RESPIRATORY TRACT INFECTIONS

ABSTRACT BOOK

GLASGOW
5 - 7 FEBRUARY 2024

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6TH FORUM ON RESPIRATORY TRACT INFECTIONS

GLASGOW

5-7 FEBRUARY 2024

Important note:

The abstracts in this book are listed as per forum programme order as follows:

- Rising Star Abstracts
- Abstracts for oral presentations – Part 1
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RISING STARS

RISING STARS SESSION: SELECTED TALKS FROM ABSTRACTS WITH Q&A

[RS1] Investigating the influence of pseudomonas aeruginosa growth, biofilm formation and genetic variation on persistence in bronchiectasis infections

Rebecca Hull[1]; Amy Gilmour[1]; Eve McIntosh[1]; Pieter C. Goeminne[2]; Charles Haworth[3]; Merete B. Long[1]; Amelia Shoemark[1]; James D. Chalmers[1]
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Background: Chronic *P. aeruginosa* airway infections in patients with bronchiectasis (BE) are associated with increased disease severity and exacerbation frequency. Unlike cystic fibrosis lung infections, there is limited research into the characteristics of *P. aeruginosa* chronic infections in BE. Multiple trials of inhaled antibiotics have failed to eradicate chronic *P. aeruginosa* infections or consistently prevent exacerbations in BE. *P. aeruginosa* biofilms are common and reduce the efficacy of antibiotics and immune-mediated clearance. Quorum sensing is regulated by systems including *las*, *rhl* and MexEF-OprN which impact biofilm formation and virulence gene expression.

Aims: To measure the genetic diversity of *P. aeruginosa* from BE patients with chronic infections and its impact on growth and biofilm formation, and to determine if these three factors predict *P. aeruginosa* eradication following inhaled antibiotic treatment.

Methods: *P. aeruginosa* clones were isolated from sputum from 100 BE patients with chronic *P. aeruginosa* infection across Europe and Australasia from patients enrolled in the ORBIT trials of inhaled liposomal ciprofloxacin. *P. aeruginosa* infection was monitored for 48 weeks after the initial *P. aeruginosa* isolation (treatment n=67, placebo n=33). *P. aeruginosa* eradication was defined by 3 consecutive negative sputum samples over at least 1 month. Illumina sequencing identified genetic changes in genes compared to PAO1 (*lasB*, *lasR, lasI, rhlR, mexF, mexE, oprN*) or PA14 (*mexT*) reference strains. *P. aeruginosa* isolate growth was measured at A600nm for 24h. Biofilm formation was measured by crystal violet staining after 24h growth. *P. aeruginosa* density in sputum was measured by culture.

Results: 450 high/moderate impact variants were found in 93 clones from 93 patients across the genes studied. 7 clones had no variants in these genes. Overall, there was a growth defect in clones with variants in these genes (Wilcoxon rank-sum test, p=0.021, no variants=11.2±0.703 A600/h2 [median±IQR], variants=9.07±2.73 A600/h2), linked particularly to variants in *lasR* (p=0.028, WT *lasR*=10.2±3.28 A600/h2, variants=8.77±2.00 A600/h2) or *rhlR* (p=0.020, WT *rhlR*=9.51±3.06 A600/h2, variants=8.20±3.21 A600/h2). Biofilm formation increased in clones with *lasB* (p≤0.001, WT *lasB*=0.258±0.250 A600, variants=0.655±0.627 A600) and *oprN* variants (p=0.044, WT *oprN*=0.288± 0.571 A600, variants=0.566±0.504 A600).

17% of patients cleared their *P. aeruginosa* infections over the 48-week ciprofloxacin treatment period. Patients with lower starting *P. aeruginosa* densities were more likely to clear the infection (p=0.040, eradicated= 7.78±2.53, persistent=8.26±1.23). There was no relationship between *P. aeruginosa* density in sputum and *P. aeruginosa* growth (spearman correlation, R=-0.11, p=0.29) or *P. aeruginosa* biofilm formation (spearman correlation, R=0.05, p=0.62). The clones' growth in vitro did not predict *P. aeruginosa* eradication (eradicated=9.31±2.81, persistent=9.18±2.97, p=0.240). Eradication was also not predicted by biofilm formation (eradicated=0.631±0.573, persistent=0.380±0.530, p=0.317) or variants in any of the 8 genes at day 1.

Conclusions: *P. aeruginosa* from BE patient airway infections have heterogenous genotypes, which influence growth and biofilm formation. These genotypes did not predict *P. aeruginosa* eradiation, nor did bacterial growth or biofilm formation parameters, indicating additional factors influence *P. aeruginosa* persistence.

Conflict of interest(s) (if any – not included in the 500 words):
EMBARC3 is supported by project partners Armata, AstraZeneca, Boehringer Ingelheim, Chiesi, CSL Behring, Glaxosmithkline, Grifols, Insmed, Janssen, Lifearc, Novartis, and Zambon.

[RS2] Investigating adaptive pathogen variants identifies macrophage targets for host-directed therapies

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Background/Aims: Antimicrobial resistance of medically important bacterial pathogens necessitates diversification of our therapeutic approach to bacterial disease, including investigation of host-directed therapies. Host defence is usually successful in preventing pathogen exposure and colonisation from progressing to invasive disease. However, efforts to identify specific host microbicidal responses that can be therapeutically targeted to treat bacterial disease (host-directed therapy) have not readily translated into clinical utility. Insight from bacterial immune-adaptive pathogen variants provides a novel approach to identify critical host microbicidal responses. Genetic diversity and plasticity equip bacterial pathogens for evolutionary adaptation under host immune selective pressure. Serotype 1 pneumococci are associated with severe clinical phenotypes, representing putative adaptive variants that may have evolved to resist host microbicidal responses. We aimed to use serotype 1 isolates to investigate macrophage bacterial killing, a bottleneck in host defence.

Methods: Bacterial isolates underwent whole genome sequencing. Human monocyte derived macrophages (hMDM) or murine bone marrow derived macrophages (mBMDM) were challenged with bacteria, and intracellular bacterial killing was quantified using a modified gentamicin protection assay. hMDM transcriptional responses were analysed by RNA sequencing. Lipofectamine-mediated siRNA transfection was used for gene knockdown. Pneumococcal bacteraemia was established by intra-peritoneal administration of 103 CFU *Streptococcus pneumoniae* in C57BL/6J mice.

Results: Bacterial genome analysis and quantification of hMDM intracellular bacterial killing identified two pairs of phylogenetically-similar, differentially-killed pneumococci. hMDM transcriptional differences associated with this differential killing were then identified. Differentially expressed host genes of interest were validated by siRNA knockdown in hMDM, identifying novel anti-pneumococcal host factors including ACOD1 and P2RX7. mBMDM from *ACOD1-/-* mice exhibited defective intracellular killing of pneumococci.

Itaconate, the product of ACOD1 enzymatic activity, was directly microbicidal against pneumococci at physiologically-relevant concentrations, and enhanced hMDM and mBMDM intracellular bacterial killing. Chemical modification of P2RX7 signalling altered hMDM intracellular killing of pneumococci (enhanced by the agonist bz-ATP and inhibited by the antagonist KN-62). Clemastine, a licenced anti-histamine drug with off-target P2RX7 potentiation, enhanced hMDM and wild type mBMDM intracellular killing of pneumococci. This effect was specific to clemastine, host-directed, and P2RX7-dependent. In a mouse model of

pneumococcal bacteraemia, clemastine treatment increased bacterial clearance from the bloodstream.

Conclusions: Investigation of pathogen adaptive variants identifies mechanisms of host defence and therapeutic targets. Clemastine represents a candidate for re-purposing as a potential host-directed therapy for pneumococcal infections.

Conflict of interest(s) (if any – not included in the 500 words): No conflicts of interest.

ABSTRACTS FOR ORAL PRESENTERS

ORAL PRESENTATIONS SESSION – PART 1

[OP1] Recognising the Clinical Impact of the Diverse Range of Respiratory Viral Pathogens in Hospitalised Adults

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Background/Aims: The SARS-CoV-2 pandemic re-emphasised the potential severity of respiratory viral infections (RVIs) in adults. Additionally, influenza has long been associated with significant mortality. Furthermore, respiratory syncytial virus (RSV) is increasingly acknowledged for it's potential to cause severe illness in hospitalised adults.

However, there are a wide variety of other RVIs such as rhino/enterovirus (RhV/EV), parainfluenza virus (PIV), human metapneumovirus (HMPV), seasonal/ human coronaviruses (HCoV) and adenovirus (AdV). These viruses have classically been characterised as causing largely self-limiting upper respiratory illness but are increasingly detected by multiplex polymerase-chain reaction (PCR) assays in adults hospitalised with acute respiratory infection (ARI).

Our aim was to assess the impact of Influenza/RSV/Covid-19 (IRC) infections compared to Non-Influenza/RSV/Covid-19 (NIRC) infections in hospitalised adults.

Methods: UNIVERSAL is an ongoing multicentre UK prospective observational study in adults hospitalised with RVI. Adults with ARI were prospectively recruited and tested for RVI using point of care multiplex PCR. Clinical characteristics were collected prospectively. We compared admission oxygen requirement, presence of radiologically confirmed pneumonia and length of stay in adults with IRC and NIRC infections.

Results: We recruited 367 hospitalised adults with PCR evidence of RVI. This included SARS-CoV-2 n=123 (33.51%), RhV/EV n=73 (19.90%), influenza n=71 (19.35%), RSV n=50 (13.62%), Other viruses n=50 (13.62%), including PIV n=21 (5.72%), HMPV n=13 (3.54%), HCoV n=12 (3.27%), AdV n=4 (1.09%).

The mean age was 65 (SD 17), 49.6% of patients were male sex and 244 patients had IRC infection (66.49%), while 123 (33.51%) were hospitalised with NIRC infection. There was no difference in age between these groups (p=0.248). Additionally, 63.1% of IRC and 57.7% of NIRC infections were aged ≥65 and there was no significant difference between groups (p=0.601).

The Charlson comorbidity index (CCI) was lower in the NIRC (median CCI- 4 IQR:4-13) vs the IRC group (median CCI-7 IQR:4-13) but the difference was non-significant (p=0.597). Additionally, there was no significant difference in the proportion of patients with asthma or COPD between groups p=0.130.

Regarding the presence of pneumonia, the proportion of patients with consolidation reported on admission chest radiograph was similar in IRC (30.3%) vs NIRC infections (30.9%) p=0.965.

Interestingly, with respect to admission oxygen requirement, the IRC and NIRC groups showed no significant difference (p=0.134), with 62.7% of IRC, and 60.5% of NIRC infections requiring oxygen on admission.

There was no significant difference in length of stay between IRC and NIRC infections (p=0.248), with a median length of stay of 4 days for both groups.

Conclusions: While hospitalisation with Influenza/RSV/Covid-19 infections were more common, Non-Influenza/RSV/Covid-19 infections were associated with comparable admission oxygen requirement, presence of pneumonia and length of stay. This highlights the importance of a broad range of viral pathogens in driving severe illness. Novel host directed therapies may be required to deliver improvements in outcome across this diverse range of infectious agents.

Conflict of interest(s) (if any – not included in the 500 words): Supported by Synairgen, Funding from Janssen and Astra Zeneca

[OP2] Right place, right time: consequences of preterm birth for the early-life airway microbiota and respiratory health.

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Introduction

Abundant evidence suggests that early-life respiratory microbiota plays a key role in one's future respiratory health trajectory, including susceptibility to respiratory infections and chronic disease. Recent studies support that this is likely mediated by interactions between the microbiota and host epigenetics. Preterm-born (PT) infants experience multiple unbeneficial early-life exposures relevant to microbiota development and are at high risk of developing respiratory diseases such as bronchopulmonary dysplasia (BPD). Yet, the respiratory microbiome formation and development in this vulnerable group are incompletely understood. We therefore aimed to dissect the impact of preterm birth (PTB) on the respiratory microbiota development and its association with respiratory health (BPD) and host DNA methylation (DNAm).

Methods

The nasopharyngeal microbiota was assessed in 80 PT infants and 50 full-term (FT) controls using 16S rDNA sequencing at 1 week of life, term-equivalent age, 4.5 months, 9 months and 2 years of corrected age. Genome-wide DNAm was assessed in matched saliva samples at term-equivalent and 9 months of age using the Illumina 850K EPIC microarray. Statistical analysis of the alpha and beta diversity, differential taxa abundance and random forest modelling were applied to identify the association between gestational age at birth (GAb) and other early-life factors on the respiratory microbiota. Weighed gene correlation network analysis was used to identify groups of functionally related DNAm regions (DNAm modules) and their correlation with microbiota features.

Results

We found that GAb is the major driver of the neonatal microbiota. PT infants had a delayed microbiota maturation, modelled using microbiota age, between birth and term-equivalent age. This was further characterized by a persistent *Staphylococcus*-dominated community, low alpha diversity and an enrichment of potentially nosocomial pathogens such as *Escherichia/ Shigella, Klebsiella* and *Staphylococcus*. Following discharge, the microbiota maturation trajectory and composition in PT infants gradually converged with that of FT controls. Yet, past (neonatal) co-

exposures of PTB – antibiotics, pulmonary surfactant treatment and exclusive maternal breast milk consumption – also showed an association with microbiota dynamics between 4.5 and 9 months of corrected age. We also identified a BPD-associated microbiota signature. PT infants with a future BPD diagnosis had enrichment of *S. haemolyticus*, a potential nosocomial pathogen, soon after birth; infants with established BPD had enrichment of *Staphylococcus* and oral-type bacteria (including *Streptococcus)* at 4.5 months of corrected age. In addition, we observed associations between multiple microbiota features and the activity of 4 out of 9 DNAm modules. PTB-driven microbiota features associated with the activity of DNAm modules involved in predominantly immune, neurological and developmental functions.

