Table 2. Adjusted Relative Risk Between Receipt of Unemployment Insurance Benefits and Health-Related Social Needs, Health Care Access, and Mental Health Outcomes[a]

Outcome	Relative risk (95% CI)[b,c]	P value[c]	Q value
Food insufficiency	0.83 (0.77-0.88)	<.001	<.001
Missed housing payment	0.63 (0.58-0.69)	<.001	<.001
Lacking confidence in affording next month			
Food	0.94 (0.92-0.97)	<.001	<.001
Housing	0.84 (0.80-0.88)	<.001	<.001
Uninsured	0.97 (0.92-1.03)	.36	.36
Delayed health care	0.93 (0.89-0.98)	.003	.003
Delayed non-COVID-19 health care	0.91 (0.87-0.96)	<.001	<.001
PHQ2 depression score ≥3[d]	0.90 (0.85-0.95)	<.001	<.001
GAD2 anxiety score ≥3[d]	0.93 (0.89-0.97)	.001	.001

Abbreviations: COVID-19, coronavirus disease 2019; GAD2, Generalized Anxiety Disorder 2-item; PHQ2, Patient Health Questionnaire-2.

[a] Models were adjusted for age, gender, race/ethnicity, education level, income, household size, marital status, state, and week of survey. The models for food insufficiency and lacking confidence in affording food next month were additionally adjusted for prepandemic food insufficiency.

[b] Relative risk compares risk for outcome in those who received unemployment insurance benefits to those who did not receive unemployment insurance benefit. A relative risk <1 indicates lower risk for a given outcome (eg, less likely to experience food insufficiency).

[c] Point estimates, 95% CIs, and P values are from log-Poisson regression models fit using generalized estimating equations (to account for repeated survey responses within individuals), person weights, and robust variance estimation. Models were fit in 10 Markov Chain Monte Carlo multiple imputation data sets and combined for a summary estimate.

[d] For the PHQ2 and GAD2, scores range from 0 to 6 (more depressive or anxiety symptoms); in keeping with scoring recommendations, we used a cut point of ≥3 on both to indicate potentially clinically significant symptoms.

Seth A. Berkowitz, MD, MPH
Sanjay Basu, MD, PhD

Author Affiliations: Division of General Medicine and Clinical Epidemiology, Department of Medicine, University of North Carolina at Chapel Hill School of Medicine (Berkowitz); Center for Primary Care, Harvard Medical School, Boston, Massachusetts (Basu).

Corresponding Author: Seth A. Berkowitz, MD, MPH, Division of General Medicine and Clinical Epidemiology, Department of Medicine, University of North Carolina at Chapel Hill, 5034 Old Clinic Bldg, CB 7110, Chapel Hill, NC 27599 (seth_berkowitz@med.unc.edu).

1. US Department of Labor. Unemployment insurance weekly claims. Accessed August 4, 2020. https://www.dol.gov/ui/data.pdf

2. Coronavirus Aid, Relief, and Economic Security (CARES) Act, S 3548, 116th Cong (2019-2020). Accessed August 4, 2020. https://www.congress.gov/bill/116th-congress/senate-bill/3548/text?q=product+actualizaci%C3%B3n

3. Renahy E, Mitchell C, Molnar A, et al. Connections between unemployment insurance, poverty and health: a systematic review. *Eur J Public Health*. 2018;28(2):269-275. doi:10.1093/eurpub/ckx235

4. Alaimo K, Briefel RR, Frongillo EA Jr, Olson CM. Food insufficiency exists in the United States: results from the third National Health and Nutrition Examination Survey (NHANES III). *Am J Public Health*. 1998;88(3):419-426. doi:10.2105/AJPH.88.3.419

5. Kroenke K, Spitzer RL, Williams JBW. The Patient Health Questionnaire-2: validity of a two-item depression screener. *Med Care*. 2003;41(11):1284-1292. doi:10.1097/01.MLR.0000093487.78664.3C

6. Kroenke K, Spitzer RL, Williams JBW, Monahan PO, Löwe B. Anxiety disorders in primary care: prevalence, impairment, comorbidity, and detection. *Ann Intern Med*. 2007;146(5):317-325. doi:10.7326/0003-4819-146-5-200703060-00004

Assessment of SARS-CoV-2 RNA Test Results Among Patients Who Recovered From COVID-19 With Prior Negative Results

