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POSTER ABSTRACT BOOK

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MICROBIOLOGY SOCIETY

P001

Occurrence and Diversity of Fungal Communities in Indoor Environments: A Pilot Study from the Czech Republic

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Abstract

Indoor fungal contamination constitutes a significant public health concern, as ventilation systems in residential buildings may function as reservoirs and dispersal pathways for micromycetes. These fungi are implicated in a spectrum of clinical forms of many diseases, including aspergillomas, chronic pulmonary aspergillosis, allergic bronchopulmonary aspergillosis, invasive aspergillosis, and pneumonitis, particularly among immunocompromised individuals. Despite the prevalence of older buildings with natural ventilation in Central Europe, comprehensive data on their fungal communities remain limited. To address this knowledge gap, we conducted a systematic investigation of the mycobiome in ventilation systems of prefabricated panel buildings. Dust samples were collected from ventilation ducts in multiple older residential buildings across eight Czech cities during different seasons to capture spatial and temporal variability. Fungal communities were characterized using a dual approach: culture-based isolation on selective media to assess viability and taxonomic diversity, and DNA-based high-throughput sequencing to determine relative abundance and community structure. Sequencing revealed that the genus *Cladosporium* was consistently present in all samples, with an average relative abundance of 15.7%, reaching up to 63% in certain cases. Culture-based methods yielded 45 viable isolates, predominantly belonging to Aspergillus, *Penicillium*, and Cladosporium, confirming the persistence of micromycetes within ventilation systems. Seasonal fluctuations in community composition were observed, suggesting environmental factors influence fungal diversity and distribution. This study provides essential baseline data for understanding fungal contamination in Central European housing and contributes to the broader discourse on indoor air quality and occupant health.

P002

Diversity analysis of indoor and outdoor fungal bioaerosols in UK households: a longitudinal study

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Abstract

Background:
In the Global North, individuals spend up to 90% of their time indoors, yet indoor air quality remains far less studied than outdoor pollution. Long-term exposure to fungal bioaerosols is associated with respiratory illness, including asthma exacerbations and allergic sensitisation. However, exposure levels remain poorly defined due to limited routine monitoring, constraining robust risk assessment and preventing the introduction of quantitative, evidence-based thresholds into housing and public health legislation.

Methods:
As part of the WellHome project, we conducted a longitudinal surveillance study of fungal bioaerosols in 118 West London households between 2022 and 2024. Passive air samplers were deployed for 28-day periods across two seasonal campaigns, with parallel outdoor sampling. Fungal communities were characterised using ITS2 amplicon sequencing, and absolute fungal burden quantified using broad-range fungal qPCR. Concurrent VOC measurements enabled correlation analyses between fungal composition and chemical exposures.

Results:
Indoor air exhibited significantly higher fungal richness and diversity than outdoor environments, with indoor communities enriched for common moulds including *Penicillium*, *Aspergillus*, and *Wallemia*. Several case studies showed the highest abundances of clinically relevant taxa were observed in households with severe visible mould or documented respiratory sensitisation. Indoor fungal communities showed stronger seasonal dynamics than outdoor air, and fungal community composition was significantly correlated with indoor VOC profiles.

Conclusion:
This study presents the first large-scale surveillance of indoor fungal bioaerosols in UK homes. By integrating longitudinal sampling with molecular quantification, it establishes baseline exposure data and provides critical evidence to inform indoor air quality regulation and public health policy.

P003

Bioaerosol deposition across different scales

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Abstract

A bioaerosol spray released into the open air is subject to dispersion downwind due to fluctuating meteorological effects such as the wind speed, meander, and atmospheric stability. The transport of evaporating droplets is also affected by the ambient relative humidity. These uncontrolled conditions result in a spatially heterogenous surface deposit of bioaerosol.

For a hazardous and environmentally persistent pathogen, it is critical that material deposited onto surfaces can be reliably quantified to determine the extent of the hazard, and again following decontamination to confirm the effectiveness of bioremediation. Surface samplers, such as swabs or sponges, can be used for estimating surface contamination using a quantitative assay. It is important that such technologies are qualified for their high sampling efficacy through a robust test method, predicated on the ability to produce a controlled bioaerosol deposit onto a range of relevant surfaces.

Capabilities have been developed at Dstl to deposit aerosols of a surrogate bacteria (*Bacillus thuringiensis*, HD-1 cry -strain) over multiple size-scales; from centimetre-sized coupons to more complex representative surfaces. During larger scale experiments the coupons were inserted into rigs to provide confidence in the estimation of bacterial density due to the well-validated method for recovery from these smaller coupons. This work is a systematic study to minimise variability, while enabling a practical footprint within which several types of surfaces can be treated within a single dissemination event.

P004

Ambient air microbiota in rural residential areas: influence of nearby livestock farms on diversity and composition

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Abstract

The adverse environmental and public health impacts of livestock-related air pollution are increasingly recognized, yet research has largely focused on chemical pollutants and specific toxins. The influence of livestock emissions on airborne microbiota remains poorly understood. This study therefore investigated spatial and temporal variation in the diversity and composition of ambient air microbiota in a livestock-dense rural area.

Ambient air was sampled at nine residential sites from April-November 2021 (7-day measurements). All sites, except the background site, were within 500m from minimally one livestock farm. Particulate matter was processed to extract DNA for 16S rRNA (V5-V6) sequencing. Local livestock characteristics were computed by geographical analyses, meteorological variables collected from a nearby weather station. Associations were analysed for alpha diversity (mixed models), beta diversity (PERMANOVA) and differential abundances (MaAsLin2).

Diversity and composition of microbiota in ambient air clearly varied over time and between sites. Diversity appeared significantly ($p<0.05$) associated to temperature and presence of goat, poultry and pig farms. For the total community composition, between-weeks variation was larger compared to between-sites (PERMANOVA $R2= 22.1\%$; 13.4%). Temporal and livestock variables explained notable proportions of this variation (PERMANOVA R2 range=5.5-9.5%). Some of the differentially abundant bacteria were characteristic of goat, poultry or pig sources.

In livestock-dense rural areas, both nearby livestock farms and temperature influenced the diversity and composition of ambient air microbiota. Further characterizing contributing sources, including the livestock industry, and their interaction with meteorological conditions is essential for risk assessments of airborne microbiota for public health and the environment.

P005

Exhaled proteins as indicators of human influence on indoor air quality

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Abstract

Background

To date, indoor ventilation recommendations have been based on monitoring CO_2 concentrations. However, particles from human exhalation can have a significant impact on indoor air quality and should be taken into account.

Methods

In this study particles exhaled by healthy employees and indoor air particles of their offices were collected by the PExA device (particles in exhaled air). The samples were subjected to proteomic analysis using the Thermo Astral mass spectrometer with a Data Independent Acquisition (DIA) method. Metaproteomic approaches were used for data analysis, which allow differentiation between human and microbial proteins within the samples.

Results

The investigations indicate a significant increase in particles in the indoor air after volunteers worked in their offices. A comparison of the proteins analyzed in exhaled air and room air revealed a distinct group of human proteins specific for the lower respiratory tract, as well as bacterial and fungal proteins from the respiratory microbiome. The lung-specific human proteins have been found to be associated with processes such as protein metabolism, in particular surfactant metabolism.

Conclusion

Lung-specific human proteins can be used as marker proteins to assess indoor air quality after quantification. This data could form the basis for updating ventilation guidelines by taking exhaled proteins into account in addition to CO_2 concentrations.

P006

Field Applicability Study of Selected Microbial Volatile Organic Compounds (MVOCs) as Biomarkers of Occupational Mould Exposure

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Abstract

Background: Indoor mould exposure is a major public health concern, yet existing assessment methods exhibit certain limitations. Recently, 21 MVOCs have been proposed as biomarkers of mould exposure. This study aims to validate these biomarkers under real occupational conditions.

Methods: A cheese factory and milling plant with 14 workstations and 22 workers, respectively, were studied. Airborne fungi and bacteria were sampled at the workstations using a six-stage Andersen impactor (28 L/min) and cultured (CFU/m³). Concentrations of MVOCs were measured in the same workstations using adsorbent tubes (Tenax TA + Carbograph 1TD; 50 mL/min, 2 h) and analyzed by TD-GC-MS/MS. Exhaled air, blood, and urine from participants were collected pre- and post-shifts and analyzed by TD-GC-MS/MS or HS-SPME-GC-MS/MS.

Results: Airborne mould and bacteria ranged from 0–1170 and 0–2080 CFU/m³, respectively. Ten MVOCs were detected in > 60% of air samples. Oct-1-en-3-ol showed significant Pearson correlations with mould ($r = 0.663$, $p < 0.05$) and bacteria ($r = 0.691$, $p < 0.05$). Several MVOCs were inter-correlated, suggesting common sources (oct-1-en-3-ol/octan-3-one: $r = 0.899$; nonan-2-one/methyl-3-butan-1-ol: $r = 0.844$; $p < 0.001$). Four MVOCs in blood, four in urine, and two in exhaled air increased significantly after shifts. Exhaled oct-1-en-3-ol correlated with ambient air (Pearson $r = 0.441$; $p < 0.05$). Intra-matrix correlations suggested simultaneous exposure and accumulation during shifts.

Conclusion: Several MVOCs, especially oct-1-en-3-ol, show promise as biomarkers of occupational mould exposure. A larger sample size is needed to characterize additional MVOCs and validate this biomonitoring approach.