Conclusion

In conclusion, this study revealed that PTB leads to stunted microbiota assembly and delayed maturation and that the early-life microbiota dynamics may precede the development of BPD. Despite the eventual convergence to an age-appropriate community, the associations with DNAm suggest that even transient microbiota adversity may be reflected in the host epigenome, indicating a possible mechanistic link to long-term respiratory sequala. Given the potential for microbiota modulation, this provides a new direction for prospective diagnosis and management of BPD and other respiratory complications of PTB.

wordcount = 493

Conflict of interest

The authors have no conflict-of-interest disclosures to report.

[OP3] Circulation of respiratory viruses during the COVID-19 pandemic in urban and rural Malawi

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Background/Aims: Many countries reported substantial reductions in endemic respiratory virus circulation during the COVID-19 pandemic, which were attributed to non-pharmacological interventions. We aimed to investigate circulation patterns of respiratory viruses in Malawi, particularly as no formal lockdown was adopted.

Methods: We conducted a prospective longitudinal cohort study of randomly selected households in urban Lilongwe and rural Karonga in Malawi, with 3-monthly visits February 2021 - April 2022. A subset of adult participants provided self-obtained upper respiratory tract samples at each visit. SARS-CoV-2 PCR and multiplex RT-PCR for endemic respiratory viruses were performed. Comprehensive metadata including demographics, medical history, socioeconomic indicators, symptoms, prevention behaviours, and recent exposures were collected.

Results: We analysed 1626 samples from 945 participants in 542 households. Median age was 36.0 years (IQR 25.5 – 48.2), 58.8% female, and 51.0% recruited from Lilongwe. 7.5% samples tested positive for ≥1 respiratory virus; SARS-CoV-2 the most frequently detected (4.4%), followed by rhinovirus (2.0%), adenovirus (0.6%), and bocavirus (0.3%). Influenza B and C viruses, parainfluenza virus, RSV, enterovirus, human metapneumovirus, and parechovirus were detected in small numbers. No influenza A viruses were detected. Higher levels of respiratory virus circulation were detected in Karonga versus Lilongwe (OR 2.58, 95% CI 1.37-4.91) and positivity of samples diminished over the study period.

Conclusions: Endemic respiratory viruses continued to circulate in the community in Malawi during the pandemic. However, the rarity of influenza/RSV viruses and the reduction in endemic virus detection over time suggest that behaviour change and border closures may have impacted virus circulation.

Conflict of interest(s) (if any – not included in the 500 words): EV has received funding from MRC and lecture fees from Janssen. AH has received funding from UKRI, MRC, BSAC, Wellcome Trust, BSAC and MRF unrelated to this work. JMR and CJ have received funding from UKRI (MR/V038613/1). The other co-authors have no conflicts of interest to declare.

ORAL PRESENTATIONS SESSION – PART 2

[OP4] The effect of age and multimorbidity on symptom severity in adults hospitalised with respiratory viral infections

Olivia Cox[1]; Tommaso Morelli[1]; Martha Purcell[1]; Paul Lee[2]; Kerensa Thorne[2]; Charlie Roberts[2]; Angelica Cazaly[2]; Will Herbert[2]; Emma Tilt[2]; Alexander Allen[2]; Victoria Goss[2]; Jacqueline Nuttall[2]; Matthew Pavitt[3]; Salman Siddiqui[4]; Neil Greening[5]; Michael Crooks[6]; Stefan Marciniak[7]; Cyrus Daneshvar[8]; James Myerson[3]; Pedro Rodrigues[9]; Tristan Clark[1]; Anna Freeman[1]; Tom Wilkinson[1]

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Background/Aims: Respiratory viral infections (RVIs) are associated with significant morbidity. The InFLUenza Patient-Reported Outcome (FLU-PRO Plus) is a 34-item patient-reported outcome (PRO) measure which objectively rates RVI symptom severity. Understanding symptom impact is central to improving outcomes and quality of life in adults with RVIs. This analysis aims to characterise factors associated with symptom severity in adults hospitalised with RVIs.

Methods: UNIVERSAL is an ongoing multi-centre UK prospective observational cohort study in adults hospitalised with RVI. Adults admitted with symptomatic acute respiratory infection undergo PCR testing for RVIs. Clinical characteristics were collected prospectively. The FLU-PRO Plus was completed by participants on admission (symptoms are rated from 0-4 (0=none, 1=mild, 2=moderate, 3=severe and 4=very severe)).

We investigated the effect of pathogen, age and Charlson comorbidity index (CCI) on symptom severity.

Results: We recruited 356 adults hospitalised with RVIs who completed the FLU-PRO Plus on admission. The mean age of participants was 65 (SD 17), 50.8% were male. Median CCI was 7 (IQR 4-13).

Viruses included SARS-CoV-2 (n=115, 32.3%), rhinovirus (n= 71, 19.9%), influenza (n=65, 18.3%), RSV (n=43, 12.1%), other viruses (parainfluenza, metapneumovirus, seasonal human coronavirus and adenovirus) (n=44, 12.4%)) and viral coinfection (n=18, 5.1%).

The mean total FLU-PRO Plus score for all viruses was 1.28, SD 0.63. Total FLU-PRO Plus scores were similar between virus groups, p= 0.381. The mean total FLU-PRO Plus scores for each virus group were as follows: SARS-CoV-2 1.32 (SD 0.65), rhinovirus 1.27 (SD 0.67), influenza 1.38 (SD 0.64), RSV 1.20 (SD 0.57), other viruses 1.24 (SD 0.57), viral coinfection 1.07 (SD 0.52).

There was no significant difference in admission domain scores between virus groups. For all viruses the mean scores for each domain included: throat 0.83 SD 1.13 p=0.448, nose 1.12 SD 0.95 p=0.229, eyes 0.57 SD 0.86 p=0.197, gastrointestinal 0.53 SD 0.79 p=0.158, respiratory 2.31 SD 0.92 p=0.052, systemic 1.47 SD 0.92 p=0.241, and sense 0.23, SD 0.39, p=0.458.

Younger participants were more likely to report moderate/severe/very severe symptoms. Of those aged 18-64 25.2% reported moderate/severe/very severe symptoms (classified as a mean total FLU-PRO Plus score 2 or above) whereas 7.3% of adults aged 65 or greater reported moderate/severe/very severe symptoms ($p<0.001$).

Individuals reporting a greater symptom severity were more likely to have fewer comorbidities. Those with moderate/severe/very severe symptoms had lower CCI scores than those with mild symptoms (median 4 IQR 2-7 vs 7 IQR 4-14, p=0.003).

Conclusions: This cohort showed no difference in symptom severity between viral pathogens. Respiratory symptoms caused the greatest symptom burden. Interestingly, younger adults reported more severe overall symptoms. Adults with more severe symptoms had lower multimorbidity scores. Age and multimorbidity likely influence the perception of symptom severity in adults hospitalised with RVI. This could be postulated to be because older and multimorbid patients are more accustomed to dealing with a higher symptom burden in general, so perceive symptoms differently, but further work should interrogate this relationship.

Conflict of interest(s) (if any – not included in the 500 words): Study supported by Synairgen, Janssen and Astra Zeneca.

[OP5] Long read 16S rRNA sequencing identifies a link between sputum microbiome dysbiosis and disease severity in Chronic Obstructive Pulmonary Disease.

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Background/Aims: Most studies of the airway microbiome in COPD utilise short read amplicon sequencing. A limitation of this method is the inability to identify organisms to species level. We tested the relationships between species identified by utilising a novel long read 16S gene sequencing technique (LoopSeq) and compared the results to clinical severity in cohort of patients with COPD.

Methods: We recruited 388 patients with a diagnosis of COPD and a FEV1/FVC ratio <0.7. Patients were clinically stable at baseline with no antibiotic or corticosteroid treatment for 4 weeks. DNA was extracted from sputum samples and long read 16S rRNA sequencing was performed. Bioinformatic analysis of the sequences was performed using DADA2 and Phyloseq in R. Dysbiosis was defined by a single bacterial species accounting for >40% relative abundance within a sample.

Results: A total of 971 sputum samples from 388 patients were analysed. The microbiome was highly heterogeneous between patients. 143 patients were “dysbiotic” at baseline. There was a strong relationship between the % relative abundance of the dominant species and the Shannon diversity index ($p<0.0001$). While most species were associated with increased diversity, *Haemophilus influenzae*, *Moraxella catarrhalis* and *Pseudomonas aeruginosa* showed associations with reduced diversity. Dysbiosis was strongly associated with lung function in the 143 patients with dysbiosis, only 4 (7.7%) of patients with GOLD 1 had dysbiosis, compared to 35 (24.0%) of GOLD 2, 46 (48.9%) of GOLD 3 and 52 (82.5%) of GOLD 4 patients ($p<0.0001$). Shannon, Simpson and Chao1 indices were all significantly different between GOLD groups indicating lower diversity with worse lung function, and there was a significant difference between groups in beta diversity analysis (PERMANOVA $p=0.002$).

Conclusions: Long read sequencing identifies dysbiosis at the species level associated with severity of COPD. COPD dysbiosis is associated with a limited number of bacterial species which may be key treatable traits.

Conflict of interest(s) (if any – not included in the 500 words): Funded by GlaxoSmithKline through an investigator-initiated research grant.

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or speaker fees from GlaxoSmithKline, Bayer Healthcare, Aradigm Corporation, Grifols, Pfizer, Boehringer Ingelheim, Napp and Insmed

[OP6] Altered peripheral blood transcriptomes in bronchiectasis patients with co-morbid cardiovascular disease: data from the EMBARC-BRIDGE study

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Background/Aims: Patients with bronchiectasis have an increased incidence of cardiovascular disease (CVD), which is associated with higher exacerbation rates. Furthermore, an increased rate of cardiovascular events following a respiratory tract infection has been observed in bronchiectasis patients. The inflammatory mechanisms contributing to these comorbid conditions are not fully understood, but the link with CVD indicates a systemic component. The present study compared the peripheral blood immune cell transcriptome in bronchiectasis patients with and without CVD to investigate factors contributing to co-morbid disease.

Methods: Multi-centre, international observational study of patients with bronchiectasis (BRIDGE study; NCT03791086). Stabilised peripheral blood was collected from patients enrolled in the UK, Spain, Italy, Germany, Netherlands and Belgium with stable disease and processed for mRNA sequencing. Based on the gene expression data, imputation of immune cell proportions was performed using CIBERSORTx and gene ontology analysis was carried out using R-studio. Measurement of 45 serum cytokines were measured by immunoassay.

Results: 335 patients with bronchiectasis were included: 78 had a history of CVD (age 70.26±11.64 (mean±SD); 53.85% female) and 257 had no recorded CVD (63.30±14.91; 57.98% female). Patients with CVD were significantly older than those without CVD (p=0.0002; Mann-Whitney U test) and had significantly higher bronchiectasis severity index (BSI) score (p<0.0001; 7.74±3.50 vs. 5.68±3.31, respectively), but there were no differences in the proportion of patients in each group ever having recorded *Pseudomonas aeruginosa* sputum culture (19.8% vs 25.6%, Fishers exact test p=0.2723). In peripheral blood immune cells, 1188 significant differentially expressed genes (DEGs; adjusted p-value<0.05; Wald test with Benjamini-Hochberg correction)

were identified between the two patient groups. Genes relating to neutrophil activity including myeloperoxidase (MPO), defensin alpha 4 (DEFA4), azurocidin 1 (AZU1) and bactericidal/permeability increasing protein (BPI) were significantly upregulated in those with CVD. Just 108/1188 of these DEGs overlapped with those in individuals with mild/moderate disease aged above vs. below 65, and none in an age analysis in severe disease. CIBERSORTx analysis identified increased proportions of neutrophils (p=0.026) and mast cells (p=0.049) in those with a history of CVD. Whereas natural killer cells (p=0.0371), naive B-cells (p=0.0075) and memory resting CD4 T-cell (p=0.0106) proportions were lower. Upregulated pathways associated with CVD included response to type II interferon and positive regulation of interleukin-1 beta (IL-1B) production, whereas T-cell differentiation and CD4-positive, alpha-beta T-cell proliferation were significantly downregulated. Compared to individuals without CVD (n=70), those with CVD (n=29) had significantly lower serum granulocyte colony stimulating factor (CSF3) (p=0.0305) and epidermal growth factor (EGF) (p=0.0035) levels, whereas interleukin-10 (IL-10) was significantly elevated (p=0.0051) in this group.

Conclusions: Significant differences in the peripheral blood immune cell transcriptome and in circulating immune cell proportions were identified between bronchiectasis patients with and without CVD which were not explained by age differences in these patient groups. Patients with co-morbid CVD tended to have more severe bronchiectasis, but did not have higher recorded incidence of *P. aeruginosa* infection. Gene expression data indicated a role for the systemic immune response, particularly neutrophil activation and pro-inflammatory cytokine production including IL-1B, in CVD pathology in patients with bronchiectasis.

Conflict of interest(s) (if any – not included in the 500 words): This work was supported by the Innovative Medicines Initiative (IMI) and EFPIA companies under the European Commission funded project, iABC (grant 115721) and by the European Respiratory Society through the EMBARC3 consortium. EMBARC3 is supported by project partners Armata, AstraZeneca, Boehringer-Ingelheim, Chiesi, CSL Behring, Grifols, Insmed, Janssen, LifeArc and Zambon.

