About the Author

Dr. Petersen is an associate professor at the University of the Faroe Islands, a senior researcher at the Faroese Hospital System, and head of the Centre of Health Sciences, Tórshavn, Faroe Islands. Her primary research interests include epidemiological research, and she has initiated and conducted multiple COVID-19 health science research projects in the Faroe Islands.

References

1. World Health Organization. Population-based age-stratified seroepidemiological investigation protocol for coronavirus 2019 (COVID-19) infection, 2020 May 26 [cited 2020 Apr 1]. https://www.who.int/publications/i/item/WHO-2019-nCoV-Seroepidemiology-2020.2
2. Kristiansen MF, Heimustovu BH, Borg SA, Mohr TH, Gislason H, Møller LF, et al. Epidemiology and clinical course of first wave coronavirus disease cases, Faroe Islands. Emerg Infect Dis. 2021;27:749–58. https://doi.org/10.3201/eid2703.202589
3. Strøm M, Kristiansen MF, Christiansen DH, Weihe P, Petersen MS. Elimination of COVID-19 in the Faroe Islands: effectiveness of massive testing and intensive case and contact tracing. Lancet Reg Health Eur. 2021;1:100011. https://doi.org/10.1016/j.lanepe.2020.100011
4. Petersen MS, Strøm M, Christiansen DH, Fjallsbak JP, Eliasen EH, Johansen M, et al. Seroprevalence of SARS-CoV-2–specific antibodies, Faroe Islands. Emerg Infect Dis. 2020;26:2761–3. https://doi.org/10.3201/eid2611.202736
5. Pollán M, Pérez-Gómez B, Pastor-Barriuso R, Oteo J, Hernán MA, Pérez-Olmeda M, et al.; ENE-COVID Study Group. Prevalence of SARS-CoV-2 in Spain (ENE-COVID): a nationwide, population-based seroepidemiological study. Lancet. 2020;396:535–44. https://doi.org/10.1016/S0140-6736(20)31483-5
6. Bogogiannidou Z, Vontas A, Dadouli K, Kyritsi MA, Soteriades S, Nikoulis DJ, et al. Repeated leftover serosurvey of SARS-CoV-2 IgG antibodies, Greece, March and April 2020. Euro Surveill. 2020;25. https://doi.org/10.2807/1560-7917.ES.2020.25.31.2001369
7. Iversen K, Bundgaard H, Hasselbalch RB, Kristensen JH, Nielsen PB, Pries-Heje M, et al. Risk of COVID-19 in health-care workers in Denmark: an observational cohort study. Lancet Infect Dis. 2020;20:1401–8. https://doi.org/10.1016/S1473-3099(20)30589-2
8. Speybroeck N, Devleesschauwer B, Joseph L, Berkvens D. Misclassification errors in prevalence estimation: Bayesian handling with care. Int J Public Health. 2013;58:791–5. https://doi.org/10.1007/s00038-012-0439-9
9. Ioannidis JPA. Infection fatality rate of COVID-19 inferred from seroprevalence data. Bull World Health Organ. 2021;99:19–33F. https://doi.org/10.2471/BLT.20.265892
10. Stringhini S, Zaballa ME, Perez-Saez J, Pullen N, de Mestral C, Picazio A, et al.; Specchio-COVID19 Study Group. Seroprevalence of anti-SARS-CoV-2 antibodies after the second pandemic peak. Lancet Infect Dis. 2021;21:600–1. https://doi.org/10.1016/S1473-3099(21)00054-2

Address for correspondence: Maria Skaalum Petersen, Department of Occupational Medicine and Public Health, The Faroese Hospital System, Sigmundargøta 5, 100 Tórshavn, Faroe Islands; email: maria@health.fo

Postmortem Antigen-Detecting Rapid Diagnostic Tests to Predict Infectivity of SARS-CoV-2–Associated Deaths