Some patients who have recovered from coronavirus disease 2019 (COVID-19) with documented negative real-time polymerase chain reaction (RT-PCR) results at the time of recovery have had subsequent positive RT-PCR test results for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)[1,2] in the absence of any symptoms suggestive of new infection.[3] It is unknown whether such patients are infectious and whether they should be quarantined. Real-time PCR is not a viral culture and does not allow determination of whether the virus is viable and transmissible. We investigated RT-PCR retested positive nasal/oropharyngeal swab (NOS) samples from recovered patients

Supplemental content

Table. Testing Results for NOS Samples Obtained at COVID-19 Diagnosis or After COVID-19 Recovery in 32 Study Patients[a]

Sample No.	COVID-19 samples tested								RNA load, copies/mL	Serology (positive or negative result)		Days of recovery sampling since diagnosis
	Diagnosis				Recovery							
	Genomic RNA (C$_T$ value)			Subgenomic RNA (C$_T$ value)	Genomic RNA (C$_T$ value)			Subgenomic (C$_T$ value)				
	E gene	*RdRP* gene	*N* gene	*E* gene	*E* gene	*RdRP* gene	*N* gene	*E* gene	*N* gene	IgG	IgA	
1	31.6	31.3	31.2	34.5	29.3	30.7	31.2	39.1	1.2×10^4	Positive	Positive	39
2	27.0	26.9	30.0	36.0	30.0	30.5	31.2		8.9×10^3	Positive	Positive	31
3	19.3	20.8	22.1	35.2	31.5	34.7	32.8		3.3×10^3	Positive	Negative	44
4	21.6	22.0	22.9	36.4	31.8	31.4	32.3		5.5×10^3	Positive	Positive	34
5	30.0	32.8	38.1	30.2	31.8	34.3	34.5		3.2×10^3	Positive	Positive	62
6	20.8	20.9	22.3	37.3	32.2	32.8	34.1		5.3×10^3	Positive	Positive	37
7	27.3	29.9	31.3	36.9	32.3	30.9	32.7		6.4×10^3	Positive	Positive	39
8	26.9	27.0	31.2	38.1	35.0	34.4	36.1		4.0×10^2	Positive	Positive	71
9	22.5	23.7	24.9	31.0	38.8	33.6	33.9		2.6×10^3	Negative	Negative	42
10	21.3	21.4	28.9	38.9		32.2	33.4		1.2×10^4	Positive	Positive	56
11	26.6	26.9	28.1	33.0		32.8	33.2		1.3×10^4	Positive	Positive	54
12	22.8	24.2	25.3	31.0		34.2	33.7		6.9×10^3	Positive	Positive	55
13	25.8	25.8	26.1	39.8	NA	34.8	39.1		3.0×10^2	Positive	Positive	36
14	20.8	20.4	21.1	32.0		35.0	35.1		1.9×10^3	Positive	Positive	56
15	29.4	30.1	32.2	37.0		36.5	39.2		3.2×10^3	Positive	Positive	36
16	27.9	29.1	31.1	32.0		38.1	39.3		1.6×10^1	Positive	Positive	77
17	30.6	29.9	31.8	32.1			35.7	NA	5.4×10^3	Positive	Positive	53
18	28.5	29.1	30.8	36.8			36.8		2.9×10^3	Positive	Positive	43
19	26.9	22.2	26.1	30.1			37.5		1.1×10^3	Positive	Positive	36
20	25.7	25.2	28.9	38.0			37.9		2.6×10^3	Positive	Positive	48
21	27.0	29.0	30.2	32.3			38.1		1.9×10^3	Positive	Positive	41
22	28.5	29.4	30.0	32.3			38.4		4.9×10^1	Positive	Negative	76
23	27.1	28.6	29.3	36.1			38.9		4.5×10^2	Positive	Positive	29
24	25.4	22.9	24.1	34.8	NA		39.0		5.6×10^1	Positive	Positive	70
25	28.7	29.5	31.4	37.3			39.1		5.4×10^3	Negative	Positive	46
26	27.1	27.7	29.2	37.1			39.1		1.9×10^3	Positive	Positive	34
27	26.7	27.7	29.6	39.2			39.2		2.0×10^3	Positive	Positive	45
28	17.1	19.1	19.9	33.0			39.2		8.5×10^2	Positive	Positive	40
29	27.0	28.9	30.0	32.1			39.3		5.0×10^1	Positive	Positive	56
30	22.9	23.8	25.8	37.1			39.4		1.6×10^2	Positive	Positive	55
31	28.6	30.4	30.9	33.0			39.6		5.3×10^2	Positive	Positive	61
32	29.1	28.0	30.9	36.2			39.8		3.4×10^2	Positive	Positive	53

Abbreviations: COVID-19, coronavirus disease 2019; C$_T$, cycle threshold; *E* gene, envelope gene; NA, not applicable; *N* gene, nucleocapsid gene; *RdRP*, RNA-dependent RNA polymerase; RT-PCR, real-time polymerase chain reaction.

