Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

months). A retrospective chart review comparing patients' clinical metrics pre- and post-rollout was then conducted. Usability and Acceptance were also measured with patients (p) and staff (s) via a number of standardised surveys: System Usability Scale (SUS), TeleHealth Usability Questionnaire (TUQ), IT Familiarity, and our own quality-survey.
Results: The Covid Pack permits adequate spirometric assessment of patients (mean bias –2.5%). Preliminary data collected from 52 patients and 11 staff members show an overall positive response to our remote-clinics. The SUS received a median score of 90 (p) and 87.5 (s) out of 100. The TUQ received a total score of 6.52 (p) and 6.1 (s) out of 7, with ease of Use and Learnability as the highest-rated category in the TUQ (median 7, range 3.6–7) and Reliability as the lowest-rated category (median 5.33, range 2–7). The IT Familiarity questionnaire received an average median score of 1 (very familiar) from both groups. Qualitative data collected via a custom survey show that while patients and staff are positive to the convenience of the remote clinic, the facility for an in-person. face-to-face review remains important, as does good WiFi connection.
Conclusion: Initial 6-month data are positive for the remote clinic as a first default during the pandemic. Preliminary data shows a positive trend for the usability and acceptance by all stakeholders, but it is not a replacement for physical clinics.

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Has the COVID-19 pandemic affected medication adherence to inhaled nebulised therapy for patients at a large adult cystic fibrosis centre?

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Objectives: The COVID-19 pandemic has led to immense challenges for healthcare systems worldwide. People with cystic fibrosis (CF) were included in the clinically extremely vulnerable group for complications of coronavirus by the UK government and advised to shield during a national lockdown. Data suggests that pandemic-related restrictions have been linked to a reduction in pulmonary exacerbation events (PEx). We sought to explore whether an increase in medicine possession ratio and potentially adherence may be a factor in this finding.
Methods: 50 patients who received medication through a homecare delivery system at a single large adult centre were randomly selected. Data from 12 months 'pre-lockdown' was compared to data for 9 months following start of shielding in March 2020. MPR was calculated and capped at 100%. Medications that were started or stopped during the pandemic were not included. Wilcoxon signed rank test was used to compare pre- and post-values.
Results: 91 prescription medications were valid for analysis (45 nebulised antibiotics, 34 mucolytics and 12 CFTR modulators). MPR increased for 41 prescriptions (45.1%), decreased for 21 medications (23.1%) and remained unchanged for 29 medications (31.9%). Median MPR increased from 83% [57–100%] to 89% [66–100%], p = 0.037. MPR for nebulised antibiotics significantly increased (median 75% [54–100%] vs 89% [61–100%], p = 0.027). Median MPR for CFTR modulators was 100% throughout and did not change for mucolytics (75% [42–100%] vs 78% [53–100%], p = 0.419).
Conclusion: We report a significant change in medication possession in adults with CF during the coronavirus pandemic in the UK. It is unclear whether this change translated to an increase in adherence but may be one factor in the reported decrease in PEx events described during this time. It is notable that increases were largely driven by inhaled antibiotics and this may represent a concerted effort to achieve maximal protection from infection.

Microbiology/Antibiotics

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Lung and gut microbiota signatures in cystic fibrosis mice challenged with *Pseudomonas aeruginosa*

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Objectives: Among the many facets of cystic fibrosis (CF), the microbiological status of patients is of great interest due to the recurrent, chronic microbial infection of the airways. In addition to airway microbiome alteration, CF patients show altered faecal microbiomes as well, correlated with gastrointestinal inflammation and nutrient malabsorption. However, whether this dysbiosis is directly caused by mutations in the *CFTR* gene is not fully clarified. The aim of this work was to evaluate the response of the lung and gut microbiota in wild type and CF mice in the naïve status and after *Pseudomonas aeruginosa* chronic infection.
Methods: We focused our analysis on lung, stool, and gut microbiota targeting the 16S ribosomal RNA gene aiming to shed light on the comparative response of lung and gut microbiota following infection by *P. aeruginosa* in wild-type and gut-corrected CF mice.
Results: Alpha diversity indices showed in WT mice higher values than in KO mice for stool and gut, while lung microbiota was similar. In CF mice, infection with *P. aeruginosa* did not affect the microbiota diversity in both stool and gut, while a drop of lung microbiota occurred with respect to the control, as would be expected as a consequence of the massive colonisation by the *P. aeruginosa* strain. We found that *P. aeruginosa* infection affected the gut microbiota of CF mice, while no effect was found in wild-type mice. This finding indicates that the pulmonary chronic infection in CF mice may lead to intestinal mucosa not directly related to CFTR lack of expression in the gut.
Conclusion: Overall our results reinforce the hypothesis of an indirect correlation between the lung and gut microbiota in the presence of CF lung colonisation by *P. aeruginosa.*
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Microevolution of *Pseudomonas aeruginosa* in the lungs of patients with cystic fibrosis

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Objectives: Bacteria undergo evolution during chronic infection in the CF lung. The study aimed to investigate molecular mechanisms of microevolution of *P. aeruginosa* in the lungs.
Methods: The whole genome of 3 *P. aeruginosa* strains isolated from a patient with CF in 2006 (70L), 2012 (203–2) and 2016 (159B) were sequenced. For genome analysis, we used BLAST, RAST, ResFinder, Provean programs.
Results: BLAST analysis showed that strains were of clonal origin: they have a common ancestor. Genome analysis showed microevolution of strains during persistence for 10 years. The evolutionary process was because of genetic changes: 1. horizontal gene transfer, for example, the strain 203-2 had aac(3)-IIa and blaTEM genes obtained with plasmid; 2. mutations in