Fabian Heinrich, Ann Sophie Schröder, Anna-Lina Gerberding, Moritz Gerling, Felicia Langenwalder, Philine Lange, Axel Heinemann, Eric Bibiza-Freiwald, Dominik Sebastian Nörz, Martin Aepfelbacher, Susanne Pfefferle,[1] Benjamin Ondruschka,[1] Marc Lütgehetmann[1]

Author affiliation: University Medical Center Hamburg-Eppendorf, Hamburg, Germany

We investigated the infectivity of 128 severe acute respiratory disease coronavirus 2–associated deaths and evaluated predictive values of standard diagnostic procedures. Maintained infectivity (20%) did not correlate with viral RNA loads but correlated well with anti-S antibody levels. Sensitivity >90% for antigen-detecting rapid diagnostic tests supports their usefulness for assessment.

DOI: https://doi.org/10.3201/eid2801.211749

Deaths associated with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) have raised concerns that contact with the corpses of deceased persons might pose a risk for transmitting infection (*1*). Nasopharyngeal SARS-CoV-2 RNA loads were shown to remain stable up to 20 days postmortem (*2*), and the maintained infectivity of corpses has sporadically been examined (*2*–*4*). In contrast, body surfaces of corpses have been considered noninfectious (*5*). Systematic studies on the infectivity of corpses and predictive values of standard diagnostic procedures remain scarce.

For this study, we prospectively collected nasopharyngeal swab specimens from 128 SARS-CoV-2 RNA-positive and 72 RNA-negative corpses ≤14 days postmortem to assess infectivity and predictive values of virologic parameters (Table). We excluded corpses exhibiting advanced putrefaction. For initial assessment, we determined RNA loads using quantitative reverse transcription PCR (qRT-PCR) (Appendix, https://wwwnc.cdc.gov/EID/article/28/1/21-1749-App1.pdf).

We found SARS-CoV-2 RNA up to 325 hours postmortem, but RNA loads did not correlate with

[1]These senior authors contributed equally to this article.

Table. Baseline characteristics of corpses received by the Institute of Legal Medicine, Hamburg, Germany, 2020–2021*

Characteristic	SARS-CoV-2 RNA positive,† n = 128	SARS-CoV-2 RNA negative,† n = 72	Total, n = 200
Age, y, median (IQR)	83.5 (71.5–89.1)	81.0 (73.0–87.0)	82.3 (72.9–88.5)
Sex			
M	71 (55.5)	36 (50.0)	107 (53.5)
F	57 (44.5)	36 (50.0)	93 (46.5)
Place of death			
Home	28 (22.0)	30 (41.7)	58 (29.1)
Nursing home	38 (29.9)	3 (4.2)	41 (20.6)
Hospital	39 (30.7)	25 (34.7)	64 (32.2)
ICU	20 (15.7)	10 (13.9)	30 (15.1)
Other	2 (1.6)	4 (5.6)	6 (3.0)
Postmortem interval,‡ h, median (IQR)	8.7 (5.3–82.6)	4.9 (3.5–8.8)	7.0 (4.3–49.9)
Putrefactive changes	11 (8.9)	1 (1.4)	12 (6.1)
SARS-CoV-2 RNA load,¶ copies/mL, median (IQR)	7.0×10^6 (5.5×10^4–5.2×10^7)	Below LOD	Not applicable

*Values are no. (%) except as indicated. In case of missing data points, valid percentages are indicated. ICU, Intensive care unit; LOD, limit of detection; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2
†B.1.1.7 variants (2/128) identified by multiplex-typing PCR (*5*). SARS-CoV-2–associated deaths were tested in a multiplex typing PCR for SARS-CoV-2 spike variants.
‡Interval from time of death until initial sampling and cooling at 4°C.

the postmortem interval (PMI; r = 0.003, p >0.99) (Figure, panel A). RNA loads were comparatively high (median 7.0×10^6 copies/mL, interquartile range [IQR] 5.5×10^4–5.2×10^7 copies/mL) (Figure, panel B) and in some cases exceeded loads in the acute phase of the disease (*6*), possibly because of postmortem mucosal softening and higher exfoliation of tissue during sample collection.

