

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.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.

Acinetobacter	Klebsiella	Pseudomonas	Stenotrophomonas
49% (19/39)	21% (6/28)	18% (2/11)	67% (2/3)
3% (1/36)	0% (0/27)	0% (0/12)	0% (0/5)
10% (38/368)	2% (12/720)	1% (2/262)	0% (0/217)
8% (9/108)	6% (5/89)	0% (0/69)	0% (0/29)
59% (64/108)	30% (27/89)	9% (6/69)	48% (14/29)
	49% (19/39) 3% (1/36) 10% (38/368) 8% (9/108)	49% (19/39) 21% (6/28) 3% (1/36) 0% (0/27) 10% (38/368) 2% (12/720) 8% (9/108) 6% (5/89)	49% (19/39) 21% (6/28) 18% (2/11) 3% (1/36) 0% (0/27) 0% (0/12) 10% (38/368) 2% (12/720) 1% (2/262) 8% (9/108) 6% (5/89) 0% (0/69)

All-cause mortality data are from the CREDIBLE-CR trial.¹ Detected resistance data (minimum inhibitory concentration >4 µg/mL) are from the CREDIBLE-CR trial¹ or SIDERO-CR study,⁵ or were generated by disk diffusion assay on carbapenem-resistant isolates from GA, USA, according to Clinical and Laboratory Standards Institute guidance. Heteroresistance data were established by population analysis profile to identify minority resistant subpopulations within an isolate. *All-cause mortality data for *Klebsiella*, *Pseudomonas*, and *Stenotrophomonas* spp are for patients who did not have *Acinetobacter* spp coinfection. †Data not available for all isolates in the CREDIBLE-CR trial.

Table: All-cause mortality and cefiderocol non-susceptibility among carbapenem-resistant pathogens

We surveyed for cefiderocol heteroresistance among carbapenem-resistant bacteria collected in the Georgia Emerging Infections Program, GA, USA, including Acinetobacter baumannii (2012–15), Klebsiella spp (2011–15), Pseudomonas aeruginosa (2015–16), and Stenotrophomonas maltophilia (2018-21; appendix p 1). By standard disk diffusion AST, the vast majority of isolates were classified as susceptible to cefiderocol, consistent with the CREDIBLE-CR trial and the SIDERO-CR surveillance study of 1873 carbapenem non-susceptible, Gram-negative pathogens.^{1,5} However, sensitive testing by population analysis profile identified cefiderocol heteroresistance in each pathogen, with particularly high rates in Acinetobacter (table; appendix pp 1, 4). Importantly, these data indicate that cefiderocol heteroresistance was present in the USA before clinical approval of this drug by the US Food and Drug Administration in 2019. The frequency of heteroresistance was far greater than that of detected resistance for all four pathogens and was similar to the all-cause mortality rate, suggesting that heteroresistance might have contributed to cefiderocol treatment failure in the CREDIBLE-CR study.

Hallmarks of heteroresistance are the resistant subpopulation increasing in frequency with antibiotic treatment

and decreasing in frequency after removal from the drug. We observed both effects in a representative carbapenem-resistant A baumannii isolate (appendix pp 3, 5). In the CREDIBLE-CR study, the minimum inhibitory concentration of some isolates exposed to cefiderocol increased after treatment, which might be consistent with heteroresistance.¹

CREDIBLE-CR involved isolates from 16 countries and SIDERO-CR involved those from 52 countries, with similar frequencies of detected cefiderocol resistance (by standard AST) as observed in our research, suggesting that the GA, USA, isolates are representative. Therefore, the widespread and undetected cefiderocol heteroresistance among carbapenemresistant pathogens observed here might explain the discordance between this drug's excellent susceptibility profile in vitro and its association with increased patient mortality.

DSW reports grants from National Institutes of Health, Veterans Health Administration, and Burroughs Wellcome Fund Investigators in the Pathogenesis of Infectious Disease award. DSW also has a pending patent for exploitation of heteroresistance for combination therapy. JTJ reports grants from Centers for Disease Control and Prevention. JEC reports grants from the Cystic Fibrosis Foundation and National Institutes of Health (T32 DK108735). All other authors declare no competing interests. We would like to thank the Georgia Emerging Infections Program led by Monica Farley, and its Multi-Site Gram-negative Surveillance Initiative, as well as the Emory Antibiotic Resistance Center's Investigational Clinical Microbiology Core, for providing isolates. This work was supported by the National Institutes of Health (Al141883, Al148661, Al158080) and the Department of Veteran's Affairs (BX002788). The Georgia Emerging Infections Program and the Multi-Site Gram-negative Surveillance Initiative are funded by the Centers for Disease Control and Prevention.

