SARS-CoV-2 shedding and infectivity

Fei Zhou and colleagues[1] estimated mean duration of viral shedding by assessing the presence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) viral RNA in patient samples. Assessing potential infectivity is a labour-intensive process, but the presence of nucleic acid alone cannot be used to define viral shedding or infection potential, as the authors state is possible within their methods.

For many viral diseases (SARS-CoV, Middle East respiratory syndrome coronavirus, influenza virus, Ebola virus, and Zika virus) it is well known that viral RNA can be detected long after the disappearance of infectious virus.[2–7] With measles virus, viral RNA can still be detected 6–8 weeks after the clearance of infectious virus.[8] The immune system can neutralise viruses by lysing their envelope or aggregating virus particles; these processes prevent subsequent infection but do not eliminate nucleic acid, which degrades slowly over time.

We were surprised to note the absence of viral load data in this study.[1] Although the use of sensitive PCR methods offers value from a diagnostic viewpoint, caution is required when applying such data to assess the duration of viral shedding and infection potential because PCR does not distinguish between infectious virus and non-infectious nucleic acid.

The timely publication of insightful data is paramount in responding to outbreaks of novel pathogens. However, the findings in this study should not be used to conclude prolonged viral shedding or provide rationale to amend isolation policies, as concluded by the authors; infectivity data are required to demonstrate these specific aspects.

We declare no competing interests.

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1 Zhou F, Yu T, Du R, et al. Clinical course and risk factors for mortality of adult inpatients with COVID-19 in Wuhan, China: a retrospective cohort study. *Lancet* 2020; **395:** 1054–62.
2 Peiris JS, Chu CM, Cheng VC, et al. Clinical progression and viral load in a community outbreak of coronavirus-associated SARS pneumonia: a prospective study. *Lancet* 2003; **361:** 1767–72.
3 Chan KH, Poon LL, Cheng VC, et al. Detection of SARS coronavirus in patients with suspected SARS. *Emerg Infect Dis* 2004; **10:** 294–99.
4 Oh MD, Park WB, Choe PG, et al. Viral load kinetics of MERS coronavirus infection. *N Engl J Med* 2016; **375:** 1303–05.
5 Wang Y, Guo Q, Yan Z, et al. Factors associated with prolonged viral shedding in patients with avian influenza A(H7N9) virus infection. *J Infect Dis* 2018; **217:** 1708–17.
6 Sissoko D, Duraffour S, Kerber R, et al. Persistence and clearance of Ebola virus RNA from seminal fluid of Ebola virus disease survivors: a longitudinal analysis and modelling study. *Lancet Glob Health* 2017; **5:** e80–88.
7 Paz-Bailey G, Rosenberg ES, Doyle K, et al. Persistence of Zika virus in body fluids—final report. *N Engl J Med* 2017; **379:** 1234–43.
8 Lin W-HW, Kouyos RD, Adams RJ, Grenfell BT, Griffin DE. Prolonged persistence of measles virus RNA is characteristic of primary infection dynamics. *Proc Natl Acad Sci USA* 2012; **109:** 14989–94.

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