[OP7] Investigating The Effects Of AXL Inhibition During Respiratory Viral Infections

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Background/Aims: AXL is a member of the TAM family of receptor tyrosine kinases with important roles in efferocytosis and in balancing/dampening immune responses and inflammation. With oncogenic potential, AXL is overexpressed and activated in cancer cells enhancing survival, tumour progression and drug resistance. In addition, AXL facilitates entry for enveloped viruses including SARS-CoV-2 by apoptotic mimicry. Bemcentinib, selected for investigation in the ACCORD trial (EudraCT 2020-001736-95), is an AXL inhibitor with anti-neoplastic activity and antiviral properties, capable of inhibiting SARS-CoV-2 entry. In addition, AXL inhibition has been shown to attenuate *in vivo* lethality of infections with viruses that do not use apoptotic mimicry for cell entry. We aimed to determine whether bemcentinib carries broad anti-viral and anti-inflammatory activity against respiratory viruses.

Methods: We chose BCi-NS1.1, an established lung epithelial cell line, in submerged cultures as an *in vitro* model of respiratory viral infection. Based on cytotoxicity and viability assay results cells were exposed to 1μM bemcentinib or DMSO control for a 16-hour pre-incubation and during subsequent infection with the following viral strains (n=5 each): Influenza, A/Wisconsin/67/2005 (H3N2) multiplicity of infection (MOI)=1; RSV A, strain Memphis 37 MOI=1; RhinoVirus 16 MOI=0.2. The viruses were added for 2h before the cells were washed to remove excess extracellular virus and either harvested immediately or after 24h incubation.

Viral genes and transcripts of interest were measured by real time quantitative PCR in cDNA reverse transcribed (Taqman assay and High Capacity cDNA Reverse Transcription, ThermoFisher) from RNA extracted from cell lysates (QIAZOL, Qiagen). Ct values were normalised against Actin-Beta (ACTB) and β2-microglobulin (B2M) and compared against the 2h DMSO samples using the $2^{-\Delta\Delta Ct}$ method.

Supernatants from the cultures were also collected at each timepoint. AXL and inflammatory cytokine protein expression were measured by ELISA (DuoSet ELISA, R&D Systems).

Results: BCi-NS1.1 cells, although permissive to respiratory viral infection and expressing AXL at the gene and protein level did not show a reduction in viral replication in cells exposed to bemcentinib compared to DMSO controls, and showed no changes or a downregulation in antiviral, interferon-stimulated genes (ISGs) and related transcription factors (DDX58, IFITM1,

IFNβ, IRF3, ISG15, MX1, MX2, NFKb, OAS1, SOCS3 and STAT3). Bemcentinib resulted in strong downregulation of both IL6 and IL8 expression (Fig.1).

Conclusions: IL6 exhibits both pro- and anti-inflammatory effects and IL8, a potent neutrophil attractant, plays a crucial role during severe influenza infection. Bemcentinib's downregulation of both ILs may suggest potential therapeutic benefits in managing patients experiencing viral-driven local and systemic inflammation, associated with poor outcomes.

This aligns with ACCORD clinical data where bemcentinib treatment, compared to standard of care alone, reduced elevated IL6 and IL8 in the acute stage of hospitalisation in patients with severe COVID19 and was also associated with fewer patients progressing to ventilation and death. Confirmatory in vitro data in differentiated primary cell models will help to inform the design of future clinical trials for this important indication.

Conflict of interest(s) (if any – not included in the 500 words): CMS has received a research grant from BerGenBio; JA has not any conflict of interest; GG, LHN, DM and AJ are employed by BerGenBio and TW has a consultancy agreement with BerGenBio.

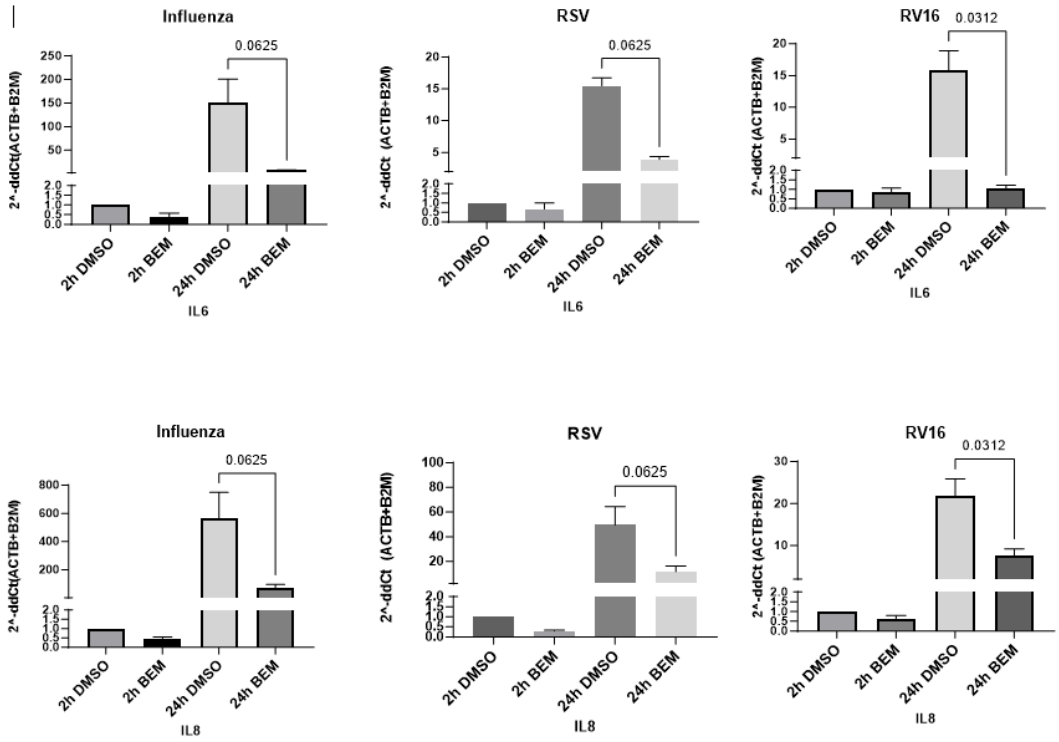

FIG.1 The strong inflammatory response caused by the virus on cells is downregulated in the presence of bemcentinib (BEM). These results mirror the clinical data from the ACCORD trial. (Wilcoxon t-test, non parametric, paired, two tailed)

[OP8] Lung stromal cells display innate immune memory that facilitates enhanced viral control following re challenge with influenza virus

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Background/Aims: Stromal cells can be permanently altered by insults, a process termed trained immunity. Whether these cells contribute to protection or pathology in infections including influenza A virus (IAV) is unclear. We hypothesize that trained stromal cells may participate in protective immunity via interactions with local immune cells.

Methods: We performed transcriptional analysis on sorted lung epithelial cells and fibroblasts isolated from naïve and IAV infected mice (primary, memory, and re-challenge timepoints). Stromal cell dynamics and interactions with immune cells were investigated using imaging and flow cytometry, including detecting infected cells *via* IAV-Nucleoprotein (NP). Following IAV re-challenge *in vivo*, T cells were depleted during the memory phase to examine viral control by lung stromal cells. T cell re-activation by naïve or IAV infected stromal cells was measured *in vitro*.

Results: RNA-sequencing provided transcriptional evidence of stromal training following IAV infection. Enrichment in immune related genes at primary/memory timepoints in lung stromal cells was enhanced upon re-challenge, particularly genes involved in antigen processing and presentation (*Ciita*, *B2m*). Spatially, stromal expression of molecules involved in communication with T cells (*Spib*, *Cxl10*) was localised near dense clusters of immune cells, indicating cellular crosstalk may facilitate early viral control. Functionally, depletion of CD4/8 T cells prior to a re-challenge infection did not alter enhanced viral control in IAV-memory animals. Stromal cells from naïve and IAV-memory mice were infected with IAV *in vitro,* less IAV-NP was found in stromal cells taken from memory animals. This was independent of type I interferon, suggesting IAV-memory stromal cells display enhanced intrinsic viral control. Interestingly, infected IAV-memory stromal cells presented antigen to CD4/8 T cells, although to a lesser extent than infected naïve-stromal cells.

Conclusions: IAV-experienced lung stromal cells play dual roles in anti-viral control. Retaining an imprint of infection may enable lung stromal cells to enhance subsequent immune responses.

Conflict of interest(s) (if any – not included in the 500 words): The authors have no conflicts of interest to declare.

ABSTRACTS FOR POSTER PRESENTERS

Strolling Poster Sessions - SESSION 1 PNEUMONIA

[1] Case Report: Successful Management of Refractory advanced Non-Tuberculous Mycobacterial Infection with Bedaquiline.

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Background/Aims: Non-tuberculous mycobacterial (NTM) infections, especially in advanced stages, pose considerable therapeutic challenges due to the limited efficacy of conventional antimicrobial regimens. This case report highlights the complexity of managing advanced refractory NTM infection, and the urgency for novel therapeutic intervention, with the use of Bedaquiline proving to be a crucial turning point. The decision to administer Bedaquiline was made following detailed discussions with the British Thoracic Society (BTS) MDR-TB Clinical Advice Service and subsequent approval from the relevant drug regulatory authorities. The patient demonstrated significant clinical and radiological improvement, highlighting the potential of Bedaquiline in the management of advanced NTM infections.

Methods: A 41-year-old female with a history of chronic obstructive pulmonary disease (COPD) and previous heroin abuse presented with recurrent chest infections and abnormal imaging. Bronchoalveolar washings and sputum cultures were persistently positive for fully sensitive Mycobacterium Chimera. In September 2019 she commenced Ethambutol (900 mg once daily), Moxifloxacin (400 mg once daily), and Azithromycin (250 mg once daily); Rifampicin was avoided due to interaction with Methadone. Despite compliance with treatment, sputum cultures remained positive in January, February, May, and July 2020.

Due to worsening symptoms, she was admitted in October 2020, with an exacerbation of COPD. A subsequent CT scan revealed the progression of cavitating lesions, prompting discontinuation of Moxifloxacin and initiation of intravenous (IV) Amikacin (975 mg once daily) and oral Rifabutin (600 mg once daily). The choice of IV Amikacin was made considering the potential risk of bronchospasm from nebulized Amikacin due to the patient's Forced Expiratory Volume 1 (FEV1) of 0.63L.

Despite the altered treatment approach, the patient experienced further positive sputum cultures until February 2021. In March 2021, she was readmitted with haemoptysis, and CT scan revealed continued radiological progression of the disease.

Results: Following further discussion with the BTS MDR-TB Clinical Advice Service in April 2021, compassionate use of Bedaquiline was initiated, with the following treatment regimen:

- Bedaquiline 400 mg once daily for two weeks, then 200 mg three times weekly.
- Clofazimine 200 mg once daily for two months, then 100 mg daily.
- Azithromycin 250 mg once daily.

- Ethambutol 800 mg once daily, reflecting her reduced weight.

Remarkably, all sputum results received after initiation of treatment were culture negative. She completed 12 months of treatment following culture conversion, with significant clinical and radiological improvement (including 16kg weight gain). The treatment was well tolerated, and there has been no evidence of recurrence. The patient is now being assessed regarding potential lung transplant or lung volume reduction surgery.

Conclusions: This case report underscores the challenges in managing advanced refractory NTM infection. The successful utilization of Bedaquiline, along with a comprehensive multidisciplinary approach, highlights the potential of novel therapeutic interventions in addressing complex NTM cases. Further research and clinical trials are warranted to explore the broader application of Bedaquiline in the management of refractory NTM infections.

Conflict of interest(s) (if any – not included in the 500 words): No conflict of interests.

[2] Applying High-Frequency Oscillatory Ventilation (HFOV) Successfully in Idiopathic Pulmonary Fibrosis Patient, Potential Challenge

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Background/Aims: Patients with Idiopathic pulmonary fibrosis (IPF) are known to frequently experience the life-threatening consequence of pneumothorax. Pneumothorax is a buildup of air around the lung but inside the pleural cavity. It happens when air gathers inside the chest between the visceral and parietal pleura. This idiopathic pulmonary fibrosis and pneumothorax lead to surgical emphysema. It occurs when gas or air seeps into the subcutaneous tissue (the skin's lowest layer). The main objective of this clinical case study is to determine how the patient's requirements and ABG change when one condition leads to another. A patient of 60 years with a medical history came to the emergency department with a chief complaint of shortness of breath and chest pain. On his arrival, the oxygen saturation was 68% at room air, and a chest X-ray revealed pneumothorax. He was then shifted to a pulmonary team to floor as surgical emphysema, secondary pneumothorax (right) on intercostal space chest tube, and CAP (community-acquired pneumonia). ABG tests were taken after every step of the lung-protective strategy: postintubation, post-HFOV connection, after disconnection, after switching to PCMV, and post-HFOV disconnection. These results indicate the severity of the patient's condition. Even after the percutaneous tracheostomy procedure, the patient was still experiencing the challenges of increased oxygen requirements and recurrent spontaneous pneumothorax

Methods: it is a ase report

Results: using High-Frequency Oscillatory Ventilation (HFOV) gave a good result with Idiopathic Pulmonary Fibrosis Patient

Conclusions: using High-Frequency Oscillatory Ventilation (HFOV) gave a good result with Idiopathic Pulmonary Fibrosis Patient

Conflict of interest(s) (if any – not included in the 500 words):

[3] DIROFILARIASIS AS A CAUSE OF PLEURAL EFFUSION – A CASE REPORT

Dora Darapi Marušić[1]; Ivona Markelić[1]; Vesna Trkeš[1]; Zagorka Boras[1]; Denis Baričević[1]; Ena Tolić[1]; Helena Kovačić[1]; Andrea Vukić Dugac[2,1]
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INTRODUCTION Dirofilariasis is a parasitic zoonosis caused by a nematode *Dirofilaria spp*. In Europe, *D. repens* is the most prevalent species, although there have also been reported cases of *D. immitis*. The primary hosts are domesticated and wild dogs, with mosquitoes serving as vectors. While *D. repens* typically causes subcutaneous and ocular dirofilariasis, *D. immitis* commonly leads to pulmonary dirofilariasis, although there have been reports of other organ systems being affected as well. In this report we describe a case of dirofilariasis affecting the lungs.