P007

Practical Sampling Strategies Enable Detection of Respiratory Virus RNA in the Air and on Surface Areas of a Daycare and a Primary School

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Abstract

Understanding respiratory virus presence and transmission in everyday environments is important for guiding infection prevention and control strategies. Schools and daycare centers are high-contact settings where viral transmission frequently occurs, yet systematic data on virus circulation among school-aged children who may be asymptomatic are limited. In this study, we used practical environmental sampling approaches suitable for educational settings, combining short-duration, low-flow air sampling with surface sampling to detect respiratory viruses. This approach eliminates the need for sampling individuals and enables rapid response and assessment during acute outbreaks.

Air samples were collected using a BioSpot-VIVAS bioaerosol sampler operating at 15 L min^{-1} for 30 minutes per session, and surface swabs were obtained from frequently touched surfaces. Samples were obtained from one daycare center and one primary school across seven consecutive weeks during peak influenza A virus (IAV) and respiratory syncytial virus circulation. All samples were analyzed by multiplex rRT-PCR and virus culture for common respiratory viruses.

Viral RNA of seasonal coronaviruses, SARS-CoV-2, human bocavirus, and rhinovirus was found in 40% of daycare and 29% of school air samples. In addition to these viruses, RNA of IAV, human metapneumovirus, and adenovirus was found in 80% of daycare and 71% of school surface samples. All air sample culture attempts were negative.

Overall, respiratory virus RNA was frequently detected in air samples from both the daycare center and the primary school, demonstrating the applicability of easy-to-use sampling strategies during acute outbreaks to rapidly generate actionable information on virus circulation in community settings.

P008

Real-time *Alternaria* spores detection and classification based on morphological feature extraction and Random Forest Classifier with SwisensPoleno Jupiter

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Abstract

Airborne Alternaria spores cause allergies in humans and diseases in plants . This study aimed to validate continuous, automatic, real-time monitoring of these spores with the SwisensPoleno Jupiter and a Random Forest classifier to identify them. A key innovation is the holography data based chain detection. chains and measure their length and width. As a reference, trained experts operated Hirst spore traps and performed manual counting and identification. Measurements were conducted in 2023 and 2024 from May to August (Main Spore Season MSS) at sites near potato fields in Reckenholz and Zollikofen, Switzerland. Based on airflow rate and measurement efficiencies, we determined the detection limits for daily concentrations of both sensors: 0.84 particles/m³ for the Poleno and 24.7 particles/m³ for the Hirst.

For Alternaria alternata and *A. solani*, we compared median daily concentrations (MDC) from the SwisensPoleno Jupiter and Hirst using Kendall's Tau over the MMS. We also compared median and maximum daily concentrations. In 2023, Kendall's Tau fo A. solani was 0.48 in Reckenholz and 0.45 in Zollikofen. Hirst MDC were 66 and 1.7 particles/m³, and maxima were 342 and 3.1 particles/m³, respectively. In 2024, Kendall's Tau for *A. alternata* was 0.57 in Reckenholz and 0.38 in Zollikofen, with Hirst MDC of 4.6 and 1.7 particles/m³ and maxima of 231 and 20 particles/m³.

We observed an agreement between the Poleno and Hirst when daily concentrations were higher than the Hirst's detection limit.

P009

Crop-associated structuring of airborne fungal communities above wheat and oilseed rape in Spring 2024

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Abstract

Background: Previous studies show greater species richness in 10m rooftop samples than at 1m in fields, indicating more mixed air at 10m representing a larger regional footprint than near the ground. Here, airborne fungal communities above crops were analysed to show crop-specific influences on airborne fungal communities.

Methods: Rotorod spore-traps collected weekly samples in plots (wheat, oilseed rape and bare fallow) at 0.5 m and 2.5 m, or 1m heights in autumn and spring. DNA was extracted and analysed using ITS metabarcoding on the Oxford Nanopore MinION platform. Community composition was assessed using relative abundance profiles, alpha and beta diversity metrics, differential abundance testing, and crop-resolved co-occurrence network analysis based on strong positive Spearman correlations.

Results: Wheat and OSR shared a core set of dominant genera, including Alternaria, Cladosporium, Solicoccozyma, and Phaeosphaeria, but differed markedly in relative abundance structure. Wheat-associated communities were dominated by Alternaria and showed higher relative abundance of cereal-associated taxa e.g. Neoascochyta. OSR samples exhibited a more even community structure enriched in Botrytis, yeast-like basidiomycetes (Solicoccozyma, Cystofilobasidium), and other epiphytic fungi. Shannon diversity did not differ significantly between crops, but beta diversity analyses revealed clear compositional separation (PERMANOVA $R^2 = 0.056$, $p = 0.002$).

Conclusions: Despite similar alpha diversity, airborne fungal communities above wheat and OSR differed significantly in composition and interaction structure during spring 2024, demonstrating strong crop-associated structuring of the aerobiome driven by a small number of dominant taxa and distinct co-occurrence patterns, with implications for understanding pathogen dispersal and crop-specific disease risk.

P010

Surface hydrophobicity and propensity for airborne transmission of mycobacteria.

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Abstract

Nontuberculous mycobacteria are readily recovered from surface waters and water distribution systems. For many years Falkinham and colleagues have advanced the hypothesis that the hydrophobicity of nontuberculous mycobacterial cells supports their tendency to be aerosolised and their transmission into lung infections. Stimulated by Minnikin's suggestion that an increase in hydrophobicity underpinned the transformation of *M. tuberculosis* ancestors into an airborne infection, we have been investigating this property in mycobacterial isolates. Using multiple assays of cell hydrophobicity and experimental aerosol generation studies we illustrate the challenges of investigating this hypothesis and present some initial conclusions

P011

Biogenic atmospheric ice-nucleating particles over the Southern Ocean

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Abstract

Our ability to simulate global climate, particularly in remote regions such as the Southern Ocean, is hampered by poor representation of aerosol-cloud interactions, such as the role of ice-nucleating particles (INPs). This rare aerosol type can trigger the freezing of supercooled liquid cloud water droplets and can comprise of mineral dusts, sea spray aerosol, and bioaerosols. It is crucial to measure their concentrations, types, sources, and sinks – information we currently lack in the Southern Ocean. In late 2024, we undertook a research cruise in this region aboard the *RRS Sir David Attenborough* to measure concentrations of aerosols, bioaerosols, and INPs. INPs were measured using a combination of state-of-the-art online instrumentation and filter sampling with offline analysis, including a comparison of traditional INP filter sampling and a more recent variant. Here, we report preliminary findings of INP measurements from the cruise. We found higher than anticipated concentrations throughout the cruise despite being in a remote marine environment. Crucially, we found differences in results between the two different methods of filter-based sampling and analysis. Lab-based testing suggests that some INPs, particularly those of a biological nature, may be undercounted when using the traditional offline filter sampling techniques for INP analysis.

P012

Bacterial composition of settled dust samples across UK railway stations

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Abstract

1.6 billion journeys were made across the UK rail network between 2023 and 2024. As such, characterising the pollution and presence of bioaerosols at railway stations across the UK is essential to be able to improve air quality for millions of passengers using the rail network. Recently published work determined the metal and fungal composition from railway stations across the UK using settled dust samples. Station location, layout and season independently contributed to urban fungal richness, diversity, and composition. For the metal analysis, iron, zinc and copper were consistently detected.

To better characterise the UK stations, this study has used the same dust samples to determine the bacterial diversity and identify the bacterial composition. DNA was extracted from the dust samples and sequenced using the 16S metagenomics kit as part of the ion torrent system. Results may identify differences within regions and between the layouts of railway stations. It is hoped these results can be correlated with the existing metal and fungal analysis to inform strategies to improve air quality in urban public spaces proving beneficial for both workers and passengers travelling across the rail network.

P013

Investigating the Impact of Relative Humidity on Airborne *Streptococcus pyogenes* Viability

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Abstract

Over the past decade there has been a significant increase in both superficial and invasive infections of *Streptococcus pyogenes* in the UK. This is clearly demonstrated when looking at incidence rates of scarlet fever, a superficial infection of *S. pyogenes*, which have been consistently elevated since 2014 with regular springtime peaks. Many UK cases are currently caused by $M1_{UK}$, an emergent strain of *S. pyogenes*. Although scarlet fever transmission is commonly attributed to direct contact, growing evidence points to aerosols as a significant route for *S. pyogenes* dispersal. However, the airborne transmission of *S. pyogenes* and how its viability is affected by varying environmental conditions remains poorly understood.

This research investigates the effect of relative humidity (RH) on the airborne viability of *S. pyogenes* H1490, an $M1_{UK}$ strain, over a 2-minute period using the Controlled Electrodynamic Levitation and Extraction of Bioaerosols (CELEBS) instrument. CELEBS is a relatively new approach to studying bioaerosols, and allows for the study of monodisperse bacteria-containing droplet populations within a controlled environment while maintaining a high sampling efficiency.

It was found that *S. pyogenes* H1490 viability was highest at 2 minutes in a 30% RH environment (78%), compared with 50% RH (36%) and 80% RH (42%). Across all RH conditions tested, a significant viability loss is typically observed after 0.25 minutes of aerosolisation. Future work aims to extend the exposure timeframe, compare the data collected on $M1_{UK}$ to other *S. pyogenes* strains, and investigate the impact other environmental conditions have on the $M1_{UK}$ strains.

P014

Multilayered aerosol generation to improve test and evaluation

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Abstract

Detecting, identifying, and monitoring aerosolised biological threat agents is critical for security and public health, yet remains a challenging task. Air is a complex matrix consisting of a range of compounds of both biological and non-biological particles with varying particle sizes and concentrations. Biological threat agents may be present at low concentrations relative to the aerosol background, hindering detection.

