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Improving Antimicrobial Stewardship in Critically-Ill Patients with COVID-19

To the Editor—We read with interest the study by Valerie Vaughn [1] and colleagues. As the authors point out, the later development of hospital-acquired secondary bacterial infections is another important consideration. We reviewed all microbiology results for 77 COVID-19 patients admitted to Intensive Care (ICU) at a London UK hospital between March 12, 2020 and April 23, 2020 from admission to discharge (obtaining local approvals). Our aim was to develop an approach supporting antimicrobial stewardship, as all patients were commenced on antibiotics upon ICU admission, 75% changed to a second antibiotic, 55% to a third (only 9% and 14% prompted by culture results, respectively).

Respiratory specimens were sent from 66% (51/77) of patients, 59% (30/51) in the first 72 hours, only 3 isolated potential community pathogens (*Haemophilus influenzae*, *Staphylococcus aureus* and *Moraxella catarrhalis*). Pneumococcal urinary antigens were sent in 56% patients with 2 positives; legionella urinary antigens in 60% with no positives. Pre-antibiotic blood cultures were taken in 56%, none isolated a respiratory pathogen. Possible community co-infections were thus identified in 6% of patients, likely higher compared with previous studies [1, 2] as our patients were critically ill.

A total of 180 respiratory specimens were processed with traditional microbiological techniques (Figure 1). Most community organisms were isolated in the first 2 days, switching to hospital-associated organisms by day 3, though most cultures were negative or yielded commensals in the first 9 days. *Pseudomonas aeruginosa* emerged after the first week on the unit, becoming the most commonly isolated organism thereafter. This illustrates how the balance quickly shifted from community to hospital-acquired pathogens in our cohort.

No particular clinical, radiological, or laboratory features set those with community pathogens apart from those with negative early cultures, though ultimately the former did have an 80% mortality (4/5) versus 49% (33/72) for the latter. The expected pathogenicity of the organism did not always match the reality (*S. aureus* with minor changes on chest imaging, or *M. catarrhalis* and *H. influenzae* with extensive bilateral consolidation). The challenge lies in determining where the line between commensal and pathogen has been crossed. On the one hand, the 1.8% positive blood cultures reported by Vaughn and colleagues [1] are clear-cut; on the other, the use of RT-PCR techniques as reported by Zhu et al. [3] with a 94% respiratory pathogen co-infection mostly illuminates a microbiome with pathogenic potential. Nevertheless, determining the significance of respiratory isolates is very difficult no matter the method, especially with gram-negative hospital-acquired respiratory infections.

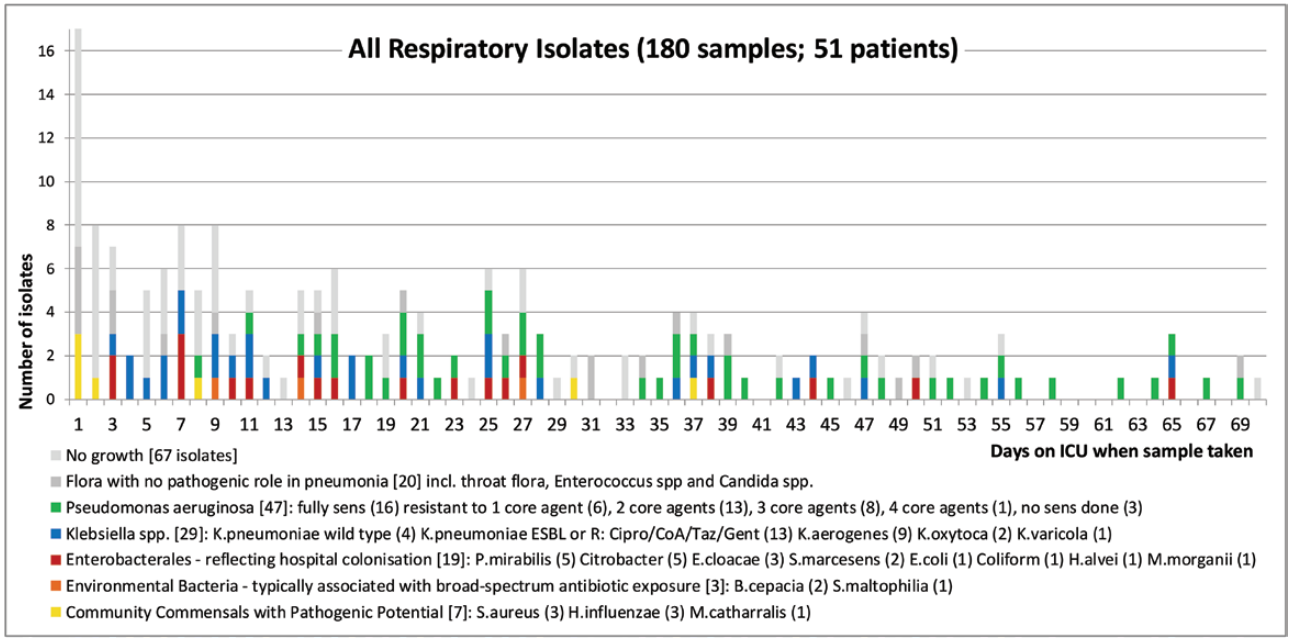

Figure 1. All respiratory isolates, from 51 patients, 180 samples in total. Abbreviation: ICU, intensive care unit.

Though we are interested to know what pathogens were identified by Vaughn and colleagues, ultimately, community-acquired pathogens should be covered by first-line antimicrobials—hence admission respiratory specimens are unlikely to alter management. Sequential procalcitonin levels from admission for all critically-ill COVID-19 patients may assist antimicrobial stewardship and monoclonal antibody treatment decisions. The aim should be discontinuation of antibiotics within the first 72 hours where supported by a multidisciplinary team assessment. Focus should then be placed on obtaining cultures when there is evidence of hospital-acquired infection to facilitate targeted antibiotic use in response to clinical deterioration.

Note

Potential conflicts of interest. The authors: No reported conflicts of interest. All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest.

Daniel R. Stevenson,[1] Manpreet Sahemey,[2] Joaquim Cevallos Morales,[2] Juan Martín-Lázaro,[2] Ruaridh Buchanan,[1] and Robert Serafino Wani[1]

[1]Department of Infectious Diseases and Microbiology, Newham University Hospital, Barts Health NHS Trust, London, United Kingdom, [2]Department of Intensive Care Medicine, Newham University Hospital, Barts Health NHS Trust, London, United Kingdom

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Correspondence: D. R. Stevenson, Infectious Disease and Microbiology Registrar, Department of Infection, Newham University Hospital, Barts Health NHS Trust, Glen Rd, London E13 8SL, London, UK (danielstevenson@nhs.net).

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