CASE REPORT A previously healthy 44-year old male patient presented to the emergency department with a one-month history of chest pain and coughing. He reported no fever or weight loss. The patient had previously received antibiotics at another institution due to suspected pneumonia with pleural effusion detected on chest X-ray. However, the pain persisted despite treatment. A CT-scan of the thorax was performed, revealing a pleural effusion extending from the base to the apex of the lungs, with consequent atelectasis of the right lower and middle lobe. Within the pleural effusion there was a 70x9mm thickening of the parietal pleura. The patient was hospitalized, and a thoracocentesis was performed, which revealed an eosinophilic effusion, with no malignant cells detected. Bronchoscopy showed no pathology and there were no significant microbiological findings. The patient started pulmonary rehabilitation, and the pleural effusion was in regression. During a follow-up appointment a CT scan of the thorax was repeated and it showed a complete resolution of the pleural effusion but an increase in size of the parietal pleura thickening. Consequently, an uniportal video-assisted thoracoscopic surgery was performed, during which a pathological deposit of the parietal pleura was identified and removed in its entirety. Histological examination of the tissue revealed an infection caused by the parasite *Dirofilaria spp*. The patient had no perioperative complications and remained symptom-free during follow-up appointments. As complete surgical excision of the parasite is usually curative, there was no further treatment indicated so far, but frequent follow-up appointments were recommended.

CONCLUSION This case report presents a rare cause of pleural effusion and emphasizes the importance of considering uncommon etiologies, especially in patients with persistent or atypical clinical features. Recent reports have shown dirofilariasis cases emerging in previously unaffected regions of Europe, with higher frequency in areas already known to be affected. Therefore it is important to familiarize clinicians with the existence of this disease.

[4] Diagnostic target product profiles for managing infections and exacerbations in cystic fibrosis

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Background/Aims: The CF AMR syndicate (Cystic Fibrosis Antimicrobial Resistance Syndicate; CF Trust, Medicines Discovery Catapult and LifeArc) has developed a suite of diagnostic target product profiles (TPPs) to address the unmet needs in managing infections and pulmonary exacerbations in cystic fibrosis. Diagnostic TPPs describe the characteristics diagnostic tests would need to meet to address a specific need.

Methods: The TPPs were developed through first engaging with people with lived experience of cystic fibrosis and their multidisciplinary care teams via focus groups, to understand the current and evolving unmet diagnostic needs. The TPP characteristics were refined through extensive stakeholder engagement, a series of surveys and a virtual symposium.

Results: We present high-level TPPs on 1. prediction and management of pulmonary exacerbations, 2. pathogen detection and identification and 3. antimicrobial susceptibility testing, as well as a more detailed TPP (4.) outlining the desired characteristics of tests for the detection of non-tuberculous mycobacteria.

Conclusions: The TPPs are presented in the form of a guidance document, aimed at stimulating innovation and bringing diagnostic solutions to people living with cystic fibrosis.

Conflict of interest(s) (if any – not included in the 500 words): nonw

[5] Risk Factors for Poor Outcomes in Children Hospitalised with Virus-Associated Acute Lower Respiratory Infections: A Systematic Review and Meta-Analysis

Daira Trusinska[1]; Si Thu Zin[2]; Emmanuel Sandoval[1,3]; Nusrat Homaira[4,5,6]; Ting Shi[1]
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Background/Aims: Acute lower respiratory infection (ALRI) caused by respiratory viruses is among the most common causes of hospitalisation and mortality in children. We aimed to identify risk factors for poor outcomes in children <5 years old hospitalized with ALRI caused by influenza, SARS-CoV-2, and respiratory syncytial virus (RSV).

Methods: We searched Medline, Embase and Global Health databases and included observational studies reporting risk factors for poor outcomes (defined as use of supplemental oxygen, mechanical ventilation, intensive care unit admission, prolonged hospital stay, and mortality) published between January 2011 and January 2023. Two authors independently extracted data on study characteristics, outcomes, and risk factors. Meta-analyses were conducted when there were at least three studies using random effects model.

Results: We included 30 studies. For influenza related ALRI, chronic conditions and age 6-24 months were identified as risk factors for poor outcomes. Cardiovascular disease, immunosuppression, chronic kidney disease, diabetes, and high blood pressure were reported as risk factors for mortality due to SARS-CoV-2 associated ALRI. For RSV related ALRI, significant risk factors based on meta-analysis were: neurological disease (odds ratio (OR) 6.14; 95% confidence intervals (95% CIs) 2.39-15.77), Down's syndrome (5.43; 3.02-9.76), chronic lung disease (3.64; 1.31-10.09), immunocompromised status (3.41; 1.85-6.29), prematurity (2.98; 1.93-4.59), congenital heart disease (2.80; 1.84-4.24), underlying disease (2.45; 1.94-3.09), age <2 months (2.29; 1.78-2.94), age <6 months (2.08; 1.81-2.39), viral coinfection (2.01; 1.27-3.19), low birth weight (1.88; 1.19-2.95), being underweight (1.80; 1.38-2.35).

Conclusions: These findings might contribute to the development of guidelines for prophylaxis and management of ALRI caused by influenza, SARS-CoV-2, and RSV.

Conflict of interest(s) (if any – not included in the 500 words): None declared.

[6] Comparison of clinical and laboratory features in Influenza A virus infection and other viral infections, including SARS-CoV-2: Data from the INNOVATE observational cohort study

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[1]*University of Dundee, Dundee, United Kingdom*

Background/Aims: With widespread vaccination and the development of effective therapeutics, COVID-19 is now one of a number of circulating respiratory viruses, alongside influenza virus, respiratory syncytial virus and others. There is a need to describe the clinical features and immune responses to different respiratory viruses in the post-pandemic era. To describe clinical features and markers of immune response available in standard care in patients with influenza A virus infection compared to other respiratory viral infections.

Methods: INNOVATE is a single-centre prospective observational cohort study based at Ninewells hospital, Dundee, United Kingdom. From December 23rd 2022 to March 14th 2023, 91 hospitalised patients with positive polymerase chain reaction (PCR) test for Influenza and/or other viruses were enrolled in the study. Influenza infection cohort A comprised 20 patients. 27 patients with SARS-CoV-2 virus infection and 9 patients with RSV were included in the study cohort B. Clinical data and inflammatory marker levels (white blood cell (WBC), neutrophil (Ne) and lymphocyte (Ly) counts and C-reactive protein (CRP)) were documented. The World Health Organisation (WHO) clinical status scale was used to assess the severity of illness. To account for the imbalance in age and sex when comparing cohorts, inverse probability weighting using propensity scores was performed.

Results: Median age of patients with Influenza in cohort A was significantly lower (59.5 years, inter-quartile range (IQR) 46.5-79.5) than in cohort B (71.5 years, IQR 61-76.5) (p=0.0021). WHO severity scale was similar between groups. 35% of patients in cohort A and 31% in cohort B therefore required supplemental oxygen or ventilatory support (p=0.694). Analysis of blood biomarkers suggested lower lymphocyte counts in cohort A, although not significantly so, with no difference in C-reactive protein. (Table 1). In cohort A, asthma and chronic obstructive pulmonary disease (COPD) were common co-morbidities. Overall, 43/91 (47.3%) of patients had either asthma or COPD; 16/20 (80%) patients with Influenza virus, 11/27 (40.7%) patients with SARS-CoV-2 and 4/9 (44.4%) patients with RSV infection had a respiratory co-morbidity.

Conclusions: Patients with influenza A presented with similar severity of illness to patients with COVID-19 and RSV, but at a younger age. Lymphopenia was common and more pronounced with influenza A infection. This baseline data from the INNOVATE cohort which will be used to profile inflammatory responses and neutrophil proteomics in patients with different respiratory viral infections.

Parameter	Unadjusted Mean (±SD)	Estimated percentage difference [95% CI], adjusted for age and sex imbalance	2-sided p-value
WBC	Cohort A: 9.9 (±5.3) Cohort B: 10.1 (±4.2)	-10.8% [-36.5%, +25.1%]	0.507
Neutrophils	Cohort A: 7.8 (±4.8) Cohort B: 7.9 (±3.9)	-9.5% [-40.8%, +38.5%]	0.647
Lymphocytes	Cohort A: 1.3 (±0.8) Cohort B: 1.4 (±0.8)	-17.5%* [-36.3%, +6.8%]	0.145
CRP	Cohort A: 103.4 (±111.5) Cohort B: 77.3 (±85.7)	-0.7%* [-54.8%, +118.0%]	0.986

Table 1: Average Treatment Effect between Cohorts A and B (% difference, Cohort A relative to Cohort B).

*- True difference is noted for lower level of Ly and CRP in group A which verifies tendency to lymphopenia.

Conflict of interest(s) (if any – not included in the 500 words):

Strolling Poster Sessions - SESSION 2 COVID-19

[7] Scoping Review of the Effectiveness of Noninvasive Ventilation in the Management of COVID-19 Patients

AHMAD ALESSA[1]
[1]*Respiratory Specialist,, MAKKAH, Saudi Arabia*

Background/Aims: The aim of this scoping review was to map the existing literature on the use of NIV for COVID-19 patients and identify gaps in knowledge.

Methods: A systematic search using appropriate keywords was conducted on three selected electronic databases; PubMed, Cochrane Library, and CINAHL by two independent reviewers. After applying the inclusion and exclusion criteria, a total of 30 studies were used for the scoping review. Data was extracted from the studies and the results were presented and discussed.

Results: The results of the scoping review showed that some studies presented evidence that supported the effectiveness of NIV. However, some other studies could not provide strong evidence for the efficiency of NIV based on statistical grounds. Also, no negative consequences were identified from the studies regarding the use of NIV in managing patients with COVID-19.

Conclusions: Hence, the findings from this study suggest that even though NIV improved the conditions of patients, more studies of high-level and high-quality ratings are needed to provide strong evidence regarding its efficiency.

Conflict of interest(s) (if any – not included in the 500 words):

[8] Scoping Review of the Use of High-Flow Nasal Cannulas in Covid-19 Patients

AHMAD ALESSA[1]
[1]*Respiratory Specialist,, MAKKAH, Saudi Arabia*

This study aimed to explore the outcomes of using HFNC for patients with COVID-19. Forty-two studies were scanned using a scoping review, of which 22 were found eligible, satisfying the inclusion and inclusion criteria. Multiple patient outcomes were considered, including recovery time, oxygenation levels, reduced need for intubation in the future, ICU avoidance, and chances of respiratory distress. The findings suggest that HFNC remains more effective in treating patients with COVID-19-induced respiratory problems than traditional methods by indicating significantly improved oxygenation, reduced recovery time, reduced respiratory distress levels, and the need for invasive methods in the future. However, a few complications were also notable while considering its implementation on a wider scale, the most prominent being particle dispersion or airborne infection. However, the studies indicate that the complications and risks can be mitigated using precaution. The research seeks the validation of its findings through more comprehensive research in the future

Conflict of interest(s) (if any – not included in the 500 words):

[9] The impact of calculating ROX index in delaying intubation with COVID-19 patients at King Abdullah medical city

AHMAD ALESSA[1]
[1]*Respiratory Specialist,, MAKKAH, Saudi Arabia*

Background/Aims: Background: HFNC is a respiratory mask that covers the nose like an oxygen mask, with the addition of nasal prongs to deliver extra oxygen. At 12 hours, a ROX score above or equal to 4.88 predicts a decreased probability of progressing to mechanical ventilation. Objective: The aim of this study was to evaluate using a high-flow nasal cannula as a potential predictor of delaying intubation. In doing this, the study also sought to verify whether the ROX index accurately predicts HFNC failure for COVID-19 patients treated in the intensive care unit (ICU).

Methods: Method: Using retrospective observational analysis of prospectively collected data and the study population of patients in the ICUs at KAMC, the study collects and analyzes data using SPSS.

Results: Results: P values that are < 0.05 show that the mean differences are statistically significant, and this is seen on days 1-1, day 1-2, day2-1, day 2-2, day 3-1, day 3-2, day 4-2, day 10-1,

and day 10-2. This suggests that ROX index can be used in intubation prediction with COVID-19 patients who have respiratory failure type I that received HFNC therapy

Conclusions: Conclusion: The study establishes that ROX index is a suitable parameter in intubation prediction in patients with Covid-19 that received HFNC therapy. It can be inferred from the analysis that the ROX index's higher value is linked with a higher chance of the success of the HFNC therapy and, consequently, a lower risk of mortality.

Conflict of interest(s) (if any – not included in the 500 words):

[10] Risk factors for in-hospital and one-year mortality of elderly patients hospitalized due to COVID-19 pneumonia.

Vasiliki Georgakopoulou[1,2]; Aikaterini Gkoufa[2]; Sotiria Makrodimitri[2]; Aristeidis Tsakanikas[2]; Dimitrios Basoulis[1,2]; Pantazis Voutsinas[1]; Georgios Karamanakos[2]; Irene Eliadi[2]; Stamatia Samara[2]; Maria Triantafyllou[2]; Ioanna Eleftheriadou[2]; Olga Kampouropoulou[2]; Chrysovalantis Papageorgiou[3]; Amalia Anastasopoulou[4]; Petros Papalexis[4]; Ilias Trakas[2]; Nikolaos Trakas[5]; Paschalis Steiropoulos[6]; Nikolaos Sipsas[1,2]
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Background/Aims: Coronavirus disease 2019 (COVID-19) is characterized by poor outcomes and high mortality, particularly among elderly patients. Since the beginning of the pandemic, older age has been recognized as an important risk factor for disease severity, with increasing mortality rates in each decade of life. This phenomenon may be a consequence of poor previous health status, with a higher prevalence of pre-existing comorbidities and a higher degree of frailty. Most studies of elderly patients' outcomes and risk factors refer to the first waves of the pandemic and predictors of in-hospital mortality in these patients. The purpose of the present research is a detailed description of the clinical characteristics and management of a cohort of elderly patients ≥ 65 years of age who were hospitalized with COVID-19 pneumonia in all phases of the pandemic, presenting their outcomes and investigating predictors of in-hospital and out-of-hospital mortality over period of one year in this particularly vulnerable population.

