Barn to Breeze: Characterising the Airborne Microbiome and Antimicrobial Resistance in Irish Livestock Environments

Anita Grasso[1], Aaron Walsh[2], Fiona Crispie[2], Marta Martins[1], Julie Renwick[1]

[1]Trinity College Dublin, Dublin, Ireland. [2]Teagasc Food Research Centre, Cork, Ireland

Abstract

Farm environments are known to generate high levels of bioaerosols, particularly during activities such as animal handling, cleaning operations, and the management and application of manure and slurry. Bioaerosols generated in farm environments are characterised by bacteria and fungi, some of which may be pathogenic and act as zoonotic agents with the potential to be transferred to humans. Therefore, it is important to address the current knowledge gap regarding the characterisation of farm bioaerosols in Ireland in order to establish prevention strategies and mitigate the airborne transmission of pathogens.

Although bioaerosols are known to comprise a diverse cohort of microorganisms, the EPA 2021 gap analysis identified air and bioaerosols as among the least studied routes for the transmission of antimicrobial-resistant organisms (AROs) and antimicrobial resistance genes (ARGs).

This study aims to characterise and investigate the aerosol microbiome in Irish farm environments, including both bacterial and fungal communities, using culture-dependent and culture-independent approaches.

Ten aerosol samples were collected during aerosol-generating activities on a single farm using the AirPrep™ Cub Sampler ACD210. Microbial communities were characterised using next-generation sequencing (NextSeq™ 2000 P4 XLEAP-SBS™). The results provide new insights into the presence and composition of bioaerosols in Irish agricultural environments. These data contribute to the broader ResistAMR programme, addressing antimicrobial resistance through a One Health perspective.

The Microbiology Society is a membership charity for scientists interested in microbes, their effects and their practical uses. It has a worldwide membership based in universities, industry, hospitals, research institutes, schools, and other organisations. Our members have a unique depth and breadth of knowledge about the discipline. The Society's role is to help unlock and harness the potential of that knowledge.

Microbiology Society @microbiosoc @microbiosoc @MicrobiologySocietyOrg1945 Microbiology Society MS Microbiology

We are now on Bluesky @microbiologysociety.org

Microbiology Society 14–16 Meredith Street, London EC1R 0AB, UK +44 (0)20 3034 4870 microbiologysociety.org