Jacob E Choby, Tugba Ozturk, Sarah W Satola, Jesse T Jacob, *David S Weiss

david.weiss@emory.edu

Emory Antibiotic Resistance Center and Emory Vaccine Center, Atlanta, GA 30329, USA (JEC, TO, SWS, JTJ, DSW); Division of Infectious Diseases, Department of Medicine, Emory University School of Medicine, Atlanta, GA, USA (SWS, JTJ, DSW); Georgia Emerging Infections Program, Georgia Department of Public Health, Atlanta, GA, USA (SWS, JTJ)

- Bassetti M, Echols R, Matsunaga Y, et al. Efficacy and safety of cefiderocol or best available therapy for the treatment of serious infections caused by carbapenem-resistant Gram-negative bacteria (CREDIBLE-CR): a randomised, open-label, multicentre, pathogen-focused, descriptive, phase 3 trial. Lancet Infect Dis 2021; 21: 226–40.
- 2 Band VI, Satola SW, Smith RD, et al. Colistin heteroresistance is largely undetected among carbapenem-resistant Enterobacterales in the United States. *mBio* 2021; **12**: e02881–20.
- 3 Band VI, Crispell EK, Napier BA, et al. Antibiotic failure mediated by a resistant subpopulation in Enterobacter cloacae. Nat Microbiol 2016; 1: 16053.
- 4 Band VI, Satola SW, Burd EM, Farley MM, Jacob JT, Weiss DS. Carbapenem-resistant Klebsiella pneumoniae exhibiting clinically undetected colistin heteroresistance leads to treatment failure in a murine model of infection. mBio 2018; 9: e02448–17.
- 5 Hackel MA, Tsuji M, Yamano Y, Echols R, Karlowsky JA, Sahm DF. In vitro activity of the siderophore cephalosporin, cefiderocol, against carbapenem-nonsusceptible and multidrug-resistant isolates of Gram-negative bacilli collected worldwide in 2014 to 2016. Antimicrob Agents Chemother 2018; 62: e01968–17.

Structured serological testing is an essential component to investigating SARS-CoV-2 reinfection

We read with interest Belén Prado-Vivar and colleagues' findings of suspected severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) reinfection



January 20, 2021 https://doi.org/10.1016/ S1473-3099(20)30990-7 This online publication has been corrected. The corrected

been corrected. The corrected version first appeared at thelancet.com/infection on February 15, 2021 in a 46-year-old man in Ecuador.¹ As reported elsewhere,² Prado-Vivar and colleagues describe a more severe symptomatic course during the second infection than during the first. Understanding factors associated with potential reinfection might enable early decision-making for the clinical management of suspected cases. Reporting of such cases, supported by sequencing, including whole-genome sequencing (WGS), as presented by Prado-Vivar and colleagues, or Sanger sequencing, and preferably viral cell culture, is necessary to identify reinfection rather than prolonged viral shedding. Although a vital step, WGS requires retention of the initial sample and a biosafety 3 laboratory, is resource intensive,² and samples with very low viral loads might not be successfully sequenced, limiting its use as a highthroughput tool.

By comparison, serological testing is increasingly widely available, yet in cases of reinfection has so far provided little insight into whether the risk of reinfection correlates in any way with an inability to produce an effective humoral response. Prado-Vivar and colleagues' patient was IgMreactive, IgG-negative on a lateral flow assay, with presumably an assigned significance of at least an initial response to SARS-CoV-2.¹ Other reported cases of reinfection have likewise described serology at initial presentation as IgM only, negative, or not tested.² Our experience with lateral flow assays suggests that early IgM-only positive results should be interpreted with caution: six of 12 health-care workers tested in a delayed case identification programme³ underwent retesting with both an anti-nucleocapsid (anti-NP) IgG and an anti-receptor binding domain (anti-RBD) IgG assay and had a seronegative result (appendix pp 3-4). Conversely, among patients who had a documented IgG response (both anti-NP and anti-RBD), we found three cases of possible reinfection, albeit they were not substantiated by WGS (appendix pp 3-4).