[a] For RT-PCR testing, the Seegene Allplex 2019-nCoV and Clonit Quanty COVID-19 assays were used for total RNA detection and quantification, respectively, whereas replicative (*E* gene) RNA was detected by an in-house RT-PCR assay.[4] Results were expressed as C$_T$ values (<40 for positive detection) or quantified as RNA (*N* gene) copies per mL. NA indicates the absence of positive detection for the indicated gene. For serological testing, SARS-CoV-2 IgG/IgA Euroimmun enzyme-linked immunoassays were used, and positive and negative results were assessed using the 1.1 or greater or less than 1.1 times the manufacturer's cutoffs as reference IgG/IgA values, respectively.

with COVID-19 with prior negative results for the presence of replicative SARS-CoV-2 RNA.[4]

Methods | We studied 176 recovered patients with COVID-19 who were admitted to the postacute outpatient service of our institution (Rome, Italy) from April 21 to June 18, 2020, for COVID-19 follow-up.[5,6] Before that, patients had discontinued isolation according to current criteria,[5] which require no fever for 3 consecutive days, improvement in other symptoms, and 2 negative RT-PCR results for SARS-CoV-2 RNA 24 hours apart.

Nasal/oropharyngeal swab samples from patients at follow-up were analyzed for total (genomic) and replicative (subgenomic) SARS-CoV-2 RNA using RT-PCR assays (eMethods in the Supplement). For patients with positive results for total RNA, samples previously obtained at the time of COVID-19 diagnosis and kept at −112 °F until testing were also tested for replicative RNA. Serological testing was performed for SARS-CoV-2 IgG/IgA detection (eMethods in the Supplement). The ethics committee of the Fondazione Policlinico Universitario A. Gemelli IRCCS (Rome, Italy) approved the study, and written informed consent was obtained from each patient.

Results | As shown in the **Table**,[4] 32 of 176 NOS samples (18.2%) tested positive for total SARS-CoV-2 RNA, with viral loads ranging from 1.6×10^1 to 1.3×10^4 SARS-CoV-2 RNA copies per mL. One of the 32 samples (3.1%) had replicative SARS-CoV-2 RNA.

Samples from the 32 patients at the time of COVID-19 diagnosis were also tested and, expectedly, had replicative SARS-CoV-2 RNA. All but 1 of 32 patients had a positive serology result against SARS-CoV-2 (Table), as well as 139 of remaining 144 patients (data not shown), at COVID-19 follow-up. The patient who tested serologically negative was not the one with a positive test result for replicative SARS-CoV-2 RNA. The mean (SD) time from COVID-19 diagnosis to follow-up was 48.6 (13.1) days in 32 patients (Table) and 57.7 (16.9) days in 144 patients (data not shown).

Discussion | Similar to that reported elsewhere,[2] 18% of patients with COVID-19 in our institution became RT-PCR positive for SARS-CoV-2 RNA after clinical recovery and previous negative results.[5] As positivity in the patients was suggestive, but not necessarily a reflection, of viral carriage, we used replicative SARS-CoV-2 RNA detection as a proxy for virus replication in culture.[4]

Only 1 of 32 patients retesting positive had replicating virus in the NOS sample, suggesting either recurrent infection or reinfection, which is impossible to separate because no whole-genome sequencing and phylogenetic analyses were performed.[3] The patient retested positive 16 days after COVID-19 recovery (ie, 39 days from COVID-19 diagnosis) and was symptomatic. The patient was an older adult with hypertension, diabetes, and cardiovascular disease but no evidence of close contacts with people with SARS-CoV-2 infection or persons who became RT-PCR positive. In the 31 remaining patients (who were asymptomatic), their positive result likely represented either recurrent or resolving infection, but in either case, they were unlikely to be infectious. The limitations of our study are the lack of data from viral cultures or whole-genome sequencing analysis and the small sample size.

Conclusions | This study highlights that many patients who recovered from COVID-19 may be still positive (albeit at lower levels) for SARS-CoV-2 RNA, but only a minority of the patients may carry a replicating SARS-CoV-2 in the respiratory tract. Further studies are needed to verify whether such patients can transmit the virus.