Methods:

Study design

For the purposes of this research, a retrospective recording of data was carried out on consecutive elderly patients aged ≥ 65 years who were hospitalized with COVID-19 pneumonia at the Infectious Diseases Unit of our hospital during the period 01/10/2022 to 15/07/2022, including patients who were infected from the initial strain and from the Alpha, Delta, and Omicron variants. The study was conducted in line with the Declaration of Helsinki and obtained approval by the Institutional Review Board of Laiko General Hospital (protocol no. 7950/08.06.2023).

Data collection

The demographic characteristics (gender, age), clinical symptoms, the extent of pneumonia on the chest x-ray with the Chest X-ray score (12), the vaccination status against SARS-CoV-2, the comorbidities, and the Charlson Comorbidity Index (CCI) were recorded. The

following admission laboratory findings were also recorded: hemoglobin (Hb) and hematocrit (Hct) levels; white blood cells (WBC); neutrophils (Neu); lymphocytes (Lym); PLTs and

immature granulocytes (IGs); CRP; serum albumin and LDH levels; d-dimers; fibrinogen (FIB); creatinine; ferritin; the levels of liver enzymes aspartate aminotransferase (AST) and alanine aminotransferase (ALT); and cholestatic enzymes gamma-glutamyl transferase (GGT) and alkaline phosphatase (ALP). Finally, the special treatments received by the patients for the treatment of COVID-19 pneumonia were recorded.

Recording of outcomes

In-hospital mortality rates were recorded, as well as mortality rates within one year of admission. We also investigated predictors of mortality. Patients without a reliable follow-up at one year were excluded from the study.

Results: A total of 1124 elderly patients (603 men, 53.7%) with a mean age of 78.51 (±7.42) years and a median Charlson's comorbidity index (CCI) of 5 were included in the study. Of these patients, 104 (9.3%) were hospitalized during the period of prevalence of the original strain Wuhan, 385 (34.3%) were hospitalized during the period of prevalence of the Alpha variant, 221 (19.7%) were hospitalized during the period of prevalence of the Delta variant, and 414 (36.8%) were hospitalized during the period of prevalence of the Omicron variant. Overall, in-hospital mortality was 33.4% (375 patients) and 1-year mortality was 44.7% (502 patients). Most patients had not been vaccinated or had not completed full vaccination against SARS-CoV-2 (843 patients, 75%), given the period of infection.

Age, immature granulocytes (IGs), lactate dehydrogenase (LDH), ferritin, Chest X-ray score as well as the absence of full vaccination, cough and fatigue were statistically significantly and independently associated with in-hospital mortality in the overall study population while

age, LDH, ferritin, alanine aminotransferase (ALT), CCI, Chest X-ray score, absence of cough and fatigue, and history of dementia were statistically significantly and independently associated with 1-year mortality in the overall study population. Different clinical and laboratory findings were related to mortality in the different periods of prevalence of different strains of SARS-CoV-2 but also in patients with dementia, Parkinson's disease and those who were nursing home residents.

Conclusions: The in-hospital and one year mortality of elderly patients hospitalized COVID-10 pneumonia is high. Specific clinical and laboratory characteristics are independent predictors of mortality in these patients.

Conflict of interest(s) (if any – not included in the 500 words): No conflicts of interest

[11] Continuous Positive Airway Pressure in Covid 19 Acute Respiratory Distress Syndrome: A Systematic Review

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Background/Aims: Acute Respiratory Distress Syndrome (ARDS) is a feared consequence of Covid 19 Pneumonia. Traditional guidance was for ARDS to be treated with Intubation and Mechanical Ventilation (IMV), when failing simple oxygen. However globally numbers of patients with Covid 19 ARDS (CARDS) quickly overwhelmed IMV capacity, with Continuous Positive Airway Pressure (CPAP) has been used as a bridge or alternative to IMV. However, the evidence base remains limited in quality despite widespread adoption in guidelines.

Methods: Pubmed (15.6.2022), Embase (30.7.2022) and Google Scholar (4.8.2022) were searched to identify studies with the primary outcome of IMV free survival in patients with CARDS receiving CPAP, ideally with simple oxygen as a comparator. Secondary outcomes were overall survival with CPAP, length of stay and adverse events. All studies were assessed by the relevant Critical Appraisal Skills Programme Tool (CASP).

Results: 13 studies were identified, out of which only 1 was a Randomised Control Trial (RCT) with simple oxygen as a comparator. There were 11 Cohort studies and one Systematic review.

Conclusions: There is much heterogeneity in CPAP success rates (50 – 70%), which may be linked to variation in candidate selection, resource setting, application protocols and combined use with other respiratory support modalities (Non Invasive Ventilation – NIV, and High Flow Nasal Oxygen – HFNO). Adverse events and economic data such as length of stay are under reported.

CPAP is an effective respiratory support in CARDS particularly in resource poor settings. However further research is needed to refine optimum candidate selection, application protocols and any added benefit from combination with NIV or HFNO.

No funding was received for this study. This review was not registered.

Conflict of interest(s) (if any – not included in the 500 words):

None

[12] Results of Glasgow Early Treatment Arm Favipiravir (GETAFIX) trial for early stage COVID-19

Matthew Tate[1]; Paterson Lucy[2]; McCartney Elaine[2]; Thygesen Helene[2]; Kelly Caroline[2]; Gunson Rory[3]; Scott Janet T.[4]; Divers Laura[2]; Cunningham Laura[2]; Perkins Jon[5]; Silva Vanessa[5]; Holland Poppy[5]; Illingworth Christopher RJ[4]; Vattipally Sreenu[4]; Thomson Emma C.[4]; Murphy Michael E.[6]; MacGregor Gordon[1]; Blyth Kevin G.[1,7]
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Background/Aims: Community interventions for mild COVID-19 could reduce severe disease incidence and healthcare/societal disruption during future infection waves. Favipiravir is an oral antiviral agent with in vitro activity against SARSCoV2, and has been well tolerated in previous studies. We aimed to establish the efficacy and safety of the oral antiviral favipiravir in mild COVID-19

Methods: GETAFIX was an open-label, community-based, phase II/III randomised trial conducted in a Scottish health board serving 1.3 million people. Non-hospitalised adult patients with mild COVID-19 symptoms (WHO ordinal severity scale (WHO OSS) ≤3) presenting within 7 days of symptom onset were. Exclusion criteria: symptom onset >7 days prior to enrolment, symptom severity of ≥4 on the WHO ordinal severity scale, pregnancy or breastfeeding, severe renal or hepatic dysfunction, history of gout, eligibility for licensed antivirals. Positive community cases were emailed within 24h and invited to web-based self-screening. Participants were randomised 1:1 to 10 days oral favipiravir (1800mg for first two doses, followed by 800mg twice daily) or standard care. The primary endpoint was worst recorded WHO OSS to day 15 (intention-to-treat population). Severe disease was defined as OSS ≥ 4. A sample of 302 delivered 85% power to detect an improvement in the primary endpoint equivalent to a cumulative odds ratio (OR) of 1.95. Secondary outcomes included adverse event rate, ICU admission rate and mortality rate. Registration with ISRCTN no. 31062548.

Results: Analysis was completed in May 2023. Between Dec 2020 & July 2022, 84,546 patients were pre-screened; 302(0.4%) were randomised (favipiravir (n=152), standard care (n=150)). 230/302 participants were vaccinated. Mean age was 47 (SD 13.2). The event rate (incidence of severe disease) was low (WHO OSS ≥ 4: 2/152 Favipiravir, 2/150 standard care). There was no significant difference in the primary endpoint (OR 1.26 (95%CI 0.53–2.97). The time to symptom resolution did not differ significantly between study arms. Favipiravir was well tolerated, with grade 2 adverse events occurring in 18% of participants in both study arms. A single participant

in the favipiravir arm developed a grade 3 adverse event. Treatment compliance was good, with 93% of doses taken on average.

Conclusions: Favipiravir did not reduce severe COVID-19 disease incidence in this well-vaccinated population. There was no difference in the worst recorded WHO ordinal severity score up to and including day 15 post-randomisation, nor in the time to resolution of symptoms.

Conflict of interest(s) (if any – not included in the 500 words):

Strolling Poster Sessions - SESSION 3 LUNG MICROBIOME, PNEUMONIA, TUBERCULOSIS

[13] Inflammatory markers and microbiome characteristics across the spectrum of respiratory diseases.

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Background: There is substantial overlap between COPD, asthma, bronchiectasis(BE) and cystic fibrosis(CF) and each is characterised by inflammation and mucociliary dysfunction. Within each condition there has been evidence of disordered microbiome, often dominated by *Proteobacteria* such as *Pseudomonas* and *Haemophilus*.

Aim: To investigate the microbiome across the spectrum of respiratory diseases including correlation with inflammatory parameters and endotypes.

Methods: We conducted a cross sectional observational cohort study of patients with a diagnosis of airways disease (COPD, asthma, BE or CF) in the East of Scotland. Patients were categorized by primary disease and clinical characteristics, spontaneous sputum was collected and inflammatory characteristics (neutrophil elastase(NE) and 19 cytokines) and sputum properties (DNA content, mucins, rheology, dry weight) measured. DNA was extracted from 0.1g sputum before undergoing long read microbiome sequencing. Resulting fastqs were assessed for quality using FastQC, ASVs were generated using DADA2 and taxonomy assigned against Silva v138.1 Alpha diversity was measured by determining the Shannon-Wiener Diversity Index (SWDI) and the Chao index using the MicrobiomeAnalyst. Linear discriminant analysis Effect Size (LEfSe) with false discovery rate (FDA) adjustment for multiple testing was used to further investigate differences. K-means clustering was performed and parameters compared between and within disease groups. Smokers without respiratory disease were used as controls.

Results: The study included patients with asthma(76), COPD(91), BE(54), CF(24) and controls(26). K means clustering identified 2 clusters defined by neutrophilic or eosinophilic inflammation. Both clusters were present in all disease groups with more neutrophilic inflammation in CF and BE (42% of COPD patients and 46% of asthma patients were neutrophilic vs 78% of BE and 87% of CF,$p<0.0001$). The alpha diversity was decreased in the disease groups (neutrophilic group and eosinophilic group) compared to the control group. Furthermore, the neutrophilic group had significantly reduced alpha diversity compared to eosinophilic group. The three groups (control, neutrophilic group and eosinophilic group) had distinct beta diversity clusters. LEfSe analysis revealed this difference was driven by a dominance of *Proteobacteria* such as *Pseudomonas aeruginosa* (LDA score=2.61, FDR adjusted P value=0.0041), and

Haemophilus parainfluenzae (LDA score=2.08, FDR adjusted P value=0.012) in the neutrophilic group whilst the eosinophilic group was more dominated by *Streptococcus* (LDA score=2.93, FDR adjusted P value=<0.0001), *Rothia mucilaginosa* (LDA score=2.68, FDR adjusted P value=0.0001) and *Prevotella melaninogenica* (LDA score=2.36, FDR adjusted P value=0.031). There was, however, no significant difference in lung function parameters such as FEV1% predicted between the two disease groups.

Conclusions: Chronic respiratory conditions can be categorized, regardless of disease types, into groups associated with neutrophilic or eosinophilic inflammatory markers and these groups have distinct microbiome characteristics. The group characterised by neutrophilic markers had decreased diversity but there was not a significant difference between the two disease groups concerning clinical parameters. These results support treatable traits approach and using biomarkers to apply therapies across respiratory diseases depending on the endotypes, meaning established treatments for specific respiratory diseases could be rapidly applied to other diseases with the same endotype.

Conflict of interest(s) (if any – not included in the 500 words): Amelia Shoemark reports consulting fees from Spirovant and Translate Bio and Payment or honoraria for lectures, presentations, speakers bureaus, manuscript writing or educational events from Translate Bio, Ethris and Insmed.

James Chalmers has received research grants from GlaxoSmithKline, Boehringer Ingelheim, AstraZeneca, Pfizer, Grifols, Bayer AG, Polyphor and Insmed; and consultancy, congress travel or speaker fees from GlaxoSmithKline, Bayer Healthcare, Aradigm Corporation, Grifols, Pfizer, Boehringer Ingelheim, Napp and Insmed.

[14] Comparison of full length 16S rRNA sequencing (Loopseq) and Illumina short read 16S gene sequencing in a cohort of patients with Chronic Obstructive Pulmonary Disease.

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Background: Most studies of the COPD microbiome utilise partial 16S rRNA gene sequencing which cannot accurately identify taxa beyond the genus level. In this study we utilised novel long read sequencing (LRS) and compared the results obtained with those from conventional 16S gene sequencing (SRS).

Methods: We recruited 388 patients with a diagnosis of COPD and FEV1/FVC ratio <0.7. Patients were clinically stable at baseline with no antibiotic or corticosteroid treatment for 4 weeks. DNA was extracted from sputum samples, and each underwent LRS and SRS. Reads were analysed using a DADA2 pipeline for taxonomic inference. Amplicon sequence variants from DADA2 were BLAST-ed to assign strain classifications. We compared diversity indices and the relative abundance of key taxa at the genus level to identify agreement between LRS and SRS. LRS analysis was used to describe the core species and strains present in the COPD microbiome.