Test and evaluation of biodetection equipment is commonly performed in aerosol chambers with HEPA-filtered air to achieve controlled, reproducible conditions, but this removes the natural complexity. To address this, we built a continuous-flow aerosol chamber with multilayered aerosol generation to provide more representative conditions for evaluating detection equipment. By introducing multiple aerosol layers from separate generators, the chamber can create a simplified yet realistic aerosol background that better mimics real-world environments.

Aerosols are generated in vertical columns, where they are conditioned before entering the horizontal continuous-flow chamber. Particles are mixed and homogenised before entering the sampling section, which includes interchangeable isokinetic sampling ports to accommodate various instrument flow rates.

Using a multilayered aerosol generation approach to mimic a real-world aerosol background could improve test and evaluation of equipment for detection, identification, and monitoring of biological threat agents. This approach could better identify operational challenges, ultimately supporting the development of more robust and reliable detection systems for biological threat agents.

P015

Salt & pH Effects on Influenza A Virus Stability

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Abstract

Influenza A viruses (IAVs) impose a significant epidemiological burden, with millions of cases reported annually. However, factors affecting their airborne stability and transmission remain to be fully understood. Extreme pH and high salt concentrations within infectious respiratory particles (IRPs) are considered stressors during airborne transmission, though their effects are typically studied in isolation. Here, we aimed to assess the combined effect of pH and salinity on IAV stability and infection. In bulk experiments, we measured IAV inactivation kinetics over a pH range from 3 to 11, and at NaCl concentrations ranging up to saturation. In addition, we used dynamic light scattering and transmission electron microscopy to study aggregation in IAVs at different pH and salt concentrations. Results suggest that low pH rapidly inactivates IAV but that the presence of salt stabilizes them, leading up to 33-fold slower IAV decay at pH 4.1. The stabilizing effect of salt was found to be concentration-dependent and manifested at concentrations as low as 250 mM NaCl. Stabilization only subsided at pH < 4, indicating that very low pH values must be reached within IRPs to result in efficient virus inactivation. We furthermore found that at low pH, IAVs tend to form aggregates almost immediately but that the presence of NaCl prevents aggregate formation. The stabilizing effect of salt can therefore not be attributed to virus protection by aggregation. Instead, we hypothesize that salt may stabilize the pre-fusion state of the IAV hemagglutinin (HA), thereby shifting the fusion pH to a lower pH.

P016

Salt-pH effects on Airborne Respiratory Viruses

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Abstract

Airborne transmission of respiratory viruses remains a critical concern for public health, driven by the release and inhalation of infectious respiratory particles (IRPs). Although external environmental conditions have been shown to modulate transmission dynamics, how intrinsic aerosol properties—particularly pH and ionic composition—jointly shape viral stability is not yet well characterized. In ambient IRPs, evaporation, gas–particle interactions, and mixing with inorganic salts can rapidly alter pH and ionic strength, potentially affecting viral infectivity during airborne transport.

In this study, we investigate the simultaneous effects of pH and salt conditions on the stability of three respiratory viruses: human coronavirus 229E (HCoV-229E), rhinovirus (HRV), and adenovirus type 2 (HAdV2). These viruses represent distinct structural and genomic classes and are relatively understudied than influenza A virus (IAV) in the context of their aerostability. By systematically varying pH (2.5-11) and NaCl (up to saturation) in bulk experiments, we aim to elucidate how these key environmental variables modulate viral stability.

We hypothesize that virus stability will exhibit virus-specific responses to pH and salinity, reflecting differences in capsid structure, genome type, and envelope presence. We will present results from experiments in bulk solutions, as well as from aerosol chamber experiments, to assess how extreme values within IRPs influence respiratory virus survival in airborne environments.

P017

From seconds to hours: quantifying microbial pathogen survival in airborne droplets with QELEBS

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Abstract

Airborne pathogen transmission strongly influences infection risk in clinical and built environments. However, quantitative data describing microbial survival during the earliest stages after aerosol generation, within the first 30s, and during prolonged airborne suspension over several hours remain limited. We previously addressed aspects of these gaps using CELEBS (Controlled Electrodynamic Levitation and Extraction of Bioaerosols onto a substrate), but the limitations in throughput and observation time constrained quantitative analysis of rare survival events.

To address these shortcomings, we developed QELEBS (quadrupole electrodynamic levitation and extraction of bioaerosol onto a substrate), which enables automated capture and culture-based quantification of individual bioaerosol droplets with high fidelity and high throughput under controlled environmental conditions.

Using *E.coli*K12 droplets as a model system, short term measurements within the first 5 s after aerosol generation demonstrated quantitatively accurate bacterial loading at the single droplet level, with colony forming units recovered on agar plates showing strong linear agreement with theoretical loading estimates (R^2 = 0.921). Moreover, QELEBS enabled stable airborne suspension of large droplet populations, up to 300 droplets, for periods of up to 4 h, allowing survival to be quantified at extremely low viable fractions, down to 1.07%. Beyond bacterial systems, QELEBS supports studies of viral aerosols under precisely controlled environmental conditions. By enabling systematic variation of relative humidity, temperature, and ultraviolet irradiation, the platform allows quantitative evaluation of environmental mitigation strategies.

Overall, QELEBS provides a robust approach to investigate how controlled aerosol microenvironments shape microbial persistence, supporting mechanistic studies and future bioaerosol risk assessment.

P018

Nothing beats the real thing: The bioaerosol survival of *Neisseria meningitidis* in human and artificial saliva

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Abstract

Neisseria meningitidis is the causative agent of invasive meningococcal disease, a potentially fatal disease transmitted via respiratory aerosol that occurs across the globe with a particularly high mortality rate of up to 10%. Previous data we collected using CELEBS (Controlled Electrodynamic levitation and extraction of bioaerosol onto a substrate) on the airborne survival of *N. meningitidis* found there to be a rapid loss of bacterial viability over the first fifteen seconds after aerosolisation in artificial saliva.

However we have identified that survival is significantly increased and prolonged when aerosolised in human saliva samples. This was identified in Serogroup A, B and C *N. meningitidis* strains but not in the commensal strain *Neisseria lactamica*, suggesting a species-specific effect. Furthermore, this effect was seen across saliva samples from different donors.

We have also identified that the addition of different anti-oxidants significantly increases the survival of serogroup B strains, suggesting that oxidative stress is a mechanism that drives loss of bacterial viability in the air, as previously shown for *E. coli* (Oswin, 2023). Furthermore, removing the presence of small molecules from the real saliva via dialysis, including the antioxidant glutathione, resulted in a reduction in bacterial viability in aerosol.

Although further work must be completed to determine the mechanisms by which saliva may increase survival of *N. meningitidis* upon aerosolisation, this research will help to understand the dissemination of airborne pathogens and therefore how they may be contained.

P019

Influenza A virus presents a relative humidity-dependent multiphasic decay in aerosols

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Abstract

Background

Influenza A virus (IAV) poses a significant burden to UK healthcare, especially in the winter months. The drivers of increased seasonal IAV infection rates are poorly understood but are potentially linked to changes in environmental conditions, host immunity, and human behaviour. This project investigates the impact of environmental conditions on IAV airborne stability, thereby improving our understanding of how different conditions can drive IAV seasonality.

Method

We employ the novel Controlled Electrodynamic Levitation and Extraction of Bioaerosol onto Substrate (CELEBS) technique to assess how environmental conditions, such as relative humidity (RH) and gas-phase CO_2 concentration, affect IAV infectivity. The CELEBS allows precise control over monodisperse aerosol populations, enabling high-resolution measurements of viral decay.

Results

Experiments with IAV strain A/WSN/33 demonstrated RH-dependent decay dynamics. At high RH (>55%), IAV exhibits multiphasic decay characterised by rapid decay within the first 30 seconds following aerosolisation, a delayed lag phase with minimal decay, and a subsequent increase in decay. Contrastingly, at 55% RH, IAV decay appears biphasic, with a rapid initial phase followed by a slower decay phase. By 10 minutes, the greatest IAV decay was observed at high RH (>55%). These differences in decay profile indicate that at different RHs there may be different drivers of IAV decay. Ongoing bulk-phase and molecular studies aim to identify the mechanisms driving RH-dependent decay.

Conclusion

These findings demonstrate that RH can influence IAV decay dynamics. These dynamics differ from those observed for other enveloped viruses using the CELEBs, including SARS-CoV-2 and murine hepatitis virus.

P020

Aerostability of Clade Ib and IIb mpox virus

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Abstract

Background

Mpox virus (MPXV) is transferred primarily through direct contact with infectious lesions or bodily fluids, although, indirect transmission via contact with contaminated surfaces is also considered possible. Surfaces may become contaminated through the deposition of respiratory droplets or via the resuspension and redeposition of skin squamae during activities such as bed making. While larger particles fall rapidly, smaller virus-containing particles may remain airborne for extended periods before eventually depositing onto surfaces. Although some data exist regarding MPXV surface stability, few studies have examined the aerostability of the virus.

Method

Aerosols of MPXV (either clade Ib or clade IIb), generated using an AeroMP platform (Biaera Technologies) and a 6-jet Collison nebuliser, were maintained within a Goldberg drum at either 80% (n=3) or 50% (n=3) relative humidity. Samples were collected at 5-, 10-, 15-, 30-, 60-, and 120-minute timepoints and infectious virus was quantified via plaque assay (n=1).

