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*Brisbane, Australia; [5]The University of Queensland, School of Public Health, Herston, Australia; [6]Queensland Children's Hospital, South Brisbane, Australia*

**Objectives:** Our group has investigated the extent of *Pseudomonas aeruginosa* aerosol release during cough in people with CF (Knibbs, Thorax, 2014; Wood, AJRCCM, 2018; Stockwell, AJRCCM, 2018). We have demonstrated the concentration of *P. aeruginosa* cough aerosols is highly variable between patients, yet the only factor associated with aerosol concentration is the sputum concentration of the pathogen. Therefore, we aimed to investigate (using the merged datasets) if additional clinical factors are associated with aerosol production.
**Methods:** The merged *P. aeruginosa* cough aerosol study datasets were analysed for factors associated with cough aerosol production. Participants were categorised into high producers if the *P. aeruginosa* aerosol count was ≥10 colony forming units (CFU) or low producers if the count was <10 CFU (Jones-Lopez, AJRCCM, 2013).
**Results:** Fifty-two people with CF and chronic *P. aeruginosa* infection performed 68 cough tests. *P. aeruginosa* sputum concentration was the only factor associated with *P. aeruginosa* aerosol concentration ($r = 0.61; p < 0.001$). No associations were seen for gender ($p = 0.78$), $FEV_1$% predicted ($r = -0.025; p = 0.86$), BMI ($r = -0.23; p = 0.11$), age ($r = 0.22; p = 0.13$), modulator use ($p = 0.47$), C-reactive protein level ($r = -0.24; p = 0.87$) or other pathogens in sputum ($p = 0.16$). The sputum concentration association was also seen in 12 subjects who were recruited to multiple (2–3) cough tests. Over time, the cough aerosol category did not change in 9 subjects (8/9 remained high producer; 1/9 remained low producer) but did change in 3 subjects (2/3 changed from high to low producers; 1/3 changed from low to high producer).
**Conclusions:** *P. aeruginosa* sputum concentration strongly predicts for *P. aeruginosa* cough aerosol concentration. Production of cough aerosol (high or low producers) was unchanged over time for most participants.
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### P175
**Extended incubation of cystic fibrosis cultures: is it worth it?**

R. Amado[1], J. Trejo[1], D. Romero[1], A. Cano[1], F. Barroso[1], T. Martin-Gomez[1]. [1]*Vall d'Hebron University Hospital, Microbiology, Barcelona, Spain*

**Objectives:** A characteristic feature of CF is the presence in the airway of pathobionts that may establish a chronic infection that modulates the progression of pulmonary function decline. Adaptation to a pathological environment, biofilm lifestyle, and repeated antibiotic treatment lead to phenotypic and genotypic alterations resulting in bacterial slower growth rates. Whereas extended incubation has been recommended for the recovery of Burkholderia, less is known about the optimum minimum time of incubation for the recovery of other bacteria. We sought to determine whether extending the incubation of respiratory cultures of CF patients improved the recovery rate of bacteria commonly associated to CF
**Methods:** Study period: January-December 2017. Oropharyngeal and sputum samples from patients attending the Vall d'Hebron Hospital CF Unit were plated at least in MacConkey, Chapman, Chocolate, and modified Thayer-Martin culture media, and incubated 5 d (up to 10d if Nocardia or Burkholderia were suspected) at 35°C inroom or 5% CO2 atmosphere as appropriate. Plates were checked every working d. Time-to-recovery of microorganisms [mean d, (SD)] was recorded. For the purpose of this study results from samples plated on Friday (not read during the first 48 h) were disregarded.
**Results:** Of 1077 eligible isolates, 206 (19.1%), 582 (54.1%), and 289 (26.8%) were detected at 24 h, 48 h, and >48 h of incubation (138–47.8%- detected after 96h). A mean of 5(1.58)d was necessary to recover 33.3% P aeruginosa, 41.4% S maltophilia, and 60% Burkholderia spp isolates, whereas 100% Nocardia spp required a mean of 8(1.66)d of incubation. Recovery of 16.2% S aureus, 22.9% Achromobacter spp, and 17.3% of Haemophilus spp was also delayed >48 h. 67.1% of isolates recovered after >48 h corresponded to chronically colonized patients
**Conclusion:** ¼ of FQ isolates would have been missed if cultures were incubated 48h. Extended incubation is relevant not only to recover chronic colonizers

### P176
**Detection of respiratory viruses in cystic fibrosis: comparison of nasal FLOQ Swabs™ and sputum using the FilmArray® platform**