Results: With a filter for samples with low read counts applied, no significant differences in Shannon alpha diversity were observed between samples sequenced with LRS and with SRS (P = 0.085). Results: We observed correlations between LRS and SRS key taxa including *Haemophilus, Streptococcus, Moraxella, Rothia, Neisseria* and *Veillonella*. The core species microbiome by LRS was dominated by unclassified *Streptococci*, *Rothia mucilaginosa*, *Streptococcus parasanguis*, *Streptococcus salivarus*, *Haemophilus influenzae*, *Prevotella melaninogenica* and *Prevotella histicola*. Most prevalent taxa in the strain microbiome were *Streptococcus salivarius ATCC 7073, Streptococcus parasanguinis ATCC 15912, Rothia mucilaginosa DSM 20746, Streptococcus toyakuensis TP1632* and *Streptococcus vulneris DM3B3*.

Conclusion: We observed agreement between LRS and SRS suggesting that Loopseq can provide a valid assessment of the sputum microbiome in COPD, with the advantage of accurate identification of pathogens to species or strain level.

FUNDING SOURCE: Funded by GlaxoSmithKline through an investigator initiated research grant.

[15] Ventilator associated pneumonia and its clinical outcomes: Results from a teaching hospital in western India

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Background/Aims: Patients receiving invasive ventilatory support in intensive care units (ICUs) are always at risk of developing ventilator associated pneumonia (VAP). VAP not only increases the morbidity and mortality but causes a drastic increase in the cost of treatment. Multiple factors lead to different patient outcomes. We intended to study the clinico-microbiological profile and outcomes of these patients

Methods: A prospective, cross-sectional study was conducted from January 2022 to October 2023 in an intensive care unit of a tertiary care teaching hospital in western India. Forty-nine patients diagnosed with VAP were enrolled after taking informed consent. Demographic, clinical, radiologic and laboratory data of these patients were collected. Patients were divided into two groups based on clinical outcomes, namely survivors and non-survivors. For univariate analysis, unpaired t-test, Chi-square and Fisher's Exact test were applied.

Results: Majority of patients were males (69%). Co-morbidities were equally present in the two groups. A significant proportion of patients who survived did not have any kind of addiction history ($p<0.05$). Majority of tracheal aspirates were positive for Carbapenem-resistant *Acinetobacter baumannii* (49%), Carbapenem-resistant Enterobacterales (22%) and Extended-spectrum beta-lactamases (ESBL) (14%). Significant survival was seen among females, patients without any addiction and those with ESBL pneumonia.

Conclusions: This study highlights gender, addiction history and ESBL as prognostic factors in predicting the clinical outcomes of VAP. Large multicentric studies are warranted for better understanding of the prognostic factors of VAP.

Conflict of interest(s) (if any – not included in the 500 words): None

[16] Factors associated with prolonged QTc at admission to respiratory wards, Wythenshawe hospital

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Background/Aims: Prolonged QTc is a risk factor for arrhythmias and sudden cardiac death. Previously, we reported that around 20% of patients admitted to our department are already taking QTc prolonging medications. Furthermore, potential QTc prolonging antibiotics, such as macrolides or fluoroquinolones are prescribed in 20% of our patients. The aim of this study was to assess factors that could predict prolonged QTc to mitigate the risk of arrhythmias in patients admitted under general respiratory medicine.

Methods: As part of a clinical audit, we analysed clinical and demographic data of 137 patients (67±16 years, 47% males, 26% were already on QT prolonging medications) admitted under general respiratory medicine to Wythenshawe Hospital, Manchester University NHS Foundation Trust in May 2023. QTc was calculated using both the Bazzet and Fridericia formulas (QTcB and QTcF, respectively). Prolonged QTc was defined as >450 ms in men, and >470 ms in women.

Results: Based on the Bazett formula, thirty-three patients (24%) had prolonged QTc at admission. QTcB (in milliseconds) was not related to age (p=0.60), gender (p=0.32), white blood cell count (p=0.11), neutrophil count (p=0.23), Na (p=0.55), K (p=0.61), Ca (p=0.11), Mg (p=0.97), arterial pH (p=0.39), pO2 (p=0.26), pCO2 (p=0.14) or if patients were on QT prolonging medications (p=0.75). Similarly, the presence of prolonged QTcB was not associated with any of these factors. When the Fridericia formula was used, only 12 patients (9%) had prolonged QTc. Interestingly, QTcF (in milliseconds) was significantly related to pO2 (ρ=0.49, p=0.04), and was lower in patients taking QT prolonging medications (403±21 vs. 423±39 ms, p<0.01), but there was no relationship with any other parameter. The presence of prolonged QTcF was not related to any parameter. QT prolonging antibiotics were started in 15% of patients, including 7 and 1 patients who had already prolonged QTcB and QTcF, respectively.

Conclusions: Clinical and demographic factors are not related to prolonged QTc at admission, therefore we suggest performing ECGs before and after starting QT prolonging antibiotics.

Conflict of interest(s) (if any – not included in the 500 words):

[17] Evaluating the Role of Video Observed Therapy (VOT) in Supporting People with Tuberculosis (TB): A Scoping Review

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Background/Aims: Tuberculosis (TB) remains an important cause of morbidity and mortality across the globe, particularly in low- and middle-income countries (LMIC). Despite effective treatment regimens and the widespread implementation of Directly Observed Therapy (DOT), TB control and elimination targets set by the WHO have not been achieved. One reason behind this is that DOT is inconvenient and can be associated with negative socioeconomic consequences including out-of-pocket costs, lost income, and stigma. The proliferation of digital health technologies, in particular since the COVID-19 pandemic, coupled with increasing internet and mobile phone coverage, has given an opportunity to evaluate the role of Video Observed Therapy (VOT) for people with TB, including in LMICs. This study aims to perform a scoping review to evaluate the role of VOT in supporting people with TB globally and make recommendations for future research and practice.

Methods: Pubmed, Medline, Cochrane Library, Web of Science and Google Scholar were searched systematically up to March 2023. After sifting, appropriate full-text records were identified and evaluated following the scoping review methods of the Joanne Briggs Institute (JBI) Manual and PRISMA reporting standards (see attached diagram). Data from full-text records were extracted into four implementation categories developed iteratively by the project team: Feasibility, Acceptability, Cost, and Effectiveness (FACE). Content analysis was then performed to compare and contrast implementation successes and challenges in these four categories across and between studies and contexts, comparing VOT and DOT where possible. Quality appraisal of the studies was done using the Crowe Critical Appraisal Tool (CCAT).

Results: In total, 66 records were identified: 47 primary research studies, 13 reviews, and 6 grey literature documents. All studies were graded as moderate to high quality and included reporting against at least one FACE category. Studies from urban settings (n = 34) and HIC (n = 33) predominated. Where measured and reported, VOT implementation was found to be feasible (43/43, 100%) and broadly acceptable (43/44, 97%) to people and providers. Of the 18/20 (90%) studies that reported cost data, VOT was shown to offer significant cost savings to the health system. Patient costs were under-reported. Of the 21/23 (91%) studies that commented on effectiveness on adherence, VOT was reported to be non-inferior to DOT. Research gaps found included evaluations of synchronous versus asynchronous VOT, VOT's long-term feasibility and sustainability in LMIC settings and addressing equity of access to smartphones within potentially vulnerable subgroups including rural populations living with TB.

Conclusions: VOT was found to be a feasible and acceptable alternative to DOT, but more evidence is needed from LMIC and underserved groups. VOT appears to have similar effectiveness in supporting adherence and is associated with cost savings for people with TB as well as the health system. More robust, multi-centred studies are needed to better understand the impact of VOT globally in the future.

Conflict of interest(s) (if any – not included in the 500 words): None to declare

[18] A RARE CASE OF TONSILLAR TUBERCULOSIS (TB)

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A RARE CASE OF TONSILLAR TUBERCULOSIS (TB)

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Tuberculosis of tonsils is an extremely rare variety of extra-pulmonary TB especially in elderly individuals. Chronic or recurrent tonsillitis with enlarged tonsils and sore throat is the main clinical presentation. As it is very difficult to differentiate it from tonsillar malignancy on clinical ground, histopathological examination of the tissue is necessary for the diagnosis of tonsillar TB. A 23-year-old male was admitted to the hospital after repeated episodes of tonsillitis since 6 months with fever (37.8 C^0) mainly in the afternoon, severe difficulty for ingestion and permanent pharyngalgia. The clinical examination revealed a large swelling of the tonsils mainly on the left, with tonsillar exudate and enlargement of the left anterior cervical and submandibular lymph nodes. The patient underwent a CT scan, which revealed asymmetry in the oropharynx/hypoharynx with predominant thickness on the left lateral wall of the palatine tonsil and asymmetry on both sides with a cephalocaudal length of 2.8 cm, with a mildly lobulated and irregular border as well as submandibular and left perijugular lymphadenopathy. The patient's chest x-ray was normal (Fig. 2, 3).The patient was a former cocaine user. His HIV status was negative. He underwent tonsillectomy with biopsy revealing granulomatous inflammation of the palatine tonsils of tuberculous etiology (Fig.4,5).The patient initiated therapy with four primary antituberculous drugs (rifampicin/isoniazid/pyrazinamide and ethambutol). Tuberculosis of the oral cavity in general is a rare locality and can be primary or secondary. The tonsillar TB is even rarer due to the defensive action of the saliva, the saprophytic microbes of the oral cavity and the thick epithelial layer cells that protect them.

Strolling Poster Sessions - SESSION 4 BROCHIECTASIS

[19] Investigating the microbiological efficacy of Pseudomonas aeruginosa eradication treatment in bronchiectasis patients using molecular methods.

Lucy Bidgood[1]; Alison Dicker[1]; Hollian Richardson[1]; Chandani Hennayake[1]; Daniela Alferes de Lima[1]; Jamie Stobo[1]; James Abbott[1]; Merete Long[1]; Digalaki Antonia[2]; Gkousiou Anna[2]; Tsikritsaki Kyriaki[2]; Katerina Dimakou[2]; James Chalmers[1]
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Background/Aims: *Pseudomonas aeruginosa* (PA) colonisation in bronchiectasis patients is associated with increased disease severity and mortality. Eradication with antibiotic treatment is the recommended method of tackling the infection at first isolation, with oral ciprofloxacin and inhaled colistin being frequently used and recommended by ERS guidelines. While previous studies have evaluated eradication attempts with culture only, this study also utilised multiplex PCR and 16S rRNA sequencing to investigate the effects of ciprofloxacin and colistin on the lung microbiome in patients with new isolation of *P. aeruginosa*.

Methods: 32 patients were treated with a two-week course of ciprofloxacin followed by a three-month course of nebulized colistin after culture-confirmed PA colonisation. Sputum was collected before, during, and after treatment and cultured for PA presence. DNA extraction was performed on extra sputum for 16S sequencing and multiplex PCR completed with the BioFire Pneumonia Plus Panel. Sequencing data was processed using DADA2 and RStudio, with analysis carried out in GraphPad and MicrobiomeAnalyst for R.

Results: 32 patients were recruited into the study, with 30 producing at least one sample for analysis. Of the 30 patients, the median age was 67.5 with 60% female participants, and 83% had more than one exacerbation per year. 10/30 (33.3%) of patients had negative PA culture after completion of eradication treatment at 3 months. 18% remained PA negative six months post-treatment. Daily sputum production dropped from 20ml per day pre-colistin to 10ml per day post-treatment. After *Pseudomonas* (30%), the next most common genus' in the patients detected by 16S were *Streptococcus* (21%), *Veillonella* (5%), and *Rothia* (5%). Genera unique to individual patients included *Proteus*, *Acinetobacter*, and *Cupriavidus*. There was no significant difference in the microbiome following ciprofloxacin (p=0667) and colistin treatments p=0.945) using PERMANOVA. 46% of samples had amplicon sequence variant (ASV) % reads of <1% *Pseudomonas*. 54 samples were analysed via BioFire, with 37 testing positive for PA. 15 samples testing negative for PA via BioFire had a corresponding positive culture result. BioFire results also included positive results for *Serratia marcescens* (n=4), *Staphylococcus aureus* (n=5), and human rhinovirus or enterovirus (n=6).

Conclusions: Clinical symptoms in patients improved after treatment, however the molecular methods demonstrated that it is more likely that treatment results in suppression rather than eradication in most cases. While the BioFire was also more sensitive than 16S sequencing for specific respiratory pathogens, 16S sequencing has value in monitoring the overall microbiome in bronchiectasis patients. Conflict in results regarding presence or absence of *Pseudomonas* in 16S sequencing versus culture might be explained by the existence of dead bacterial DNA being sequenced. Overall, little change was also seen in the lung microbiome post antibiotic treatment. While limited by small sample size, this study provides the foundation for a larger investigation into eradication therapy.

Conflict of interest(s) (if any – not included in the 500 words):

[20] The Clinical and Socioeconomic Burden of Bronchiectasis: Preliminary Results of A Systematic Literature Review

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Background/Aims: The overall burden of bronchiectasis (BE) continues to lack clarification even after the introduction of clinical care recommendations. A better understanding of the overall burden could support development of new therapies. Here, we present preliminary findings of a systematic literature review that aimed to assess the overall clinical and socioeconomic burden of BE across aetiologies and its associated diseases.

Methods: Following PRISMA guidelines, Embase, MEDLINE and Cochrane Library databases were searched for publications relating to BE disease burden (December 2017–2022). Journal articles and congress abstracts reporting on observational studies, randomised controlled trials and registry studies were included, as well as editorials, narrative reviews and existing systematic literature reviews, for the purpose of identifying primary studies. A reviewer screened all titles and abstracts to identify publications for full-text review, which were then screened for potential inclusion. A second reviewer verified both screening steps.