Results

Infectious virus was recovered at all timepoints for both MPXV clades under both humidity conditions, indicating that aerosolised virus remained viable over the two-hour study period. Differences in the degree of titre reduction were observed between the two clades. However, these findings are preliminary, and additional data will be required to draw firm conclusions.

Conclusion

Although preliminary, these findings demonstrate that aerosolised MPXV can remain viable for at least 2-hours. This highlights the potential for airborne virus to contribute to environmental contamination, including the re-contamination of previously cleaned surfaces, particularly in poorly ventilated spaces where aerosols may remain suspended for longer periods.

P021

Differential decay of structurally distinct respiratory viruses in deposited human saliva particles at variable relative humidity

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Abstract

Respiratory viruses move through the environment to transmit, and they must therefore retain infectivity during this transport phase to spread effectively. Yet the environmental stability of many important respiratory viruses is unknown. The main objective of this research is to evaluate the susceptibility of structurally distinct respiratory viruses to environmental exposures. Here, we generated 1 µL virus-laden human saliva particles and evaluated virus degradation following environmental exposure. Our findings indicate that adenovirus, a 100 nm nonenveloped icosahedral virus, exhibits extensive stability regardless of relative humidity (RH), whereas rhinovirus, a 30 nm nonenveloped icosahedral virus, undergoes significantly more decay at 50% and 80% RH. Influenza virus, an enveloped pleomorphic virus, displays comparable stability to adenovirus under the same conditions. These findings are counter to the assumption that enveloped viruses are less persistent than nonenveloped viruses. We hypothesize that rhinovirus' small size results in fewer protein interactions, causing reduced protection that would typically be conferred by proteins. Interestingly, our simulated saliva, generated to mimic the inorganic and protein concentrations in our human saliva, confers increased rhinovirus stability. It is possible the proteins in simulated saliva, which we simplified by using only human serum albumin, are much smaller in size than many human saliva proteins; at the same mass concentration, albumin is more extensively distributed than proteins in saliva, increasing interactions and providing additional protection. Ultimately, this work is critical to establishing mechanisms driving environmental virus susceptibility that will allow for an improved understanding of exposure risks and development of effective prevention strategies.

P022

Organic Components Modulate the Survival of RSV in the Aerosol State

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Abstract

Respiratory syncytial virus (RSV) is a leading cause of severe lower respiratory tract infections in young children worldwide, yet effective antiviral therapies and pediatric vaccines remain limited. Understanding RSV survival in the aerosol state is therefore essential for elucidating transmission pathways and informing engineering controls and public health strategies. Organic components are unavoidable constituents of respiratory fluids and are expected to play an important role in virus survival as they can shape the physicochemical microenvironment for viruses, particularly during short-range transmission. In this ongoing study, we investigate how organic constituents modulate RSV survival during aerosolization and subsequent short suspension periods. RSV is aerosolized in Eagle's Minimum Essential Medium (EMEM) supplemented with representative organic components, including sucrose, mucin, and bovine serum albumin (BSA). RNA copy number and infectious titer ($TCID_{50}$) are quantified for the stock solution, immediately after aerosolization, and at two defined aerosol residence times using droplet digital PCR (ddPCR) and standard $TCID_{50}$ cell culture assays. Viral survival during atomization and between residence times of approximately 7 s and 40 s is evaluated in a flow-tube suspension system operated at ~30% relative humidity. Preliminary results indicate that sucrose supplementation enhances RSV survival during aerosolization but reduces survival at later residence times compared to EMEM alone. Scanning electron microscopy shows smoother particle surfaces with sucrose, whereas EMEM-only particles appear more desiccated and irregular. Together, these findings suggest that organic components can exert competing effects on RSV survival by dynamically regulating aerosol microenvironments during aerosol evolution.

P023

Collection efficiency of a miniaturised electrostatic precipitator for sampling ice-nucleating particles

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Abstract

Ice nucleating particles (INPs) can initiate ice formation in cloud water droplets above -38°C, influencing climate due to their effect on cloud lifetimes and radiative properties. Improved characterisation of the spatial and vertical distribution of INPs remains limited by conventional sampling approaches; ground-based approaches such as filter sampling require mains power and limits deployment in remote or elevated environments, while aircraft sampling is costly. We are characterising and validating a novel, miniaturised electrostatic precipitator (ESP) for its application to INP sampling. The ESP is a lightweight, battery-operated aerosol sampler that collects particles by electrostatic precipitation onto a hydrophobically coated glass slide, offering potential for portable and airborne INP measurements. However, its INP collection efficiency under varying wind conditions is not fully characterised.

This study investigated effects of windspeed on INP collection efficiency by sampling aerosol particles under controlled windspeeds ranging from light to moderate breezes (2-6 m s^{-1}) that the ESP is expected to be deployed in. Collected aerosol particles were analysed using a droplet freezing assay to determine INP concentrations, then compared with concurrently measured particle size distributions and theoretical collection efficiencies to assess overall collection efficiency of the ESP. INP concentrations showed no significant variation across the tested range, indicating minimal wind-induced sampling bias under these conditions. These results support the ESP as a robust tool for portable and airborne INP measurements, such as drone deployment. Future studies should test its performance at higher windspeeds to evaluate its suitability for biological INP sampling under potentially turbulent conditions.

P024

Detection of Airborne Methicillin-Resistant Staphylococcus aureus (MRSA) in a Hospital Environment

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Abstract

Methicillin-resistant *Staphylococcus aureus* (MRSA) is recognized as a serious public health threat by the Centers for Disease Control and Prevention (CDC). The bacterium is known to be transmitted primarily through direct contact. In this study, the presence of airborne MRSA was investigated in two units of a hospital using both active (BioCascade impactor and gelatin filter) and passive air sampling methods. Identification of MRSA was performed via plate culturing, broth enrichment, and Polymerase chain reaction (PCR). From Unit 1, 61 active and 78 passive samples were collected, while 20 samples were collected by active sampling in unit 2. Amplicon bands corresponding to 16S rRNA genes were observed for at least 20 samples, which proved the presence of bacteria. Thirteen samples were positive for *mecA* gene, but below *lukS* gene's the detection limit, thus making the presence of MRSA inconclusive. Five enriched samples from unit 1 were positive for *femA, nuc, mecA* and *lukS* genes, confirming the presence of MRSA. Furthermore, size-resolved collection using the BioCascade revealed the presence of airborne MRSA across a broad size range (<0.5 µm to >10 µm), suggesting the potential for airborne transmission. These findings underscore the need for further infection control strategies for airborne MRSA.

P025

BioCascade Impactor with Temperature Control and Water Injection to Conserve Virus Viability in Air Sampling

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Abstract

The BioCascade Impactor (BC) collects size-fractionated bioaerosols into three stages (>10, 4.1–10, 1.5–4.1 µm) through gentle impingement into a liquid medium. To minimize high evaporation rates of the collection medium under low relative humidities (<40%) and long sampling durations (>3 h), we developed a "jBioCascade" system coupling temperature control with a stage-specific water-injection module. This injection system delivers sterile water to each stage at user-programmable intervals and volumes, helping offset evaporation while maintaining the intended nozzle–liquid geometry. Evaporation rates of two collection media across a range of RH values were quantified, and were used to tune injection profiles that keep stage volumes within ±15% of the initial 2 mL. The device performance in collecting airborne, viable MS2 bacteriophage was tested across varying RH (20-80%), sampling durations (60, 120 and 180 min), and corresponding injection rates. Across all matched RH–duration conditions, injection increased viable MS2 recovery by a mean of 0.54 log_{10} PFU (≈3.5-fold; 95% bootstrap CI:0.41–0.70 log_{10}) and showed a very large, standardized effect (paired Cohen's d=1.77). Injection significantly enhanced PFU yields at 20% and 40% RH and at 60- and 180-min sampling durations, with the largest relative gains occurring under low-RH, long-duration conditions. Stage-resolved analysis showed consistently higher PFU in all BC stages with injection, without altering the underlying size distribution. Taken together, these results demonstrate that the RH-tuned water-injection system effectively maintains liquid volume and substantially improves viable virus recovery over multi-hour sampling, suggesting its applicability in environmental surveillance for bioaerosols.

P026

Effect of Particle Concentration on Collection Efficiency in a Condensational Growth Tube

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Abstract

Condensational growth of aerosol particles is widely used in aerosol measurement devices and bioaerosol collection. While it is anticipated that particle concentration plays a crucial role in determining the size of the droplets formed, the effect of this parameter on the collection efficiency of the Viable Virus Aerosol Sampler (VIVAS) is still unknown. Our main objective was to investigate how variations in aerosol concentration affect aerosol growth dynamics and collection performance in VIVAS, using computational fluid dynamics (CFD) modeling with COMSOL Multiphysics®. Simulation results demonstrated that the release of latent heat during droplet growth and the depletion of water vapor associated with particle activation reduce peak supersaturation within the growth tube, thus reducing the droplet size. As the particle number concentration increased, the resulting droplet sizes decreased. Based on a 3-µm cut-off size, and VIVAS operated at 8 LPM flow rate, four inlet particle concentrations were tested, ranging from 10^3 to 10^6 particles/cm^3. The mean diameter of the final particle size decreased from 7.9 µm to 2.75 µm, and the corresponding collection efficiency decreased from 98% to 78%. These findings underscore the significance of thermodynamic and vapor mass-transfer effects in condensational growth tubes. These results provide a foundational step toward optimizing operational conditions. Future work will extend this study by evaluating how temperature gradients and particle residence time influence condensational growth and collection efficiency. Such analyses will enable more precise control over droplet growth and enhance the reliability of bioaerosol sampling across a wide range of environmental conditions.