Virus isolation proved infectivity was maintained in 26/128 (20%) corpses (Appendix). PMI (median 13

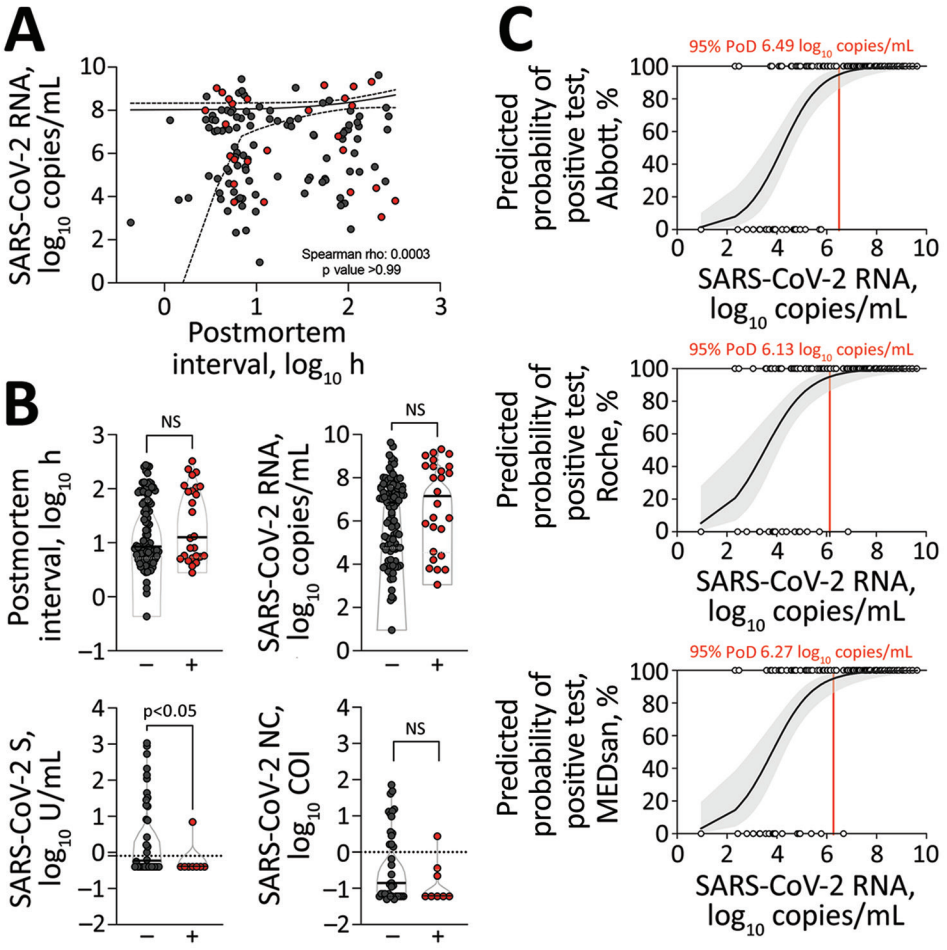

Figure. Overview of 128 consecutive records of SARS-CoV-2–associated deaths received by the Institute of Legal Medicine, Hamburg, Germany, 2020–2021. A) SARS-CoV-2 RNA loads by postmortem intervals. Spearman correlation was performed; estimates and 95% CI are shown. B) Postmortem intervals, viral RNA loads, quantitative (S), and qualitative (NC) antibody levels compared among culture-positive (+) and culture-negative (–) corpses. Comparisons were performed using Mann-Whitney-U or χ^2 testing, as appropriate. Median and interquartile ranges are shown. Horizontal dotted lines indicate cutoff value. C) Probability of positive antigen-detecting rapid diagnostic test results depending on viral RNA loads calculated by binomial logistic regression. Robust estimates with 95% CI are shown. Vertical red line indicates 95% PoD with the corresponding viral RNA load. Ag-RDT, antigen-detecting rapid antigen test; COI, cut-off index; NC, nucleocapsid; NS, not significant; PoD, probability of detection; S, spike; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