We therefore strongly advocate use of a structured approach to reporting serological data alongside WGS when exploring reinfection. When high Ct values, as reported by Prado-Vivar and colleagues, are thought to correlate with low viral burden, it is possible that the initial infection could simply lack sufficient stimulation of germinal centre reactions to generate isotypeswitching and lasting, detectable antibody production.⁴ To delineate any relevance of primary infection viral burden on isotype switch, we must allow for inter-IgG class variability and consider the impact on assay selection; anti-NP IgG assays can identify previous exposure, but it is anti-RBD IgG assays that might provide further information through correlation with neutralising activity, and expression of these antibodies might be discordant.⁵ Standardising reporting of serological data for reinfection cases might help characterise the role of the humoral response in cases of reinfection, and it would appear doing so with an anti-RBD IgG assay could have greater utility.

SJCP reports receiving a research grant from the Scientific Exploration Society/Viscount Gough, outside the submitted work. RJ reports receiving honoraria, speaker fees, travel support, or research grant funding from Gilead, ViiV Healthcare, BMS, Abbvie, Janssen, and Merck, outside the submitted work. LSPM reports personal fees from Dairy Crest, DNA Electronics, Profile Pharma, Pfizer, and Umovis Lab, grants from CW+ and the National Institute for Health Research, and educational support from Eumedica, outside the submitted work. PR and GWD declare no competing interests.

Crown Copyright $\ensuremath{\mathbb{C}}$ 2021 Published by Elsevier Ltd. All rights reserved

*Scott J C Pallett, Rachael Jones, Paul Randell, Gary W Davies, Luke S P Moore

scott.pallett@nhs.net

Centre of Defence Pathology, Royal Centre for Defence Medicine, Queen Elizabeth Hospital Birmingham, Birmingham B15 2WB, UK (SJCP); Chelsea and Westminster Hospital NHS Foundation Trust, London, UK (SJCP, RJ, GWD, LSPM); North West London Pathology, London, UK (PR, LSPM); Imperial College London, NIHR Health Protection Research Unit in Healthcare Associated Infections and Antimicrobial Resistance, London, UK (LSPM)

- Prado-Vivar B, Becerra-Wong M, Jose Guadalupe J, et al. A case of SARS-CoV-2 reinfection in Ecuador. Lancet Infect Dis 2020; published online Nov 23. https://doi. org/10.1016/S1473-3099(20)30910-5.
- 2 Iwasaki A. What reinfections mean for COVID-19. Lancet Infect Dis 2020; published online Oct 12. https://doi.org/10.1016/ S1473-3099(20)30783-0.
- 3 Pallett SJC, Rayment M, Patel M, et al. Point-of-care serological assays for delayed SARS-COV-2 case identification among health-care workers in the UK: a prospective multicentre cohort study. *Lancet Resp Med* 2020; 8: 885–94.
- 4 Baumjohann D, Preite S, Reboldi A, et al. Persistent antigen and germinal center B cells sustain T follicular helper cell responses and phenotype. *Immunity* 2020; **38**: 596–605.
- 5 Rosadas C, Randell P, Khan M, McClure MO, Tedder RS. Testing for responses to the wrong SARS-CoV-2 antigen? Lancet 2020; 396: e23

Regulatory approval of COVID-19 vaccine for restricted use in clinical trial mode

Published Online January 25, 2021 https://doi.org/10.1016/ \$1473-3099(21)00045-1

See Online for appendix

Covaxin is India's first indigenous vaccine against severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), developed through a collaboration between Bharat Biotech and the National Institute of Virology, which is a branch of the Indian Council of Medical Research, the Indian official authority for medical research. The development team isolated a strain of SARS-CoV-2 from patients with asymptomatic infection and developed a vaccine on a Vero cell-line manufacturing platform to deliver the inactivated coronavirus strain. On Jan 3, 2021, the vaccine was granted approval "for restricted use in emergency situation in public interest as an abundant precaution, in clinical trial mode",1 which raised several concerns across the scientific society.²

There is an urgency and a feeling of moral obligation to get the vaccine to the public as early as possible, based on large-scale evidence on its safety and efficacy. However, the approval of a partly studied vaccine through an accelerated process on the basis of results from phase 1 and 2 clinical trials³ and incomplete data on the