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.

Low rate of bacterial co-infection in patients with COVID-19

We agree with Michael J Cox and colleagues[1] that clinical management of COVID-19 would be enhanced by further characterisation of bacterial co-infections. A few case reports have described examples of such co-infections.[2,3,4] However, national[5] and international[6] guidelines recommend empirical antibiotics for all patients who are severely ill with suspected COVID-19, and that cessation of therapy is left to the clinicians' discretion. Pending the widespread availability of metagenomic sequencing as envisaged by Cox and colleagues,[1] we argue that traditional diagnostics still have a role.

We reviewed all microbiology results for patients admitted to Whiston hospital (Prescot, UK) with PCR-confirmed COVID-19 between March 6, 2020, and April 7, 2020. Hospital policy for patients admitted with community-acquired pneumonia, including suspected COVID-19 cases, recommends blood cultures and pneumococcal and *Legionella* urinary antigen tests based on clinical severity, in line with national guidelines.[7] We collected the data to inform and update the hospital's antimicrobial policy, with approval from the Trust Quality Improvement and Clinical Audit department. We recorded results for 7 days from the positive COVID-19 test because positive samples collected after this time period might represent hospital-acquired infections. Samples unequivocally consistent with contamination were considered negative.

We identified 195 patients (for demographics and microbiology see appendix p 1). Five (3% of 195, or 4% of 137 patients specifically tested), had pneumococcal co-infection and all survived to hospital discharge. One of 31 patients tested was positive for the *Legionella* antigen without lower respiratory tract samples to confirm legionellosis. Bacteria grew from four of 26 sputum samples (appendix p 1). All bacteria were Gram-negative bacilli more typically associated with oropharyngeal colonisation than community-acquired pneumonia.

Our findings suggest that bacterial co-infection is uncommon in patients with COVID-19 who are newly admitted to hospital. The co-prevalence of pneumococcus and severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was low, and *Staphylococcus aureus* was not detected. By contrast, in influenza infection the prevalence of bacterial co-infection in hospitalised patients can exceed 30%.[8,9] These results suggest that routine antibiotics might not be indicated in patients with COVID-19. If superimposed bacterial community-acquired pneumonia is suspected, coverage for typical pathogens such as pneumococcus might suffice, unless there is specific clinical concern for infection with atypical agents.

The main strength of our report is the correlation of microbiology results with all consecutive COVID-19 admissions. The main limitation is the variability of microbiological sampling. Our results might not be generalisable to other geographical settings.

Future studies should implement standardised microbiological sampling for all COVID-19 admissions and prospectively correlate the prevalence of co-infection with mortality rates. Such studies could also correlate clinical and laboratory findings with the presence of co-infection to support rational prescribing of antibiotics.

We declare no competing interests.

*Hugh Adler†, Robert Ball†, Michael Fisher, Kalani Mortimer, Madhur S Vardhan
hugh.adler@sthk.nhs.uk

†Joint first authors

Department of Microbiology, St Helens and Knowsley Teaching Hospitals NHS Trust, Prescot, L35 5DR, UK (HA, RB, MF, KM, MSV); and Department of Clinical Sciences, Liverpool School of Tropical Medicine, Liverpool, UK (HA)

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See Online for appendix