Results: In total, 1,585 unique publications were identified, of which 587 full texts were screened and 215 were included in this preliminary analysis. Commonly reported symptoms and complications included dyspnoea, cough, wheezing, sputum production, haemoptysis, fever, exacerbations, respiratory tract infections and reduced lung function. Disease severity was reported across several indices, and mortality was reported in several studies. BE impacted health-related quality of life across several patient-reported outcome measures and domains, with patients experiencing fatigue, anxiety and depression. Healthcare resource utilisation (HCRU; hospitalisations/readmissions/length of stay/annual hospital days) was considerable. Patients, health insurance companies and healthcare systems accrued substantial medical costs related to hospitalisations, treatments, and emergency department and outpatient visits. Indirect costs included sick pay and lost income.

Conclusions: These preliminary results show that BE causes significant clinical and socioeconomic burden. Disease-modifying therapies that reduce symptoms, improve quality of life, and reduce HCRU and costs are needed.

Conflict of interest(s) (if any – not included in the 500 words): JDC has received research grants from AstraZeneca, Boehringer Ingelheim, GlaxoSmithKline, Gilead Sciences, Grifols, Novartis, Insmed and Trudell, and received consultancy or speaker fees from Antabio, AstraZeneca, Boehringer Ingelheim, Chiesi, GlaxoSmithKline, Insmed, Janssen, Novartis, Pfizer,

Trudell and Zambon. KGN reports advisory board membership for Boehringer Ingelheim. MM participated in advisory boards for Boehringer Ingelheim. MS reports having received research grants from Novartis, Trudell pharma and GlaxoSmithKline; travel grants from Novartis, Actelion, Boehringer Ingelheim, GlaxoSmithKline and Rafa; speaker fees from Astra Zeneca, Boehringer Ingelheim, GlaxoSmithKline, Insmed, Teva, Novartis, Kamada and Sanofi; and advisory fees (including steering committee membership) from GlaxoSmithKline, Boehringer Ingelheim, Kamada, Syncrony medical, Zambon and Vertex pharmaceuticals. MS also reports data and safety monitoring board participation for Bonus therapeutics, Israel and is an ERS Task Force member on Bronchiectasis guideline development. PJM is an advisory board member for Boehringer Ingelheim's Airleaf trial and Insmed's Aspen trial. PJM is also a PI for clinical trials with the following pharmaceutical companies: Insmed: Aspen, 416; Boehringer Ingelheim: Airleaf; Paratek: oral omadacycline; AN2 Therapeutics: Epetraborole; Renovian: ARINA-1; Redhill; Spero; Armata. SDS had no conflicts to declare. SHC is on advisory boards for CSL Behring, Boehringer Ingelheim and Pneumagen Ltd, served on a data and safety monitoring board for Inovio Pharmaceuticals Inc., and has received personal fees from AstraZeneca and Chiesi Farmaceutici.

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[21] Sputum Dipeptidyl Peptidase-1 Activity Associates With Inflammation And Disease Severity in Bronchiectasis: Data From The EMBARC-BRIDGE Study

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Background/Aims: Neutrophilic inflammation in the airways and release of neutrophil serine proteases (NSPs) like neutrophil elastase drives bronchiectasis development and progression in the vicious vortex. NSPs contribute to mucociliary clearance impairment in bronchiectasis, lung damage, and subsequent airway infection. DPP1 (a.k.a Cathepsin C) is a cysteine cathepsin and a key enzyme involved in the activation of NSPs in the bone marrow in hematopoietic precursor cells. DPP1 is produced by a range of cell types, including mature neutrophils, but its role at inflammatory sites is less well defined. DPP1 inhibition is a promising therapeutic strategy in bronchiectasis; this study aimed to optimise an assay for the measurement of DPP1 activity in sputum samples and investigate associations with inflammatory markers and clinical status.

Methods: DPP1 activity was measured in soluble sputum from patients with bronchiectasis participating in the multicentre, international, observational study EMBARC-BRIDGE (NCT03791086), using a fluorescent in-plate kinetic activity assay with Gly-Phe-AMC as the substrate and recombinant DPP1 as an assay standard. Sputum IL-8, olfactomedin 4 (OLFM4), and neutrophil elastase were measured by immunoassay. A panel of cytokines including CSF3 and IL-1B were measured in serum by OLINK target 48 immunoassay, and cytokines in sputum including IL-5 were measured by multiplex immunoassay. The sputum microbiome was profiled by long read loopseq sequencing. Blood immune cell proportions were imputed from mRNAseq data using CIBERSORTx. Sputum *Pseudomonas aeruginosa* culture results and bronchiectasis severity index (BSI) were utilised for further patient characterisation.

Results: 164 bronchiectasis patients were included in the study (age 65.12 ± 15.32 [mean±SD], 46.34% female). DPP1 activity was detectable in soluble sputum, and was higher in patients with

more severe disease, defined as a BSI score of 9 or greater (p=0.0035; Mann-Whitney). DPP1 activity was also higher in sputum from patients who had ever grown *P. aeruginosa* (p=0.0003) and was significantly lower in those who had lower levels of the anti-inflammatory bacterium Rothia in long read loopseq (p=0.0033). DPP1 activity showed a positive correlation with estimated proportion of blood neutrophils (spearman; r=0.2131, p=0.0050). Sputum DPP1 activity strongly correlated with levels of the neutrophil chemoattractant IL-8 in sputum (r=0.585, p=<0.0001), and activity of the NSP elastase (r=0.469, p=<0.0001). DPP1 activity in sputum also showed moderate correlations with serum inflammatory cytokines IL-1B (r=0.325, p= 0.0015) and IL-5 (r=0.266, p= 0.0008), and both serum and sputum CSF3/G-CSF levels (r=0.355, p= 0.0005, and r= 0.199, p= 0.0123 respectively). Despite being a potential DPP1 inhibitor, levels of the neutrophil granule protein OLFM4 showed strong positive correlation with DPP1 activity (r=0.648, p=<0.0001).

Conclusions: DPP1 activity is detectible in sputum from patients with bronchiectasis. Correlation of this protease with other neutrophil granule products indicates neutrophils as a source of DPP1 in the airways. Higher levels of DPP1 activity are associated with both systemic (IL-1B, IL-8, G-CSF) and airway (elastase, G-CSF, OLFM4) inflammatory markers as well as more severe disease and associated factors including *P. aeruginosa* infection and reduction in anti-inflammatory commensal Rothia.

Conflict of interest(s) (if any – not included in the 500 words): This work was supported by the Innovative Medicines Initiative (IMI) and EFPIA companies under the European Commission funded project, iABC (grant 115721) and by the European Respiratory Society through the EMBARC3 consortium. EMBARC3 is supported by project partners Armata, AstraZeneca, Boehringer-Ingelheim, Chiesi, CSL Behring, Grifols, Insmed, Janssen, LifeArc and Zambon.

[22] Post Tuberculosis (TB) Bronchiectasis versus Non-TB Bronchiectasis in Northern Pakistan: A single centre retrospective cohort study on frequency, demographics, microbiology, and complications

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Background/Aims: While Post Tuberculous (TB) Bronchiectasis is known to be the most common cause of Bronchiectasis in South Asia, there has been little research into its prevalence, demographics, microbiology, or complications in Pakistan. This single centre retrospective cohort study at Bach Christian Hospital (BCH) in rural Northern Pakistan seeks to address this issue.

Methods: Demographic, Imaging, Aetiological and Microbiological dara were obtained from 32 patients with Bronchiectasis at BCH from between January 2023 and December 2023. Bronchoalveolar lavage (BAL) was done for microbiology in all patients but one.

Ethical approval was obtained from BCH ethics committee.

Results:

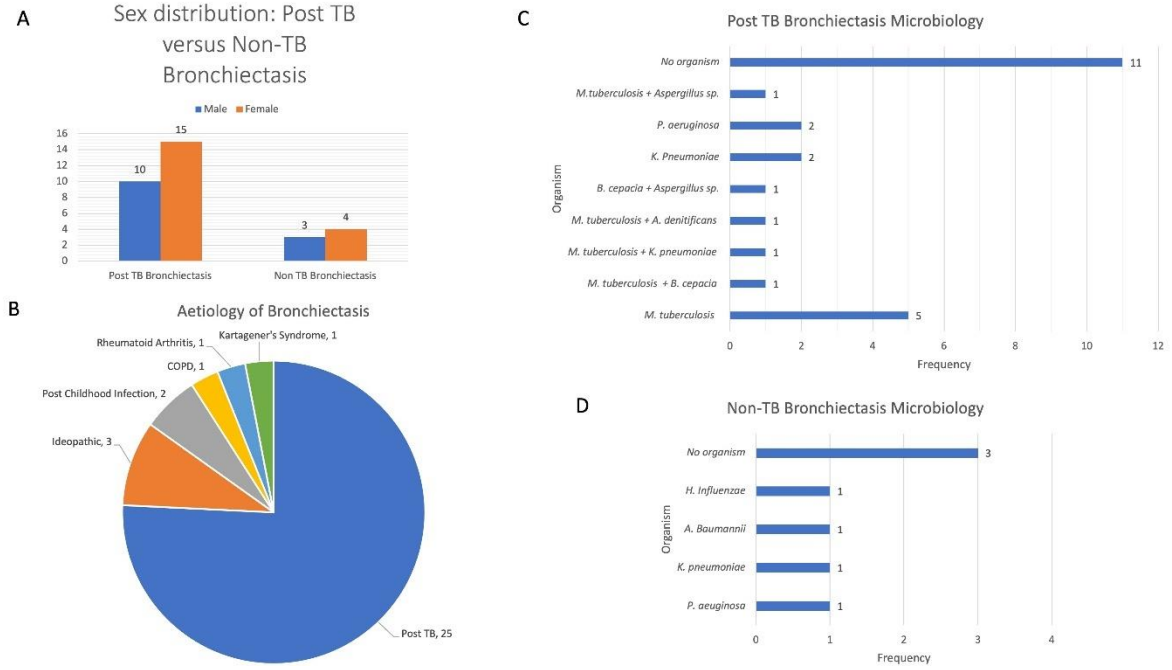

Figure 1 A. Sex distribution in Post TB vs Non-TB Bronchiectasis B. Aetiology distribution of Bronchiectasis C. Microbiology of Post TB Bronchiectasis D Microbiology of Non TB Bronchiectasis

Sex distribution, aetiological distribution, and microbiology of Post TB vs Non TB Bronchiectasis can be seen in *figure 1*. 76% (25/32) of all cases of Bronchiectasis were Post TB. TB infection was seen in 5 cases of Post TB Bronchiectasis, TB with bacterial or fungal co infections in 4, and single bacterial infections in 4. 11 patients had no growth.

In post TB Bronchiectasis 4 patients had growth of a single bacterium, and no growth in 3.

Drug sensitivities of obtained bacterial isolates are seen in *figure 2*.

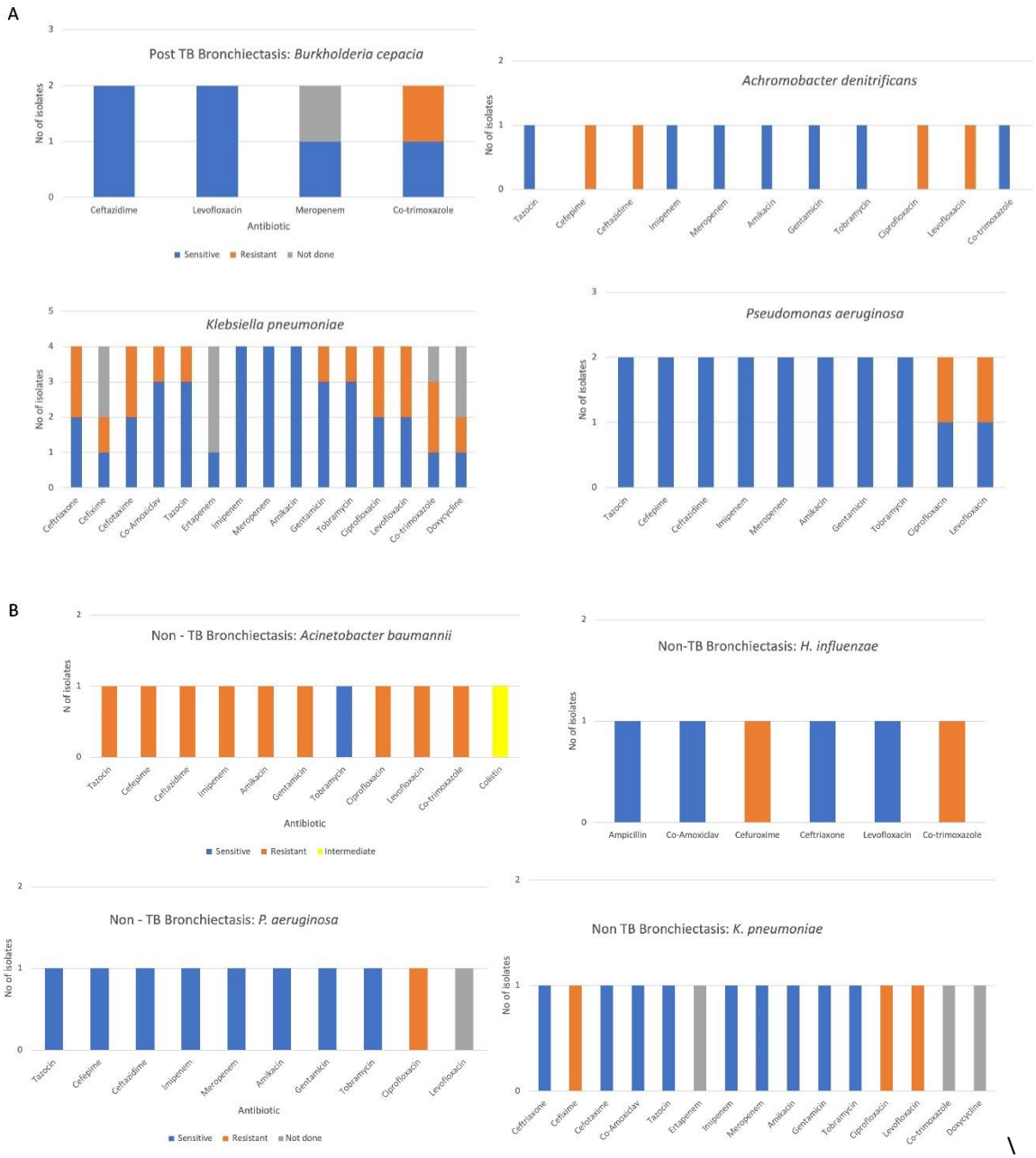

Figure 2 Drug sensitivities of bacterial isolates from Post TB Bronchiectasis (A) and Non-TB Bronchiectasis (B)

In terms of complications, one patient each with Post TB and Non-TB Bronchiectasis died from Type 2 Respiratory failure despite appropriate treatment. 2 patients with Post TB Bronchiectasis presented with destroyed left lung syndrome but improved but with ongoing significant respiratory impairment. All other patients improved with treatment.