P027

AirSeq as a tool for cereal rust surveillance

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Abstract

Cereal rusts are known to be some of the most devastating diseases in wheat, causing billions of dollars of yield loss each year globally. *Puccinia striiformis* f. sp. *tritici* and *Puccinia triticina*, causing yellow rust and brown rust respectively, are two of the most abundant cereal rust fungi, with *P. striifromis* f. sp *tritici* causing almost 5.5 million tonnes of yield loss alone annually (Beddow *et al*., 2015). As these pathogens are obligate biotrophs, they cannot be cultured, leading to limited knowledge regarding their disease spread. We have developed AirSeq, a novel sequencing-based approach for studying bio-aerosols and environmental DNA. This technology allows us to capture spores from the air before infection occurs. The use of AirSeq paired with environmental metadata could offer the possibility to make more accurate, timely predictions of infection risk, which could form part of integrated disease management strategies. Thereby helping farmers to reduce costs while remaining environmentally friendly. Here, we present AirSeq surveillance data from multiple commercial wheat growing sites, showing how abundance of *P. striiformis* f. sp. *tritici* and *P. triticina* changes both geographically and temporarily. We also benchmark our findings to climate data to demonstrate the influence the weather has on disease spread.

P028

Silicone wristbands as a novel passive sampling tool for personal microbial exposure assessment

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Abstract

Expanding on their success in chemical exposure assessment, we tested silicone wristbands (SWB) for personal microbial exposure assessment.

We first established bacterial binding affinities to SWB using dilution series of various specific bacteria and a mock community. Subsequently, in a field study we compared SWB with active personal filter-based inhalable dust air sampling among office (n=4) and farm workers (n=5). Samples underwent DNA extraction, and total (16S-rRNA gene) and bacterial specific DNA was quantified by qPCR. Bacterial species were profiled using metabarcoding (amplicon sequencing 16S hypervariable region V5V6).

Various bacterial species bound efficiently to SWB, though slight shifts in mock bacterial community populations suggested some differential binding affinity of the eight bacterial species. The field study confirmed the bacterial adherence capability of SWB, which captured various bacteria in both high (farm) and low (office) microbial load environments. Notably, bacterial community structures on SWB closely resembled those of simultaneous collected personal air samples, especially among farm workers, underscoring the potential of SWBs as a microbial sampling tool. Furthermore, participants rated wearing SWBs as more convenient than traditional air samplers with pumps.

In conclusion, SWB are a promising low-cost passive sampling tool for personal microbial exposure assessment. By expanding the bioaerosol assessment toolbox, they enable large-scale application in epidemiological studies generating more robust scientific evidence on exposure-response relationships between microbial agents and associated health effects.

P029

Monitoring biofluorescence spectra from aerosol collected onto a filter substrate for bioaerosol detection and exposure assessment

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Abstract

This abstract is sent to the conference organising committee member Richard Thomas (Dstl) directly for reviewing purposes. The organisational permissions being sought and organising committee are aware. Thank you.

P030

Detection of airborne microbes and their derivatives using a novel ambient air sampling device.

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Abstract

Airborne microbes and their derivatives can pose a range of risks such as disease transmission, food contamination, allergy and chronic health conditions. Hence there is an interest in measuring bioaerosols in indoor environments, particularly where these risks are increased such as in healthcare and waste management. Multiple methods are available to measure bioaerosols, each with different capabilities and limitations. The aim of this study was to demonstrate the ability of a novel ambient air sampler (Apollo) to collect airborne microorganisms and their derivatives.

S. aureus, E. coli, L. innocua, K. pneumoniae and the bacteriophage MS2 were aerosolised within a test chamber. Air was sampled using the filtration based Apollo device. Filters were extracted and microbes quantified using culture based techniques and qPCR. Environmental air samples were collected with Apollo for various time periods (1-7 days) in residential properties and offices. Bacteria, endotoxin and β-glucans were quantified by qPCR, recombinant factor C and Glucatell assays respectively.

Viable bacterial and viral particles from multiple species can be recovered and quantified from Apollo filters following short-duration sampling. Using qPCR techniques for quantification, the sampling time could be increased, resulting in higher quantification of bacteria from Apollo filters. Bacteria, endotoxin and β-glucans could be detected and quantified from Apollo samples in all domestic properties.

This pilot study demonstrates the ability of Apollo to sample a range of microorganisms and their derivatives which are of interest in multiple industries. Apollo provides a user-friendly solution for routine monitoring of bioaerosol exposure in indoor environments.

P031

Collection of aerosolised microspheres using corona-free electrostatic actuation

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Abstract

The transmission of pathogenic bioaerosols poses significant risks to human health, animal welfare, and agricultural productivity, often leading to economic losses and increased pressure on public health systems. Electrostatic precipitation (ESP) is an aerosol collection method (Foat *et al.* 2016); however, its reliance on corona discharge generates ozone, which can compromise bioaerosol integrity (Ouyang *et al.* 2023). To retain the advantages of ESP while eliminating ozone exposure, an ozone-free electrostatic actuation alternative was investigated.

Indium tin oxide-coated microscope slides were connected to four separate electrical conditions (positive, negative, grounded, and floating) in an $8m^3$ aerosol chamber, with four optical particle counters to measure aerosol concentration. Fluorescent 1µm polystyrene microspheres, used as model particles, were nebulised for 15 minutes and sampled electrostatically (-10kV to +10kV) for 10 minutes. Samples were imaged using an EVOS M7000 fluorescence microscope and analysed with Celleste 6 software. To enhance collection efficiency, a fan-assisted collection device was constructed. Fan speed and spatial placement were varied to optimise performance.

Both positively and negatively biased slides collected up to 17.0 and 8.5 times more particles than grounded or floating controls, respectively, with performance increasing with voltage. The fan device achieved up to 59.1% collection efficiency at an airflow rate of 10.9L/min.

These findings demonstrate that ozone-free electrostatic actuation enables effective aerosol collection, with the potential to preserve bioaerosol viability, supporting future applications in biosurveillance and agricultural biosecurity.

This work was supported by Research England-funded Biodetection Technologies Hub and the Engineering and Physical Sciences Research Council [grant number EP/X017591/1].

P032

Kromek Biosequencer: Fully automated detection and identification of bacteria and viruses in air via field-based long read sequencing for non-expert users

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Abstract

Novel methodologies for fully automated separation and concentration of bacteria and viruses from an air sample, for agnostic threat detection and identification using sequencing have enabled near-real time analysis of environmental metagenomic samples.

Kromek has developed an instrument that samples air at 4,800 lit./min and transfers the 0.5-10 µm particles present in the sample into an aqueous solution. The instrument then extracts the nucleic acids, purifies them, amplifies them and prepares the sequencing library. Sequencing is performed automatically utilising the ONT MinION, where DNA fragments are base-called, analysed and the organisms present are identified *in situ.*

Time from sample collection to identification is 90 minutes for DNA organisms and 135 minutes for RNA organisms. The pipeline can identify a pathogen at a concentration of 10^4 organisms per sample, among a complex environmental background. The built-in bioinformatics software utilises several tools with a final decision algorithm that incorporates the confidence of detection of the identified organism.

Kromek is envisioning a world where timely detection of pathogens can minimise the impact of infectious disease outbreaks and strengthen national defences from malicious bioterrorism attacks.

P033

Portable Cyclone-Based Bioaerosol System for Molecular Detection of Airborne Plant and Environmental Pathogens

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Abstract

Airborne spread of plant and environmental pathogens threatens food security and ecosystem health, yet most current monitoring methods rely on laboratory-based, off-line sampling and culture. This study presents an integrated bioaerosol monitoring system that combines a compact cyclone collector with automated loop-mediated isothermal amplification (LAMP) and complementary lateral flow immunoassays (LFA) to enable near-real-time detection of airborne pathogens in agricultural and environmental settings.

A miniaturised, high-efficiency cyclone is integrated into a standard 15 mL Falcon tube, which functions as a sealed, disposable unit for both aerosol collection and downstream analysis. Air is drawn through the cyclone, concentrating bioaerosols into a small liquid volume that is directly compatible with LAMP, LFA, and culture-based methods.

System performance was evaluated in an 8 m^3 aerosol chamber using polystyrene microspheres and *Bacillus globigii* spores as surrogates for airborne fungal and bacterial pathogens. The platform demonstrated efficient capture across the 1–10 µm size range under chamber conditions and reliable recovery of larger, spore-sized particles representative of agriculturally important fungi such as brown and yellow rust during field testing. The collected samples remained suitable for nucleic-acid amplification, antigen detection, and culture, confirming preservation of biological integrity.

The use of low-cost, commercially available consumables and a modular assay design enables rapid re-targeting to different pathogens. Overall, this cyclone-based platform provides a practical route to deployable airborne pathogen detection for early warning and biosurveillance.

