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.

SARS-CoV-2 viral load predicts COVID-19 mortality

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) detection platforms currently report qualitative results. However, technology based on RT-PCR allows for calculation of viral load, which is associated with transmission risk and disease severity in other viral illnesses.[1] Viral load in COVID-19 might correlate with infectivity, disease phenotype, morbidity, and mortality. To date, no studies have assessed the association between viral load and mortality in a large patient cohort.[2–4] To our knowledge, we are the first to report on SARS-CoV-2 viral load at diagnosis as an independent predictor of mortality in a large hospitalised cohort (n=1145).

We prospectively evaluated nasopharyngeal swab samples for SARS-CoV-2 by real-time RT-PCR (Roche cobas 6800; Roche, Basel, Switzerland). Positive samples were assessed by a laboratory-developed quantitative RT-PCR test approved for clinical use[5] and viral loads were calculated with standard curves (full method provided in the appendix [pp 1–2]).

Viral loads for symptomatic, hospitalised patients who tested positive for SARS-CoV-2 were measured on samples collected between March 13 and May 4, 2020, that tested positive on both platforms at diagnosis. Only patients with complete survival data (discharged from or died in hospital) were included in our analysis (n=1145). Mean age was 64·6 years (SD 17·5), with 651 (56·9%) male patients, and a self-reported racial distribution of 357 (31·2%) African American patients, 335 (29·3%) white patients, 42 (3·7%) Asian patients, 375 (32·8%) patients of other race, and 36 (3·1%) patients of unknown race. The overall mean $\log_{10}$ viral load was 5·6 copies per mL (SD 3·0), and median $\log_{10}$ viral load was 6·2 copies per mL (IQR 3·0–8·0). Mean $\log_{10}$ viral load significantly differed between patients who were alive (n=807; mean $\log_{10}$ viral load 5·2 copies per mL [SD 3]) versus those who had died (n=338; 6·4 copies per mL [2·7]) by the end of the study period.

A Cox proportional hazards model adjusting for age, sex, asthma, atrial fibrillation, coronary artery disease, chronic kidney disease, chronic obstructive pulmonary disease, diabetes, heart failure, hypertension, stroke, and race yielded a significant independent association between viral load and mortality (hazard ratio 1·07 [95% CI 1·03–1·11], p=0·0014; appendix p 3), with a 7% increase in hazard for each log transformed copy per mL. A univariate survival analysis revealed a significant difference in survival probability between those with high viral load (defined as being greater than the overall mean $\log_{10}$ viral load of 5·6 copies per mL) and those with low viral load (p=0·0003; appendix p 4), with a mean follow-up of 13 days (SD 11) and a maximum follow-up of 67 days.

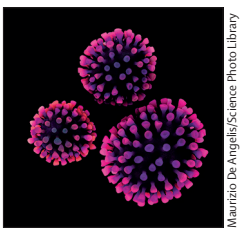
Early risk stratification in COVID-19 remains a challenge. Here, we show an independent relationship between high viral load and mortality. Transforming qualitative testing into a quantitative measurement of viral load will assist clinicians in risk-stratifying patients and choosing among available therapies and trials. Viral load might also affect isolation measures on the basis of infectivity. Future work will address SARS-CoV-2 viral load dynamics and the quantitative relationship with neutralising antibodies, cytokines, pre-existing conditions, and treatments received, among other covariates, as we develop integrative algorithms for risk prediction.

GN reports grants, personal fees, and non-financial support from Renalytix AI, non-financial support from Pensieve Health, and personal fees from AstraZeneca, BioVie, Gerson Lehrman Group, and Reata, outside of the submitted work. All other authors declare no competing interests. EP and FC contributed equally to this work.

*Elisabet Pujadas, Fayzan Chaudhry, Russell McBride, Felix Richter, Shan Zhao, Ania Wajnberg, Girish Nadkarni, Benjamin S Glicksberg, Jane Houldsworth, *Carlos Cordon-Cardo*
carlos.cordon-cardo@mssm.edu

Icahn School of Medicine at Mount Sinai, New York, NY 10029, USA

1 Drain PK, Dorward J, Bender A, et al. Point-of-care HIV viral load testing: an essential tool for a sustainable global HIV/AIDS response. *Clin Microbiol Rev* 2019; **32:** e00097-18.
2 Pan Y, Zhang D, Yang P, Poon LLM, Wang Q. Viral load of SARS-CoV-2 in clinical samples. *Lancet Infect Dis* 2020; **20:** 411–12.
3 Yu F, Yan L, Wang N, et al. Quantitative detection and viral load analysis of SARS-CoV-2 in infected patients. *Clin Infect Dis* 2020; **71:** 793–98.
4 Zheng S, Fan J, Yu F, et al. Viral load dynamics and disease severity in patients infected with SARS-CoV-2 in Zhejiang province, China, January–March 2020: retrospective cohort study. *BMJ* 2020; **369:** m1443.
5 Pujadas E, Ibeh N, Hernandez MM, et al. Comparison of SARS-CoV-2 detection from nasopharyngeal swab samples by the Roche cobas 6800 SARS-CoV-2 test and a laboratory-developed real-time RT-PCR test. *J Med Virol* 2020; published online May 8. https://doi.org/10.1002/jmv.25988.


Maurizio De Angelis/Science Photo Library

Published **Online**
August 6, 2020
https://doi.org/10.1016/S2213-2600(20)30354-4

See **Online** for appendix