hours, range 3–325 hours) and SARS-CoV-2 RNA load (1.4×10^7 copies/mL, IQR 3.7×10^4–3.3×10^8) among culture-positive corpses did not differ significantly from PMI (median 8 hour, range 0–275 hour; p = 0.38) and RNA loads (7.0×10^6 copies/mL, IQR 5.8×10^4–3.9×10^7 copies/mL; p = 0.14) among culture-negative corpses (Figure, panel B). We successfully isolated virus from samples with comparatively low amounts of RNA (<1×10^4 copies/mL), in contrast with previous findings among living patients (*6*). We observed putrefactive changes in no culture-positive corpses compared with in 11/98 (11%) culture-negative corpses ($\chi^2 = 3.20$; p = 0.11), indicative of potentially decreased infectivity.

We confirmed seroconversion in 18/44 (41%) blood samples, 15/43 (35%) anti-nucleocapsid positive and 17/44 (39%) anti-spike positive (range <0.4–1066.0 U/mL; Appendix). Levels of anti-spike antibodies, representing neutralizing antibody levels (*7*), were not significantly correlated with PMI (r = 0.07; p = 0.64), but were well correlated with viral RNA levels (r = –0.70; p <0.0001). Anti-nucleocapsid antibodies were found in only 1/8 (13%) culture-positive compared with 14/35 (40%) culture-negative corpses ($\chi^2 = 2.17$; p = 0.23) (Figure, panel C). Moreover, anti-spike antibody levels differed significantly (p = 0.04) between culture-positive (1.22 U/mL, SD 2.32) and culture-negative (86.85 U/mL, SD 240.56) corpses, indicative of inverse association of SARS-CoV-2–specific antibody levels with infectivity (Figure, panel C).

Antigen-detecting rapid diagnostic tests (Ag-RDTs) are considered adequate alternative swift diagnostic tools in living patients (*8*,*9*), but knowledge about their postmortem applicability and reliability remains scarce. We tested Ag-RDTs from 3 manufacturers and found excellent performance for postmortem use (Appendix Table 1). Compared with qRT-PCR results, for the Panbio COVID-19 Ag Rapid Test Device (Abbott, https://www.abbott.com), sensitivity was 80.3% (95% CI 72.3%–86.4%) and specificity 100.0% (95% CI 95.0%–100.0%); for the SARS-CoV-2 Rapid Antigen Test (Roche https://www.roche.com), sensitivity was 86.4% (95% CI 79.1%–91.9%) and specificity 98.6% (95% CI 93.0%–100.0%); and for the SARS-CoV-2 Antigen Rapid Test (MEDsan https://www.medsan.eu), sensitivity was 84.1% (95% CI 76.6%–90.0%) and specificity 95.8% (95% CI 88.0%–99.0%) (Appendix Figures 1, 2).

We found SARS-CoV-2 RNA load correlated with Ag-RDT positivity in univariate and multivariate analyses (p<0.001), thereby confirming their predictive value (Figure, panel C; Appendix Table 2). Subgroup analyses of corpses with >1×10^6 RNA copies/mL (n = 74) revealed 100% (95% CI 95.1%–100.0%) sensitivity in Abbott (n = 74) and Roche and MEDsan (n = 73 each) assays. In contrast, neither PMI (p = 0.34) nor putrefactive changes (p = 0.90) were predictive for testing positive in Ag-RDTs (exemplarily for the MEDsan assay; Appendix Table 2). Ag-RDT sensitivity in infectious corpses was 92.3% (95% CI 74.9%–99.1%) for Abbott, 96.2% (95% CI 80.4%–99.9%) for Roche, and 96.2% (95% CI 80.4%–99.9%) for MEDsan. We detected 2 SARS-CoV-2 variants of concern despite relatively low viral RNA loads (4.83 $\log_{10}$); the 2 samples tested positive by Abbott and Roche but were missed by MEDsan.