P034

Advanced Chemical Sensors for Biodetection

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Abstract

Bioaerosols are a significant challenge to public health and environmental monitoring due to their complex composition and the lack of rapid, field-deployable detection techniques. Microbial volatile organic compounds (MVOCs), which are produced as metabolic byproducts of microorganisms, offer a promising non-invasive chemical fingerprint for bioaerosol identification. This project focuses on the design and experimental validation of a colorimetric sensor chip for detecting MVOCs in airborne environments. Colorimetric sensors were made with chemically responsive dyes that change colour when exposed to volatile organic compounds. Detection was carried out using the Crim Track colorimetric technique, where analyte–dye interactions generate RGB responses. At this point in the study, the sensor platform has been tested under controlled laboratory conditions with known volatile analytes. The colorimetric chips showed consistent and distinct response patterns, and the resulting RGB data was extracted and analysed to evaluate colour change behaviour, sensor performance, and analyte differentiation. These findings support the functionality and sensitivity of the developed sensor system as a proof-of-concept platform. Ongoing and future research will broaden this approach to detect MVOCs produced by microorganisms in airborne environments. Overall, this study lays the groundwork for the creation of a low-cost, portable, and rapid colorimetric sensing platform with potential applications in indoor air quality monitoring, environmental surveillance, and early detection of microbial contamination.

P035

Metagenomic of Indoor Air: A Comparative Study of Sampler Efficacy

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Abstract

Routine monitoring of indoor bioaerosols for microbes is essential for public health, but the choice of an appropriate air sampler is dependent on the purpose. To detect viable bacteria and determine metagenomic content, this study evaluated the comparative efficacy of four distinct bioaerosol sampling technologies: filtration (CUB, CPAS), impingement (BioSampler), cyclonic (Coriolis), and electrostatic precipitation (ESP).

To assess reproducibility and method-dependent biases, parallel sampling of air was conducted in a university gym and a café. Samples were cultured on non-selective agar alongside DNA extraction, followed by 16S amplicon Illumina sequencing to analyse microbial community composition. Blank samples were included in the analyses.

Of the five tested units, two, the CUB and Coriolis Compact, particularly stood out for colony forming units' recovery and DNA yield from samples owing to their high flow rates, and for the CUB, great recovery efficiency from filters. The metagenome of air samples from the same setting differed depending on the air sampler, with CUB samples having the greatest Alpha diversity and SKC samples the least.

These findings indicate that sampler selection potentially impacts viable bacterial recovery and observed microbial diversity. The parallel application of multiple devices highlights that high-flow filtration offers greater sensitivity and reproducibility for characterizing indoor microbiomes, particularly where other methods face detection limitations. However, the low biomass of air samples remains challenging for metagenome studies.

P036

The comparison of nebulized DNA recovery using CUB, ESP and CPAS aerosol samplers from an aerosol chamber

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Abstract

Collecting and analyzing airborne environmental DNA (eDNA) is crucial for environmental bio-surveillance. However, the recovery of eDNA depends strongly on collectors and downstream protocol. To assess this, collection device were compared under controlled conditions and standard protocols.

Experiments were performed in aerosol chamber using fixed sampling timeline, starting with 20 min air cleaning, followed by 40 min nebulisation and sampling. Total of 3 mL of a mixture of microbial suspension (10^8 CFU) was nebulised. AirPrep™ CUB sampler (50 L/min), SKC Sampler (12.5 L/min), an electrostatic precipitator (ESP; 13.4 L/min), and CPAS (2 L/min) using multiple collection filters (Glass, Needle, and H13 filter) were tested to collect samples from air. DNA of samples were extracted using the Qiagen PowerWater Kit and quantified by Qubit. Eukaryotic and prokaryotic DNA were quantified with qPCR-assays targeting 28S and 16S rRNA genes, respectively. Results were normalised to sampled air volume for one hour for each device.

For all recovered samples, qPCR result showed that collection and recovery are achievable by all tested collectors. DNA recovery was dependent on the filter material used with the CPAS. CUB samples had the highest extract DNA concentration, although when normalised to sampled air volume, total DNA recovery (μg/m³) was highest for samples from ESP (1.44) and CPAS-H13 filter (1.08), intermediate for CUB (0.94) and CPAS-Glass filter (0.90), and lowest for CPAS-Needle filter (0.24). These findings show that device choice is important to collect DNA for downstream analysis and CPAS performance changes with filter.

P037

Real-time detection and characterisation of bioaerosols in residential environments within the UK

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Abstract

Background

Research on indoor bioaerosols is increasing due to potential health risks, yet their dynamics in UK homes remain poorly understood. Current studies rely on short-term sampling methods, which fail to capture temporal variability and impact of occupant activities and environmental factors on bioaerosols concentrations. While recent advancements in bioaerosol detection provide real-time measurements, challenges remain in distinguishing between biological and non-biological particles. This project aims to enhance our understanding of indoor bioaerosol dynamics in UK residences using an advanced UV-LIF-based sensor.

Methods

Real-time continuous measurements will be conducted in selected homes utilising Spectral Intensity Bioaerosol Sensor (SIBS), in conjunction with active and passive sampling to measure size-segregated bacteria and fungi composition, temperature, relative humidity, CO_2, total VOCs, and particles.

Results

A critical literature review identified current knowledge gaps as; challenges in discriminating fluorescent interferents, limited understanding of particle size-resolved molecular fluorescence origins, and the absence of robust frameworks for assigning spectral responses to bioaerosol classes in real time.

Conclusion

This will create reliable datasets enabling discrimination between biological and non-biological particles and categorise biological particles based on their optical properties and fluorescence, while also generating new knowledge on indoor bioaerosol composition and dynamics.

P039

Microbes in Your Home's Ventilation: A Czech Pilot Study on the Often Overlooked Risks to Air Quality and Health

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Abstract

Microbial contamination in residential ventilation systems can significantly affect indoor air quality and occupant health, particularly in panel buildings constructed between 1950 and 1995 that often feature natural ventilation systems never cleaned or maintained. This study examined microbial contamination in central air handling systems of residential buildings in the Czech Republic. Surface and dust samples were collected using swabs, preserved in DNA Shield, and DNA was isolated with the Zymo Soil Kit. Sequencing was performed using NGS targeting the 16S rRNA gene, and data were processed in R. Both cultivation and molecular biological methods were employed to identify and profile bacterial communities present in these systems. For cultivation, four types of media were used: Nutrient agar, agar for actinomycete isolation, Endo agar and Wort agar for yeasts and filamentous fungi. Analysis revealed a diverse microbial community, including potentially harmful phyla such as *Actinomycetota, Bacteroidota, Bacillota,* and *Pseudomonadota*, with higher microbial loads and diversity in poorly maintained systems. Variability in contamination was influenced by factors such as filter condition, sampling location, and maintenance history. These findings highlight the need for regular maintenance of ventilation systems to mitigate microbial risks. Although conducted in the Czech Republic, the data and methodologies are applicable to similar residential buildings worldwide, contributing to improved indoor air quality and public health strategies.

P040

Glycol Vapors in Emergency Airborne Pathogen Transmission Suppression

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Abstract

Air disinfection technologies that can be rapidly and broadly deployed during airborne pathogen outbreaks represent a critical gap in pandemic preparedness. While ventilation, filtration, and germicidal UV can reduce disease transmission, their use is constrained by cost, energy, and/or scalability. Propylene (PG), dipropylene (DPG), and triethylene (TEG) glycol vapors present a promising alternative approach for transmission suppression in occupied spaces.

We conducted a comprehensive literature review and analyzed production capacity and cost-effectiveness to understand efficacy, safety, and deployment considerations for emergency-use of these specific glycol vapors. Literature demonstrates effective inactivation of diverse pathogens, including bacteria, enveloped and non-enveloped viruses, and fungal spores. While variation exists among controlled chamber studies, there is evidence that glycol vapors can achieve ~3-6 log reductions per hour against aerosolized viruses and bacteria under optimal environmental conditions. Historical field trials in healthcare settings and military barracks have reported significant reductions in glycol-mediated disease transmission, including a 91% decrease in respiratory infections when continuously deployed in a convalescent ward with little direct patient contact. Limited adverse effects have been reported from real-world implementations, with EPA safety assessments indicating negligible to low toxicity for healthy adults at efficacious glycol vapor concentrations. Furthermore, glycols are inexpensive to produce and can be rapidly deployed using commonly available devices, enabling emergency scalability.

We are funding additional research that will help address identified remaining knowledge gaps, including efficacy studies, human safety assessments, and contemporary field observations to elucidate glycol vapors' usage as a practical, pathogen-agnostic countermeasure for emergency airborne transmission suppression.

P041

Development of a Sample Analysis Capability for Assessing Environmental Decontamination Efficacy from a Range of Sample Types with Non-Pathogenic Surrogates

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Abstract

An effective operational response to a wide area release of a hazardous and environmentally persistent biological warfare agent, in an urban environment, requires the implementation of a qualified and integrated sampling and analysis strategy and process. Many sample types will need to be collected and analyzed to determine contamination spread. Further collection and analysis after decontamination of the site to assure target levels of hazard reduction are achieved is also required before a site is returned to normal use. During a recent experimental trial we expanded our sample types further to include decontamination and sampling of more complex surfaces such as shrubs and other organic materials.

This work describes how we are developing a sample collection, processing and analysis capability at scale for the identification and quantification of *Bacillus thuringiensis* cry- (BTcry-), an ACDP Hazard Group 1 (low hazard) bacterial spore, as a simulant for *Bacillus anthracis* (BA) spores. Currently the process involves evaluating methods to optimise spore recovery from direct samples, swabs and alternative samplers, which can then be used to optimize the analysis of *Bacillus anthracis* spores at Containment Level 3.

This project is funded by Department for the Environment, Food and Rural Affairs (DEFRA) as part of the National Technical Advisory Group – Recovery (NTAG-R) project at Dstl, where the quality of advice provided by NTAG-R is critically assured through an active research project that develops, tests and evaluates remediation technologies.