Flora Marzia Liotti, PhD
Giulia Menchinelli, PhD
Simona Marchetti, BSc
Brunella Posteraro, PhD
Francesco Landi, MD
Maurizio Sanguinetti, MD
Paola Cattani, MD

Author Affiliations: Dipartimento di Scienze Biotecnologiche di Base, Cliniche Intensivologiche e Perioperatorie, Università Cattolica del Sacro Cuore, Rome, Italy (Liotti, Menchinelli, Posteraro, Sanguinetti, Cattani); Dipartimento di Scienze di Laboratorio e Infettivologiche, Fondazione Policlinico Universitario A. Gemelli IRCCS, Rome, Italy (Liotti, Menchinelli, Sanguinetti, Cattani); Dipartimento di Scienze Mediche e Chirurgiche, Fondazione Policlinico Universitario A. Gemelli IRCCS, Rome, Italy (Posteraro); Dipartimento di Scienze dell'Invecchiamento, Neurologiche, Ortopediche e della Testa-Collo, Fondazione Policlinico Universitario A. Gemelli IRCCS, Rome, Italy (Landi).

Corresponding Author: Brunella Posteraro, PhD, Dipartimento di Scienze Mediche e Chirurgiche, Fondazione Policlinico Universitario A. Gemelli IRCCS, Largo A. Gemelli 8, 00168 Rome, Italy (brunella.posteraro@unicatt.it).

1. Lan L, Xu D, Ye G, et al. Positive RT-PCR test results in patients recovered from COVID-19. *JAMA*. 2020;323(15):1502-1503. doi:10.1001/jama.2020.2783

2. Kang H, Wang Y, Tong Z, Liu X. Retest positive for SARS-CoV-2 RNA of "recovered" patients with COVID-19: Persistence, sampling issues, or re-infection? *J Med Virol*. 2020;1-3. doi:10.1002/jmv.26114

3. Alvarez-Moreno CA, Rodríguez-Morales AJ. Testing dilemmas: post negative, positive SARS-CoV-2 RT-PCR—is it a reinfection? *Travel Med Infect Dis*. 2020;35: 101743. doi:10.1016/j.tmaid.2020.101743

4. Wölfel R, Corman VM, Guggemos W, et al. Virological assessment of hospitalized patients with COVID-2019. *Nature*. 2020;581(7809):465-469. doi:10.1038/s41586-020-2196-x

5. Carfì A, Bernabei R, Landi F; for the Gemelli Against COVID-19 Post-Acute Care Study Group. Persistent symptoms in patients after acute COVID-19. *JAMA*. 2020;324(6):603-605. doi:10.1001/jama.2020.12603

6. Gemelli Against COVID-19 Post-Acute Care Study Group. Post-COVID-19 global health strategies: the need for an interdisciplinary approach. *Aging Clin Exp Res*. 2020;32(8):1613-1620.

Editor's Note

Challenges in Testing for SARS-CoV-2 Among Patients Who Recovered From COVID-19

Among patients who have recovered from COVID-19, repeated testing for SARS-CoV-2 may be done weeks or months after infection either as part of routine screening (eg, screening nursing home personnel on a weekly basis to prevent transmission of infections to patients) or because of the development of symptoms that are worrisome for reinfection. Unfortunately, the interpretation of positive test results in patients who have previously recovered from COVID-19 is fraught. The best widely available test, a real-time polymerase chain reaction (RT-PCR), is very sensitive for fragments of viral RNA and can be positive because of nonviable remnants of the virus. Currently, there is not a widely available test for determining whether the virus can reproduce and transmit infection.

In this issue of *JAMA Internal Medicine*, Liotti et al[1] describe the results of retesting 176 patients who had recovered

from COVID-19 with 2 negative RT-PCR test results 24 hours apart. At a mean of 48.6 days from their date of diagnosis, 32 patients (18.2%) had a positive PCR test result for SARS-CoV-2 RNA. Using a specialized assay, only 1 of these 32 patients (3.1%) had evidence of RNA capable of replication. Although this study cannot solve the challenge of interpreting positive PCR results in recovered patients, the data help us to better understand the scope of the problem.

To avoid unnecessary quarantine for patients who have recovered from COVID-19, routine repeated PCR testing should not be done in the 90 days following infection. However, more complicated is what to do about patients who are symptomatic and have positive results on repeated PCR tests. Reinfection with SARS-CoV-2 has been documented[2] (based on demonstration of different genetic differences between the viruses infecting the person on the first and second episode) but is rare. Until clinical laboratories have the capability to test for the reproductive capacity of coronavirus, interpretation of the epidemiologic significance of positive PCR results among recovered patients will remain challenging.