The first limitation of our study is that blood was not available from all corpses, and the serologic assays and Ag-RDTs used are not approved for cadaveric samples. Furthermore, because of a shortage of reagents and supplies, we had to use different tests to quantify RNA, and slight deviations cannot be ruled out.

In summary, we show that cadavers from SARS-CoV-2–associated deaths remain infectious long after death in a considerable proportion of cases. Postmortem infectivity does not correlate with PMI or viral RNA load but correlates with the absence of virus-specific antibodies. Ag-RDTs performed well, enabling rapid on-site detection. Because previous studies among living patients indicate that Ag-RDTs reliably detect all SARS-CoV-2 variants (*10*), we believe that our results on postmortem Ag-RDTs use can contribute to crisis management in severely affected regions and increase safety in the medical sector worldwide.

Acknowledgments

We thank Jessica Vering for her technical support and Daniela Fröb for managing records of SARS-CoV-2–associated deaths within the Institute of Legal Medicine. We offer condolences to the families and friends of all patients whose deaths were attributable to COVID-19.

The ethics committee of the Hamburg Chamber of Physicians approved this study (reference no. 2020-10353-BO-ff and PV7311).

This work was funded within the research consortium DEFEAT PANDEMIcs (grant number 01KX2021), part of National Network University Medicine, funded by the Federal Ministry of Education and Research of Germany. National Network University Medicine is coordinated at the Charité-Universitätsmedizin Berlin and supervised by the DLR Project Management Agency at the German Aerospace Center. The funders had no role in study design, data collection or analysis, decision to publish, or preparation of the manuscript.

About the Author

Mr. Heinrich is a medical student employed at the Institute of Legal Medicine, University Medical Center Hamburg-Eppendorf. His primary research interests include infectiologic and immunologic research.

References

1. World Health Organization. WHO coronavirus (COVID-19) dashboard [cited 2021 May 13] https://covid19.who.int
2. Heinrich F, Meißner K, Langenwalder F, Püschel K, Nörz D, Hoffmann A, et al. Postmortem stability of SARS-CoV-2 in nasopharyngeal mucosa. Emerg Infect Dis. 2021;27:329–31. https://doi.org/10.3201/eid2701.203112
3. Plenzig S, Bojkova D, Held H, Berger A, Holz F, Cinatl J, et al. Infectivity of deceased COVID-19 patients. Int J Legal Med. 2021;135:2055–60. https://doi.org/10.1007/s00414-021-02546-7
4. Zacharias M, Stangl V, Thüringer A, Loibner M, Wurm P, Wolfgruber S, et al. Rapid antigen test for postmortem evaluation of SARS-CoV-2 carriage. Emerg Infect Dis. 2021;27:1734–7. https://doi.org/10.3201/eid2706.210226
5. Schröder AS, Edler C, Ondruschka B, Püschel K, Schädler J, Heinemann A, et al. The handling of SARS-CoV-2 associated deaths—infectivity of the body. Forensic Sci Med Pathol. 2021;17:411–8. https://doi.org/10.1007/s12024-021-00379-9
6. Jones TC, Biele G, Mühlemann B, Veith T, Schneider J, Beheim-Schwarzbach J, et al. Estimating infectiousness throughout SARS-CoV-2 infection course. Science. 2021;373:eabi5273. https://doi.org/10.1126/science.abi5273
7. Meyer B, Torriani G, Yerly S, Mazza L, Calame A, Arm-Vernez I, et al.; Geneva Center for Emerging Viral Diseases. Validation of a commercially available SARS-CoV-2 serological immunoassay. Clin Microbiol Infect. 2020;26:1386–94. https://doi.org/10.1016/j.cmi.2020.06.024
8. World Health Organization. Antigen-detection in the diagnosis of SARS-CoV-2 infection [cited 2020 Aug 11]. https://www.who.int/publications/i/item/antigen-detection-in-the-diagnosis-of-sars-cov-2infection-using-rapid-immunoassays
9. Dinnes J, Deeks JJ, Adriano A, Berhane S, Davenport C, Dittrich S, et al.; Cochrane COVID-19 Diagnostic Test Accuracy Group. Rapid, point-of-care antigen and molecular-based tests for diagnosis of SARS-CoV-2 infection. Cochrane Database Syst Rev. 2020;8:CD013705.
10. Osmanodja B, Budde K, Zickler D, Naik MG, Hofmann J, Gertler M, et al. Accuracy of a novel SARS-CoV-2 antigen-detecting rapid diagnostic test from standardized self-collected anterior nasal swabs. J Clin Med. 2021;10:2099. https://doi.org/10.3390/jcm10102099