P042

Encapsulation technologies for improving pulmonary infection treatment with aerosolised antimicrobials.

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Abstract

The aerosolisation of antimicrobials enables the delivery of high drug concentrations directly to the site of respiratory infection, reducing the side effects frequently associated with conventional systemic antimicrobial delivery. This approach permits the use of therapeutics with poor oral or systemic bioavailability, facilitating infection resolution, while also reducing commensal exposure to antimicrobial selection pressure, mitigating the development of AMR. Despite these advantages, the clinical efficacy of aerosolised antimicrobials is frequently limited by poor deposition and retention of drugs within the deep lung, as well as limited intracellular penetration. However, the integration of encapsulation techniques into nebulisation therapy offers a means to address these challenges.

Here, we examine how emerging encapsulation technologies such as Antibiotic-loaded Ultrasound-Responsive Agents (AURAs) and Liposomes can drive the resolution of respiratory infection. With a specific focus on *Mycobacterium abscessus,* a chronic, MDR pathogen which infects alveolar macrophages, we evaluate the impact of encapsulation strategies on drug uptake, retention and intracellular efficacy within macrophages using a THP-1 infection assay. The enhanced intracellular efficacy and tuneable release observed when antibiotics are delivered in a Liposome or AURA underscores the potential for such formulations to enhance therapeutic outcomes in patients with chronic, MDR lung infections.

P044

The influence of ventilation conditions on the spread of human respiratory aerosols in indoor rooms: an experimental aerobiological study

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Abstract

It remains unclear how reliably findings from studies using artificial aerosols translate to real-life conditions. We examined the impact of ventilation on spatial distributions of human-derived respiratory/vocal emissions within a 70 m^2 test-room, resembling long-term care living rooms.

During four study days, five healthy volunteers participated in three 1.5-hour sessions per day, performing controlled vocal activities under three randomly assigned ventilation settings (150 m^3/h, 150 m^3/h + UV-C&HEPA air cleaner (~51 m^3/h CADR-ANSI (0.5-3 µm)), 400 m^3/h). Bioaerosols were sampled at 6-11 locations at <1.5m, 3m, and 6m distance from participants using passive plate sampling, NIOSH and GSP samplers, followed by culturing for total bacterial counts, and qPCR analysis of 16S rRNA, *Streptococcus salivarius*, and *Staphylococcus epidermidis* as markers of total, oral, and skin bacteria, respectively. GRIMM optical counters monitored Particulate matter (PM).

Passive plates and active NIOSH samples contained only few culturable bacterial colonies, and bacterial markers were detected in < 11 (5%) of the 216 active air samples, precluding spatial analysis. Compared to ventilation at 150 m^3/h, PM concentrations were 23-48% reduced by adding UV-C&HEPA air cleaner, and 52%-79% reduced with ventilation at 400 m^3/h. PM spatial variation was limited (~10-15%), in contrast to previous experiments with inert particles where up to 200% spatial variation was observed.

Key-lessons learned: the critical role of room contamination shielding and source-strength. While bioaerosol detection, despite targeting commensals, stays challenging, real-world PM and bioaerosol evaluations remain crucial for understanding ventilation interventions that artificial studies may overlook.

P045

Comparative Performance of Filtration or Electrostatic Precipitation using *Mycobacterium tuberculosis* Bioaerosols

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Abstract

Conventional respirator evaluation relies primarily on filtration efficiency; however, efficiency alone does not directly indicate the number of particles or organisms reaching the wearer. In this study, particle collection performance was assessed using differential quantification of absolute downstream aerosol counts. A standard N95 respirator and a prototyped miniaturized electrostatic precipitator (EP) were evaluated separately using controlled aerosols of 1 µm, 4 µm, and mixed 1 + 4 µm polystyrene latex (PSL) beads as physical surrogates. Particle transmission was quantified as particles per minute (p/min) downstream of each method and compared with a no-mask control. All masks reduce downstream particle counts by two-three orders of magnitude relative to no protection. For 1 µm PSL aerosols (~6.7×10^6 p/min without protection), EP permitted ~8.8×10^2 particles/min, slightly lower than the N95 respirator (~1.67×10^3 p/min), which served as a reference control across all aerosol sizes. The same differential quantification framework was applied to *Mycobacterium tuberculosis* bioaerosols, enabling direct comparison between inert surrogate particles and bacterial aerosols using absolute penetration metrics. Scanning electron microscopy of collection filters demonstrated dense deposition without protection and minimal downstream deposition when respirators were used, while energy-dispersive X-ray spectroscopy confirmed surrogate particle composition. Together, these results demonstrate that differential quantification of absolute aerosol penetration provides a direct, exposure-relevant approach for evaluating respirator performance across both surrogate and biologically relevant aerosols.

P047

Modeling Human Respiratory Diseases Caused by Highly Pathogenic Microorganisms at the NEIDL, Boston University.

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Abstract

The development of animal models closely resembling the pathogenesis of human diseases is essential for revealing their natural history, mechanisms and the development of efficacious countermeasures. The goal of the NEIDL Aerobiology program is to deliver pathogenic microorganisms in BSL3 and BSL4 biocontainment to appropriate animal species to induce human-like disease manifestations. This work is supported by the NEIDL Integrated Support Services including highly trained animal research personnel and the Comparative Pathology Lab. The NEIDL research community has extensive experience in working with BSL3 and BSL4 level pathogens, including Ebola, Marburg, Nipah, Lassa viruses, *Mycobacterium tuberculosis* and *Francisella tularensis*. The NEIDL aerobiology unit is equipped with two Biaera Aero3G Aerosol Management Platform systems that are installed in dedicated Class III Biosafety cabinets within BSL3 and BSL4 aerobiology suites. Prior to animal experimentation, a series of preliminary studies is performed to determine the aerosol efficiency factor for a particular agent to ensure consistent delivery of a desirable inoculum of a viable microorganism. This allows for the determination of lethal or sublethal pathogen doses and their reproducible delivery depending on experimental design. We will present the development and characterization of a mouse model of human-like pulmonary tuberculosis enabled by the consistent aerosol delivery of low doses of virulent *Mycobacterium tuberculosis*. This model has been instrumental is dissecting mechanisms of the formation of necrotic TB granulomas and testing antibiotic regiments predictive of the human TB outcomes.

P048

Optimization of Ventilation Airflow at High Containment Large Animal Research Facilities to Reduce Pathogen Spread

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Abstract

This study focuses on determining aerosol dispersion patterns of pathogens within an ABSL-3Ag veterinary hospital and investigating how varying ACH rates or configuration of animal pens impact pathogen dispersion and potential biorisks within space. We employ computational fluid dynamics (CFD) modeling with spatial-temporal bioaerosol collection to determine the movement of bioaerosols in room airflow, and design optimized airflow rates and operational parameters to reduce their concentration and mitigate potential biosafety risks.

Surrogate *E. coli* bioparticles were disseminated in the animal holding and necropsy rooms and collected at eight different locations using the wetted wall cyclone bioaerosol collectors. The experiments were followed by CFD to simulate various airflow patterns for 9, 12 and 15 air changes per hour (ACH) with and without air curtains to predict and track the dispersion of bioaerosols in the rooms.

Results show that the airstreams in the smaller holding rooms are maintained even with the HVAC system turned off resulting in the transport of airborne bacteria towards the air inlets on one side of the holding rooms while bioaerosol dissemination is more symmetrical in the larger and taller necropsy room. The collected aerosol samples show high viability, antibiotic resistance and total cell counts. Simulation data and air property measurements show turbulent vortices in the necropsy room at 15 ACH. However, the center of the room shows balanced airflow pattern, supporting the bioaerosol collection results. Modeling with bioaerosol analysis will inform engineering controls to optimize HVAC parameters and reduce the spread of airborne pathogens in agricultural facilities.

P049

Effectiveness of portable air cleaners on microbial markers in primary school classrooms: first results from a cluster-randomized trial

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Abstract

High occupancy and prolonged classroom attendance can impair air quality and increase respiratory health risk. Portable air cleaners (PACs) may reduce bioaerosols, though field-based evidence on their effectiveness remains limited.

In the winter of 2023/2024, 66 classrooms across 10 Dutch primary schools were clustered and randomized to high-efficiency particulate air (HEPA) or Plasma/Ionization PACs (clean air delivery rate ~400 m^3/h), or no PACs. During a three-week baseline and one to four three-week intervention periods per school, airborne dust was sampled using electrostatic dust fall collectors and analyzed for human-associated bacteria, a general bacterial marker, and seasonal viral markers using qPCR. Data collection continued into winter 2024/2025, totaling up to 180 classrooms and 29 schools, but only first-year results are presented.

Relative to control, HEPA-filter PACs were associated with 10% lower total bacterial load (geometric mean ratio [GMR] = 0.90, 95% CI 0.66–1.22), and Plasma/Ionization PACs with 2% lower load (GMR = 0.98, 95% CI 0.72–1.34), neither statistically significant. Species-specific bacterial markers were often near or below the limit of quantification, and viral markers were rarely detected. Species-specific detection probability was not significantly associated with either PAC type, and effect directions showed no consistent pattern across markers.

Preliminary first-year results suggest PACs did not significantly affect airborne bacterial or viral concentrations, a result that may also reflect limited power, improper PAC operation, unmodelled factors, or dynamic classroom bioaerosol behavior. These findings underscore the importance of evaluating PACs in real-world settings to determine air cleaning intervention feasibility.