Discussion

There are several notable points from this study:

1. The frequency of Post TB Bronchiectasis is very high compared with other studies even for South Asia
2. A significant number (8/24) of Post TB Bronchiectasis had re-infection or failure to improve despite appropriate drug treatment. All patients were sputum AAFB negative, and with at least one with previous negative sputum and gastric lavage TB PCR, highlighting the importance of TB PCR on BAL in the management of these patients.
3. Among patients with Post TB Bronchiectasis, those with co-infection or significant structural lung disease present a difficult treatment challenge.
4. Drug susceptible bacteria and NTM were less commonly isolated compared with other studies, but this may reflect prior antibiotic treatment and challenges in diagnostic techniques for NTM.
5. Complications such as destroyed lung in Post TB Bronchiectasis, and drug resistant organisms in Post TB and Non-TB bronchiectasis are significant treatment challenges.

Significant limitations include small sample size and single centre nature. The study could be improved with spirometry and functional status data to complete a validated scoring system such as the Bronchiectasis Severity Index (BSI).

Conclusions: Post TB Bronchiectasis is an important cause of morbidity and mortality in Northern Pakistan. Further research is needed particularly to manage Post TB Bronchiectasis patients with co-infections or complications such as significant structural lung disease.

Conflict of interest(s) (if any – not included in the 500 words): None

[23] Sputum Azurocidin-1 is a marker of disease severity and microbiome dysbiosis in adult bronchiectasis: Data from the EMBARC-BRIDGE study

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Background/Aims: Azurocidin-1 (AZU1) is a neutrophil protein similar in structure to neutrophil elastase (NE) but without protease activity. Proteomic analysis suggests it is associated with disease severity in bronchiectasis. We hypothesized that AZU1 is associated with clinical severity markers and microbiome dysbiosis in patients with bronchiectasis.

Methods: Sputum AZU1 concentration was measured by ELISA in sputum samples from the pan-European, multicentre EMBARC-BRIDGE study. Results were linked to clinical severity markers, sputum levels of other neutrophil granule proteins, and to relative abundance of taxa at species level in sputum measured by full length 16s rRNA sequencing.

Results:142 patients were included for analysis. Mean age was 64.91 (±16). 68 (48%) were female. Median sputum AZU1 was 59.68µg/ml (IQR 17.21-246.73). Sputum AZU1 correlated positively with the neutrophil proteases NE (r=0.66, p<0.001) and Proteinase-3 (r=0.76, p<0.001). Median sputum AZU1 was higher in patients with a history of bacterial infection, previous hospitalisation and greater radiological severity (Figure). Patients were grouped by high and low AZU1 levels based around the median sputum concentration. Linear Discriminant Analysis of Effect Size (LEfSe) showed that the proteobacteria *Haemophilus influenzae* and *Pseudomonas aeruginosa* were the most differentially abundant species defining patients with high AZU1 whereas *Rothia mucilaginosa* differentiated those with low AZU1. Alpha diversity, measured using the Shannon index, was lower among patients with high sputum AZU1 (p<0.013). Beta diversity analysed by PERMANOVA revealed distinct clusters defined by high and low sputum AZU1.

Conclusions: AZU1 is a novel inflammatory biomarker associated with disease severity and microbiome dysbiosis in bronchiectasis.

Conflict of interest(s) (if any – not included in the 500 words): This work was supported by the Innovative Medicines Initiative (IMI) and EFPIA companies under the European Commission funded project, iABC (grant 115721). EMBARC3-is funded by the European Respiratory Society through the EMBARC3 clinical research collaboration. EMBARC3 is supported by project partners Armata, AstraZeneca, Boehringer Ingelheim, Chiesi, CSL Behring, Grifols, Insmed, Janssen, Lifearc, and Zambon. JDC is supported by the GSK/Asthma and Lung UK Chair of Respiratory Research.

[24] Characterizing neutrophil function in bronchiectasis and the impact of neutrophil-platelet aggregates: data from the EMBARC-BRIDGE study

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Background: Bronchiectasis is a chronic lung condition with high global morbidity and mortality. A hallmark of bronchiectasis is neutrophilic airway inflammation but reports of altered blood neutrophil function are mixed. Platelets have been implicated in neutrophil activation in similar chronic lung diseases such as COPD and may activate neutrophils in bronchiectasis towards a proinflammatory phenotype.

Aims: To characterize key blood neutrophil function in bronchiectasis.

To determine whether neutrophil-platelet interaction can be detected.

To investigate the effects of platelet interactions on neutrophil activity in these patients.

Methods: Circulating neutrophil-platelet aggregates (CD11b+CD41+ cells) were assessed in bronchiectasis patients (n=20) (median FEV1% predicted 78.8%, Median BSI=4) from EMBARC BRIDGE (NCT03791086) and healthy volunteers (n=5) by flow cytometry.

Key blood neutrophil functions of apoptosis (fluorescence microscopy), phagocytosis (flow cytometry), *Pseudomonas aeruginosa* killing (CFU/ml counts), and neutrophil extracellular trap production (NETs; in-plate fluorometry) were measured in participants.

Results: Bronchiectasis patients (age 60.7 ±15.6, mean ±SD, 50% male) had increased neutrophil-platelet aggregates compared to controls (age 25.8±0.8, 20% male)(neutrophil-CD41 MFI ±SD 1288 ±838) vs 415 ±52, Mann Whitney P=0.01). CD11b expression increased in patients with above median aggregates (P=0.05). Bronchiectasis patients had increased bacterial killing vs controls (69% vs 25%, P=0.003), but this was not associated with aggregates. No differences in NETs, apoptosis or phagocytosis were found (P>0.05).

Conclusions: Increased neutrophil-platelet aggregate formation compared to controls suggests a role of platelets in neutrophil activation in bronchiectasis. Independently from controls, an increase in CD11b in patients with higher neutrophil CD41 further shows platelet activation of neutrophils. Killing of P. aeruginosa was altered in bronchiectasis while other functions did not reach significance.

Conflict of interest(s) (if any – not included in the 500 words): None

[25] Aspergillus testing and disease outcomes in Bronchiectasis: data from the EMBARC registry.

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Background/Aims: *Aspergillus fumigatus* causes airway disorders including Allergic bronchopulmonary aspergillosis (ABPA), *Aspergillus* sensitisation (AS) and *Aspergillus* bronchitis (AB). ERS guidelines propose standardized testing for ABPA in those with bronchiectasis to guide optimal treatment, but data suggests testing is not widely carried out. As such, the clinical significance of *Aspergillus* lung diseases in bronchiectasis is not well understood, especially given the lack of universally accepted diagnostic criteria for ABPA. This study aimed to investigate the incidence of ABPA testing across Europe and investigate the clinical significance of *Aspergillus* disease in bronchiectasis while comparing existing and modified ABPA diagnostic criteria.

Methods: Bronchiectasis patients enrolled into the EMBARC registry from 2015-2022 with serological testing for *Aspergillus* disease (total IgE, *Aspergillus*-specific IgE or *Aspergillus* skin test, *Aspergillus*-specific IgG and blood eosinophil counts) were included. ABPA was defined using Modified-ISHAM criteria (2021) with sensitivity analysis performed using ISHAM-ABPA criteria (2013). Elevated *Aspergillus*-specific IgE/positive *Aspergillus* skin test without ABPA was deemed 'AS'. Those with elevated *Aspergillus*-specific IgG without ABPA acted as surrogate for AB. Patients not meeting these criteria formed the control group. Exacerbations during annual follow-up were analysed using negative binomial modelling and survival analysis was performed using Cox proportional hazards regression with adjustment for relevant confounders.

Results: 18,792 patients were included. Of these patients, 9953 (53%) received serological testing for ABPA. ABPA testing varied greatly across Europe, with the lowest rates of ABPA testing occurring in South-Eastern Europe (with <7% patients tested for ABPA). Of those enrolled in EMBARC tested for ABPA, 608 (6.1%) had ABPA, 570 (5.7%) showed AS, 806 (8.1%) had raised *Aspergillus*-specific IgG, 184 (1.8%) had both AS and raised *Aspergillus*-specific IgG and 619 (6.2%) had elevated eosinophil counts without *Aspergillus* disease using the Modified-ISHAM criteria (2021). 78 ABPA diagnoses were missed using the original ISHAM-ABPA criteria (2013) (31 previously AS, 47 previously AS with raised *Aspergillus*-specific IgG). All patients with *Aspergillus* disease had more severe bronchiectasis and worse lung function at baseline. Long-term follow-up revealed patients with raised *Aspergillus*-specific IgG experience more exacerbations (RR 1.19 95%CI 1.05-1.35, p=0.008) and hospitalisations (RR 1.66 95%CI 1.37-1.99, p<0.001), while a trend towards increased mortality was observed in those with ABPA (HR 1.40 95%CI 0.99-1.99, p=0.057). Inhaled corticosteroids modified hospitalisation risk associated with AS (RR 0.70 95%CI 0.54-0.90, p=0.006 vs RR 0.91 95%CI 0.54-1.52, p=0.71) and raised *Aspergillus*-specific IgG (RR 1.32 95%CI 1.04-1.68, p=0.02 vs RR 2.26 95%CI 1.68-3.02, p<0.001).

Conclusions: Rates of ABPA testing vary greatly across Europe despite ERS guidelines. *Aspergillus* disease is common in bronchiectasis and associates with worsened disease severity

and outcomes which can be modified by ICS. The Modified-ISHAM criteria (2021) captured ABPA diagnoses that would have been missed using existing ISHAM-ABPA criteria (2013).

Conflict of interest(s) (if any – not included in the 500 words): This work was supported by the Innovative Medicines Initiative (IMI) and EFPIA companies under the European Commission funded project, iABC (grant 115721). EMBARC3-is funded by the European Respiratory Society through the EMBARC3 clinical research collaboration. EMBARC3 is supported by project partners Armata, AstraZeneca, Boehringer Ingelheim, Chiesi, CSL Behring, Grifols, Insmed, Janssen, Lifearc, and Zambon. JDC is supported by the GSK/Asthma and Lung UK Chair of Respiratory Research.

[26] Paediatric bronchiectasis in the UK: current status, challenges and opportunities – a National UK audit

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The abstract is submitted on behalf of the contributing members of the Paediatric Bronchiectasis Network UK.

Objectives: Paediatric bronchiectasis (PB) is an orphan disease. (1) In 2021, the Paediatric Bronchiectasis Network UK (PBNetUK) was set up by clinicians interested in improving the care of PB in the UK. In 2023, a national audit of 1) current bronchiectasis service provision in UK tertiary paediatric respiratory centres and 2) a snapshot of children and young people (CYP) with PB seen across these centres was initiated.

Methods: All 24 centres participating in the PBNetUK network were contacted and asked to register the audit locally. An agreed template for data capture was developed. The audit has two parts: 1) service provision data and 2) patient data. Centres were asked to provide data on as many CYPs seen over a 6-months period as possible. Submission of data from district general hospitals (DGH) in the network was encouraged. Data variables included outpatient services provided, total numbers of patients with PB in the service and demographic data for a cross-section of the patients. Data was pseudo-anonymised and analysed centrally. Only CYPs with CT confirmed bronchiectasis were included.

Results: 17 of the 24 centres (71%) have responded to date serving a total of 744 patients. Data on 375 individual patients (50% of total), have been submitted for further analysis. Eleven centres (52%) have dedicated bronchiectasis (or chronic suppurative lung disease) clinics. There was variability between centres regarding frequency of patient reviews (by clinicians, physiotherapists and respiratory nurses). Only 4/17 (24%) have access to a psychologist or a dietitian. Less than half of the centres (7/17) have a structured transition service in place despite 13/17 centres having a dedicated adult service available. Specific PB SOPs are only in place in four centres, although most centres stated they follow ERS 2021 guidelines. (2) All centres agreed with eradication of *Pseudomonas aeruginosa* on first isolation although eradication strategies varied between centres.

Conclusion: This large national audit supports benchmarking and demonstrates the scale and importance of PB. Current challenges such as inequity of service provision are revealed. The importance of paediatric centres to develop dedicated PB services for better patient care and expansion of MDT teams to include dietetic/psychology support are highlighted as areas of opportunity. It is hoped that the audit will encourage paediatricians leading DGH to capture data on PB in the future and closely work with tertiary units for support.

References

1. Regan KH, Hill AT Emerging therapies in adult and paediatric bronchiectasis. Respirology 2018
2. Chang AB, Fortescue R, Grimwood K, et al. Task Force report: European Respiratory Society guidelines for the management of children and adolescents with bronchiectasis. Eur Respir J 2021

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