S. Carter[1,2], B. Keogan[3], P. O'Reilly[3], S. Coughlan[3], G. Cooke[2,4], C. De Gascun[3], C. Gallagher[1], E. McKone[1,2]. [1]*National Referral Centre for Adult Cystic Fibrosis, St Vincent's University Hospital, Dublin, Ireland;* [2]*Conway Institute, University College Dublin, Dublin, Ireland;* [3]*National Virus Reference Laboratory, University College Dublin, Dublin, Ireland;* [4]*Institute of Technology Tallaght, Dublin, Ireland*

**Objectives:** This Prospective observational study had two aims:

1. To measure the prevalence of respiratory viruses in people with CF when clinically stable and at onset of CF exacerbation.
2. To compare results from paired Nasal FLOQ Swabs™ and sputum using the FilmArray® real time PCR respiratory panel.

**Methods:** Individuals were included at the clinically stable time point if well, and a minimum of 4 weeks since last intravenous antibiotics. Individuals were included at the exacerbation time point within 24 hours of commencing intravenous antibiotics for CF exacerbation.
Nasal FLOQ Swabs™ were collected and frozen in Universal Transport Medium (UTM™ RT) at - 80°C. 200 µl aliquot of raw sputum was frozen at −80°C until thawed and homogenized in 200 µl of Copan SL solution. Both samples were analysed using the FilmArray®respiratory panel.
**Results:** Results of viral status (either nasal swabs, sputum or both) were available for 163 of 194 episodes recorded (82%). At the clinically stable time point (n = 96) 10% of individuals tested positive for respiratory viruses: Human Rhinovirus/Enterovirus (7%), Coronavirus (2%) and RSV (1%). At the exacerbation time point (n = 67) 36% tested positive for respiratory virus: Human Rhinovirus/Enterovirus (19%), Influenza (7%), Coronavirus (4%), Mixed Infection (3%) and Para-Influenza (1%).
Of the 83 paired nasal and sputum samples 84% had concordant results. However, 16% of results were discordant with 15% negative for viral infection on nasal swab but positive in sputum.
**Conclusion:** Prevalence of respiratory viruses was lower in the clinically stable cohort compared to previous studies. However, the prevalence of respiratory viruses at exacerbation was in keeping with other published work. CF Sputum was processed using COPAN SL solution on the FilmArray® platform and these results suggest that sputum may be a more sensitive method for detecting respiratory viruses in CF.

### P177
**Characterisation of pathogens causing lung infection in people with cystic fibrosis by surface-enhanced Raman spectroscopy (SERS)**

D. Allen[1,2], J. Kelly[2], G. Carson[1], L.J. Sherrard[1], D.F. Gilpin[1], J.S. Elborn[3], S.E.J. Bell[2], M.M. Tunney[1]. [1]*Queen's University Belfast, School of Pharmacy, Belfast, United Kingdom;* [2]*Queen's University Belfast, School of Chemistry and Chemical Engineering, Belfast, United Kingdom;* [3]*Queen's University Belfast, Centre for Experimental Medicine, Belfast, United Kingdom*

**Objectives:** Culture methods are used to detect bacteria causing respiratory infection in people with CF. These methods are time-consuming and so there is a need for rapid techniques to accurately identify and characterise these pathogens. SERS is a novel technique that produces a whole-organism spectroscopic fingerprint at high speed. A range of bacterial species detected in respiratory CF samples were characterised using SERS.
**Methods:** Raman spectra of clinical isolates and reference strains were obtained from *Pseudomonas aeruginosa* (n = 66), *Staphylococcus aureus* (MSSA, n = 5; MRSA, n = 20), *Stenotrophomonas maltophilia* (n = 6), *Streptococcus pneumoniae* (n = 5), *Achromobacter xylosoxidans* (n = 3) and *Burkholderia cepacia* complex (Bcc; n = 11). Bacterial isolates were adjusted to $1 \times 10^8$–$1 \times 10^9$ CFU/mL and a resulting bacterial pellet was mixed with citrate reduced silver colloid (CRSC) and dried. Raman spectra were recorded (4 × 10 seconds at 785nm) and analysed within GRAMS/Al software.
**Results:** Two distinct spectra were observed with *P. aeruginosa*; one was dominated by the pigment pyocyanin (n = 13 isolates) with vibrational bands present at 1350, 1492, 1598 and 1615 $cm^{-1}$. The remaining 53 isolates had characteristic vibrational bands at 661, 735 and 800 $cm^{-1}$ which correspond to guanine, adenine and uracil, respectively. Variation in the