P050

Exposure Risks from Microbiological Hazards in Buildings and Their Control—A Rapid Review of the Evidence

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Abstract

Background – A rapid review was undertaken to consider the evidence for human exposure to harmful microorganisms from indoor air and surfaces. Published information about these contaminants, as well as measures to control them, including building design and energy conservation, were included in this review.

Methods – A systematic review approach, including agreed search terms, quality assessments of retrieved papers and a consistent process of data extraction, was applied to assess information on domestic dwellings, office environments, and other non-industrial settings. Recovered information was used to determine the reported prevalence, persistence, and transmission of microorganisms in these settings. Environmental factors that influence indoor microbiological colonization were also included.

Results – The evidence strongly indicates that ventilation is the primary factor for controlling indoor dampness, helping to mitigate indoor mould colonization and the accumulation of other indoor contaminants, including infectious microorganisms. Although modern building airtightness, including retrofits of older builds, contributes to thermal comfort and building energy efficiency, this may also limit a building's ventilation capacity. This in turn can potentially allow biological pollutants to accumulate, increasing the likelihood of harmful exposures and ill-health effects for building occupants.

Conclusion – Effective building design and maintenance, which promote appropriate levels of air exchange for indoor spaces, are important for the control of indoor moisture and microbiological contamination. The Government in England has recently updated the ventilation guidance for the Building Regulations (Approved Document F: volume 1). This applies to domestic dwellings only and includes improvements to required ventilation rates and related energy efficiency.

P051

Bioaerosol Risk Assessment interVention Engineering (BRAVE)

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Abstract

Indoor air quality plays a critical role in the transmission of respiratory illnesses; however, current building systems lack the ability to sense biological hazards and respond in real time. The Bioaerosol Risk Assessment interVention Engineering (BRAVE) project addresses this gap by integrating sensing, modeling, and automated interventions to reduce the risk of respiratory illness in buildings. BRAVE aims to achieve a 25% reduction in respiratory illness while delivering a 10% return on investment. The project advances three interconnected technical areas. First, we are creating a low-cost, real-time biosensing system for bacteria, viruses, fungi, and allergens in air that can detect 25 targets in under 45 minutes. Second, we are developing a respiratory risk assessment model that combines readouts from the biosensor with data from the building and environment. Third, we are using the risk assessment software to implement interventions that will reduce exposure risks to acceptable levels. Interventions include off-the-shelf air cleaning technologies (e.g., in-room HEPA filtration, upper-room germicidal UV) coupled with building-specific modifications to existing HVAC systems (e.g., higher-quality filters, modulating outside air, and improved control sequences for energy efficiency) and behavioral nudges that are acceptable to building occupants (e.g., spending time outdoors, limiting mixing of inhabitants). Through an accompanying epidemiological study and economic analysis, we will illustrate the value of our solution. BRAVE aims to revolutionize building management practices and provide cleaner, healthier air to occupants.

P052

Applying Machine Learning to Predict Influenza Viral Spillover and Airborne Transmission

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Abstract

Avian influenza virus (AIV) represents a significant challenge to global health due to its high mortality rates and its ability to spillover into new host species. The recent spillover of H5N1 in chickens and cattle resulted in massive economic burden and increased public health risk. Traditional methods of disease surveillance rely on the detection and subsequent pathogen characterization; however, this approach is reactive and may not provide sufficient lead time for effective intervention. Computational tools that allow for efficient and proactive prediction of zoonotic potential are critical in mitigation of influenza outbreaks and identifying strains with human zoonotic potential. Our approach utilizes rich large language model embeddings from ESM-2 of each individual protein in the strain in a machine learning model to predict the protein host tropism probabilities to nine animal families. The weighted precision and recall scores for the protein host tropism model are 0.95 and 0.95, respectively. Then, a zoonotic strain prediction model was built using the outputs from the protein host tropism prediction model to provide the probability that an influenza strain belongs to one of the following six groups: avian, non-human mammal, human, avian-to-human zoonotic, avian-to-non-human mammal zoonotic, or non-human mammal-to-human zoonotic. Weighted precision and recall for this model are 0.77 and 0.75, respectively. Next, we aim to develop a model to predict airborne transmissibility of strains using data collected from animal transmission models. The model will first assess the receptor binding preference, as human receptor binding is critical for infection and transmission between humans.

P053

How are Pathogens Distributed in Respiratory Emissions?

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Abstract

Pathogen-laden aerosols are the mechanism of choice for a myriad of airborne transmissible diseases. Much has been done to build a picture of the physics, biology, generation, and transport of these bioaerosols in the hopes of mitigating infection risk to those susceptible. However, the initial distribution of pathogens across different aerosol sizes generated by respiratory emissions remains unclear due to the challenges in measuring both particle size segregation and quantifying the viability of microorganisms present in the aerosols. To gain a qualitative understanding; we conducted a systematic literature review following the PRISMA methodology. The review examined 1,247 papers finding 55 describing experimental methods capable of both aerosol size segregation and/or quantifying the pathogens/microorganisms present in bioaerosol generated during respiratory activities. The review found a consensus that pathogens are concentrated in smaller infectious respiratory particles. To develop quantitative understanding; data from the reviewed papers was extracted for use in a meta-analysis. We developed a novel mathematical model combining existing work on particle size distributions with pathogen distributions across particle sizes. This new model was built with the available data in mind and used to analyse studies involving breathing, speaking, singing and coughing fitting load distributions to mycobacterium tuberculosis and SARS-COV-2. Initial results suggest that pathogens are not distributed by a constant concentration, which is the current assumption made by most modelling work used to inform mitigation strategies.

P054

The Theta Engine: An AI-Driven Framework for Real-Time Assessment of Airborne Exposure Risk

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Abstract

Airborne transmission risk reflects both immediate environmental conditions and pathogen-specific properties that have evolved over time, including aerosol stability, infectious dose, and host–pathogen interaction dynamics. We describe a proof-of-concept aerobiology modeling framework that integrates real-time environmental and mask-derived sensing with historical pathogen data to enable AI-driven adaptive, learning-based assessment of airborne exposure risk. The framework incorporates continuous measurements of carbon dioxide, temperature, and relative humidity as mechanistically grounded proxies for ventilation efficiency and aerosol persistence, while mask-mounted sensors provide localized breathing-zone data that capture short-duration deviations from ambient conditions. These real-time inputs are analyzed in conjunction with curated longitudinal datasets describing respiratory pathogen characteristics, transmission efficiency, and environmental sensitivity, allowing model parameters to be iteratively updated as new data is acquired. Evolutionary concepts, including selection pressure on transmissibility and environmental robustness, are embedded to support forward-looking prediction under changing pathogen and host conditions. A triad of competitve machine-learning programs recursively optimize predictive responses to ventilation and airflow changes, enabling refinement of risk estimation as additional environmental and pathogen data are incorporated. When validated at scale, this framework will transform how airborne risk is anticipated and managed, enabling earlier detection of high-risk conditions, adaptive mitigation strategies, and proactive preparedness for emerging respiratory pathogens before widespread transmission occurs.

P055

A Simple Atmospheric Dispersion Model with Resuspension and Decay

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Abstract

A fundamental understanding of the processes governing atmospheric dispersion is essential for
optimizing the emergency response following a biological incident. We have developed a simple vertical atmospheric dispersion model for biological contaminants that includes resuspension and inactivation which is used to investigate key concepts. The time at which the concentration of biological contaminant in the air is less than a given threshold is defined as the clearance time. The clearance time is compared for two analytically solved reference cases, (i) infinitely fast adhesion, and (ii) no adhesion. Four additionally scenarios are compared to the reference cases, (1) with a linear model for the turbulent diffusivity, (2) no decay rate, (3) with a decay rate due to inactivation, and (4) time-dependent resuspension. In all scenarios, we observe an increase in the clearance time for specific fractions of the resuspension rate and deposition velocity compared to reference case (ii); we define this as the overshoot regime. The main part of the analysis is based on a simple parametrization using a constant effective value of the turbulent diffusivity, except for the scenario with a linear parametrization. The time-dependent resuspension model is a logistic decay function which can be used to emulate scenarios with time intervals of high and low traffic. The model is a simple mechanistic concept model, and the study focuses on the fundamental understanding of the system. With further investigation, it can be implemented in more complex model frameworks describing atmospheric dispersion and health effects.

P056

Pathogen Detection for Built Environments: Predicting, Detecting, and Preventing Airborne Bio-Threats through Passive Environmental Biosurveillance

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Abstract

Background

Our built environment and its circulating air is a growing biosecurity and public health risk. The indoor microbial burden includes bacteria, fungi, mold, viruses, and allergens. COVID-19 prompted rethinking how indoor air quality, built environments, and engineering controls can be improved to further mitigate infectious disease spread. Indoor environments lack rapid, accurate, and scalable detection for airborne pathogens that is integrated with building controls for real-time interventions and risk management. The US has increased investment in biodefense and the bioeconomy and recognizes synergistic funding is needed from allies, commercial, and nonprofit entities to protect the public and provide effective early warning.

Methods

We use a safe DNA-tagged to simulate airborne pathogens to predict airflow in real world environs and a qPCR-based automated biosensor for rapid detection. Our biosensor is a desktop printer size with integrated air sampler, collector, multiplex array, and results analysis.

Results

We present findings from real-world studies applying our DNA tracer technology and qPCR biosensor in built environments with peer-reviewed research and active work.

Conclusion

Since aerosols are the most common transmission for pathogen spread, a complete biosurveillance with multiple environmental modalities and clinical syndromes is key.

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