Addresses for correspondence: Fabian Heinrich, Institute of Legal Medicine, University Medical Center Hamburg Eppendorf, Butenfeld 34, 20259 Hamburg, Germany; email: fa.heinrich@uke.de; Susanne Pfefferle, Institute of Medical Microbiology, Virology and Hygiene, University Medical Center Hamburg Eppendorf, Martinistraße 52, 22529 Hamburg, Germany; email: s.pfefferle@uke.de

Monitoring International Travelers Arriving in Hong Kong for Genomic Surveillance of SARS-CoV-2

Haogao Gu, Samuel S.M. Cheng, Pavithra Krishnan, Daisy Y.M. Ng, Lydia D.J Chang, Gigi Y.Z. Liu, Sammi S.Y. Cheuk, Mani M.Y. Hui, Mathew C.Y. Fan, Jacob H.L. Wan, Leo H.K. Lau, Daniel K.W. Chu, Vijaykrishna Dhanasekaran, Malik Peiris, Leo L.M. Poon

Author affiliations: University of Hong Kong School of Public Health, Hong Kong, China (H. Gu, S.S.M. Cheng, P. Krishnan, D.Y.M. Ng, L.D.J. Chang, G.Y.Z. Liu, S.S.Y. Cheuk, M.M.Y. Hui, M.C.Y. Fan, J.H.L. Wan, L.H.K. Lau, D.K.W. Chu, V. Dhanasekaran, M. Peiris, L.L.M. Poon); HKU-Pasteur Research Pole, University of Hong Kong, Hong Kong (V. Dhanasekaran, M. Peiris, L.L.M. Poon); Centre for Immunology and Infection, Hong Kong (M. Peiris, L.L.M. Poon)

DOI: https://doi.org/10.3201/eid2801.211804

We sequenced ≈50% of coronavirus disease cases imported to Hong Kong during March–July 2021 and identified 70 cases caused by Delta variants of severe acute respiratory syndrome coronavirus 2. The genomic diversity detected in Hong Kong was similar to global diversity, suggesting travel hubs can play a substantial role in surveillance.

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) lineage B.1.617 (*1*) and 3 of its sublineages, B.1.617.1 (Kappa), B.1.617.2 (Delta), and B.1.617.3, were first detected in India. The Delta variant started circulating widely in different continents beginning in late March 2021 (*2*,*3*). It was initially classified as a variant of interest in April 2021 and then reclassified as a variant of concern in May 2021.

Hong Kong adopted an elimination strategy to control coronavirus disease (COVID-19). A previous study reported the use of stringent measures (e.g., mandatory COVID-19 testing, travel restrictions) to detect and prevent SARS-CoV-2 importation by COVID-19–positive travelers (*4*), thereby reducing the risk of new SARS-CoV-2 introductions, and also showed that regional and international airports could be useful sentinel surveillance sites to monitor SARS-CoV-2 circulation. In this study, we tested the feasibility of using surveillance strategies similar to those used in that study to monitor sequence diversity of Delta variant