Mitchell H. Katz, MD

Author Affiliation: NYC Health and Hospitals, New York, New York.
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Corresponding Author: Mitchell H. Katz, MD, NYC Health and Hospitals, 125 Worth St, Room 514, New York, NY 10013 (mitchell.katz@nychhc.org).

1. Liotti FM, Menchinelli G, Marchetti S, et al. Positive SARS-CoV-2 RNA test results among patients who recovered from COVID-19 with prior negative results. *JAMA Intern Med*. Published online November 12, 2020. doi:10.1001/jamainternmed.2020.7570

2. Tillett RL, Sevinsky JR, Hartley PD, et al. Genomic evidence for reinfection with SARS-CoV-2: a case study. *Lancet Infect Dis*. 2020;2:30764-30767. doi:10.1016/S1473-3099(20)30764-7

Excess Mortality in California During the Coronavirus Disease 2019 Pandemic, March to August 2020

Few studies on excess deaths during the coronavirus disease 2019 (COVID-19) pandemic in the US have documented how excess mortality varies across population subgroups.[1,2] Using time-series models, we estimated excess deaths in California between March and August 2020 by age, sex, race/ethnicity, and educational level. California has a population of 39.5 million, which is approximately 12% of the US population of 328.2 million.

Methods | Using California Department of Public Health data on deaths occurring on or after January 1, 2016, we estimated excess deaths during 2 COVID-19 pandemic periods: March 1 through May 9, 2020 (statewide shelter-in-place), and May 10 through August 22, 2020 (reopening). This study followed the Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) reporting guideline. The study protocol was reviewed and approved by the institutional

Table. Excess Deaths Attributable to the COVID-19 Pandemic in California From March to August 2020, Using Time-Series Analysis of January 2016 to February 2020 Deaths

Variable	Excess deaths (95% PI)		Excess deaths per capita per week (95% PI)[a]		
	Total	Per capita[a]	March-April	May-August	Change[b]
Entire state	19 806 (16 364-23 210)	501 (414-587)	12 (8-16)	26 (21-30)	2.2
Age, y					
0-24	254 (53-453)	20 (4-36)	0 (0-1)	1 (0-2)	2.9
25-54	3377 (2987-3760)	207 (183-230)	4 (3-6)	11 (10-12)	2.7
55-64	2713 (2445-2980)	567 (511-623)	12 (8-16)	30 (27-33)	2.5
65-74	3564 (2947-4171)	1052 (870-1232)	24 (15-33)	54 (46-62)	2.2
75-84	4488 (3589-5377)	2638 (2109-3160)	71 (47-95)	128 (103-153)	1.8
≥85	5135 (3922-6307)	6849 (5230-8411)	171 (73-267)	342 (257-423)	2.0
Sex[c]					
Women	8182 (6913-9420)	596 (504-686)	13 (8-19)	31 (26-35)	2.3
Men	11 351 (9286-13 398)	859 (703-1014)	21 (14-28)	43 (36-51)	2.1
Race/ethnicity[c]					
Asian	2077 (1602-2546)	476 (367-583)	16 (11-22)	21 (16-26)	1.3
Black	1882 (1624-2135)	1206 (1041-1369)	40 (32-49)	54 (46-61)	1.3
Latino	8439 (7359-9493)	922 (804-1038)	16 (12-21)	51 (45-56)	3.1
White	5390 (3092-7632)	485 (278-687)	11 (1-20)	25 (15-34)	2.3
Educational level[c]					
No high school degree and no GED	5979 (5242-6705)	1300 (1140-1458)	21 (13-29)	72 (65-80)	3.4
High school degree or GED	6815 (5757-7857)	1230 (1039-1418)	32 (21-44)	60 (51-70)	1.9
Some college or associate degree	3242 (2091-4369)	413 (267-557)	10 (4-16)	21 (14-28)	2.1
Bachelor's degree or beyond	2606 (1989-3214)	291 (222-359)	8 (4-11)	14 (11-17)	1.8

Abbreviations: COVID-19, coronavirus disease 2019; GED, general educational development; PI, prediction interval.

[a] Per 1 000 000 living individuals.

[b] Multiplicative factor between first time period and second time period (calculated as ratio of second time period to first time period).

[c] Among decedents aged 25 years or older.