

Persistent SARS-CoV-2 RNA Shedding without Evidence of Infectiousness: A Cohort Study of Individuals with COVID-19

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Summary of article's main point

The majority of participants with mild to moderate COVID-19 continued to shed SARS-CoV-2 from the nasopharynx ≥ 10 days after symptom onset. However, we did not recover any replication-competent virus from 35 rRT-PCR-positive nasopharyngeal specimens collected ≥ 10 days after symptom onset.

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Abstract

Background: To better understand SARS-CoV-2 shedding duration and infectivity, we estimated SARS-CoV-2 RNA shedding duration, described characteristics associated with viral RNA shedding resolution¹, and determined if replication-competent viruses could be recovered ≥ 10 days after symptom onset among individuals with mild to moderate COVID-19.

Methods: We collected serial nasopharyngeal specimens at various time points from 109 individuals with rRT-PCR-confirmed COVID-19 in Utah and Wisconsin. We calculated probability of viral RNA shedding resolution using the Kaplan-Meier estimator and evaluated characteristics associated with shedding resolution using Cox proportional hazards regression. We attempted viral culture for 35 rRT-PCR-positive nasopharyngeal specimens collected ≥ 10 days after symptom onset.

Results: The likelihood of viral RNA shedding resolution at 10 days after symptom onset was approximately 3%. Time to shedding resolution was shorter among participants aged < 18 years (adjusted hazards ratio [aHR]: 3.01; 95% CI: 1.6–5.6) and longer among those aged ≥ 50 years (aHR: 0.50; 95% CI: 0.3–0.9) compared to participants aged 18–49 years. No replication-competent viruses were recovered.

Conclusions: Although most patients were positive for SARS-CoV-2 for ≥ 10 days after symptom onset, our findings suggest that individuals with mild to moderate COVID-19 are unlikely to be infectious ≥ 10 days after symptom onset.

Keywords: SARS-CoV-2, COVID-19, viral shedding, viral culture, infectivity, infectious period

¹ Viral RNA shedding resolution was defined as a first negative rRT-PCR test.

Background

SARS-CoV-2, the novel virus that causes coronavirus disease 2019 (COVID-19), has caused a pandemic that has led to business and school closures, restrictions in travel and social gatherings, and strained healthcare systems globally. As of October 16, 2020, approximately 7.9 million cases and 216,000 deaths have been reported in the United States, with almost 367,000 new cases in the last 7 days [1]. With continued community transmission of SARS-CoV-2, it is vital to better understand the duration of viral RNA shedding and the infectious period for individuals with COVID-19 to inform decisions regarding isolation duration, infection prevention and control guidance, reopening businesses, and setting return-to-work and return-to-school policies.

SARS-CoV-2 RNA shedding (detection of viral RNA from specimens) durations of up to 63 days have been reported from China [2–4]. Viral RNA shedding has been shown to continue after resolution of symptoms based on samples from the nasopharynx tested by real-time reverse transcription polymerase chain reaction (rRT-PCR) [5]. Although the CDC 2019-nCoV rRT-PCR Diagnostic Panel is a qualitative assay used for diagnostic purposes only, the cycle threshold (Ct) value has been used as an indirect measure of viral load. The Ct value appears to be related to disease progression and possible infectivity [6]. Multiple studies showed higher viral loads around the time of symptom onset and significantly reduced viral loads within a week after symptom onset [7–11]. However, only a few studies investigated the duration of replication-competent SARS-CoV-2 shedding primarily in hospitalized patients [5,12–14]. Based on available literature, shedding of replication-competent virus among patients with mild to moderate illness beyond 10 days after symptom onset is rare [5,12,13,15], but shedding of replication-competent virus can continue up to day 20 after symptom onset in patients with severe illness [14]. Further research is needed to understand

the duration of viral RNA shedding and potential infectivity among community-based individuals with mild to moderate COVID-19 to inform public health policies.

Our analysis estimates the time to resolution of SARS-CoV-2 RNA shedding in the nasopharynx, and we report on individual characteristics associated with viral RNA shedding resolution. We also evaluate whether replication-competent SARS-CoV-2 may be recovered from rRT-PCR-positive nasopharyngeal (NP) specimens collected ≥ 10 days after symptom onset among community-based people with mild to moderate COVID-19.

Methods

From March to May 2020, the Centers for Disease Control and Prevention (CDC) partnered with two local health departments in Wisconsin (Milwaukee City and North Shore) and three county health departments in Utah (Salt Lake, Davis, and Summit) to investigate the transmission of SARS-CoV-2 within local households. SARS-CoV-2 positive individuals (termed ‘source participants’) identified through diagnostic testing during clinical care and routine public health reporting were eligible for enrollment if they were not currently hospitalized, diagnosed with SARS-CoV-2 infection within 10 days prior to enrollment, and were living with ≥ 1 other individual. We recruited these source participants through referrals from public health nurses at the respective local health departments, and invited their household contacts to participate in the household transmission investigation as previously described [16,17]. We followed this investigation cohort for a 15-day period (day 0–day 14) to collect clinical and laboratory data, allowing us to estimate the duration of SARS-CoV-2 RNA shedding (detection of viral RNA from NP specimens by rRT-PCR) using symptom onset date, pre-investigation positive test date (if applicable), a day 0 test, and a day 14 test, and any interim tests as potential time points for onset and resolution of viral RNA shedding (Figure 1).

At enrollment (day 0), questionnaires were administered to all participants for collection of demographic information, underlying medical conditions, exposure history, and detailed symptom information. On day 0, NP specimens were collected from all participants. On day 1 through day 14, all participants maintained a daily symptom log and were asked to report any new or worsening symptoms to the investigation team. If new or worsening symptoms were reported among participants included in the investigation, we returned to the household to collect NP specimens from all household members. On day 14, closeout questionnaires were administered, and NP swabs were collected.

Nasopharyngeal specimens were tested by rRT-PCR using the CDC 2019-nCoV rRT-PCR Diagnostic Panel [18] at the City of Milwaukee Health Department Laboratory and Utah Public Health Laboratory. The CDC's 2019-nCoV rRT-PCR Diagnostic Panel showed clinical sensitivity of 100% (13/13; 95% CI: 77.2%–100%) and a clinical specificity of 100% (104/104; 95% CI: 96.4%–100%) [19–21].

To better understand potential infectivity of participants who were rRT-PCR positive beyond 9 days, we performed viral culture on 35 rRT-PCR-positive NP specimens that were collected 10–36 days after symptom onset. Presence of culturable virus was detected by limiting dilution culture in Vero CCL-81 cells as previously described [22,23]. If cytopathic effects were observed, cell monolayers were harvested, and total nucleic acid was extracted for confirmatory testing using rRT-PCR. In order to define a specimen as culture positive, the passage 1 viral isolate had to be positive by rRT-PCR and have a Ct of at least two less than the clinical specimen, indicating more viruses coming out of the cell culture than was put into the cell culture.

Participants Included in the Investigation

A total of 261 participants (62 source participants and 199 contacts) from 62 households (26 in Wisconsin and 36 in Utah) were enrolled in the household transmission investigation. Among the household contacts, 50 were rRT-PCR positive for SARS-CoV-2 during the study. Of the total 112 participants with confirmed COVID-19, three (2.7%) withdrew on the same day of their symptom onset and first rRT-PCR-positive specimen collection. These participants were excluded from the analysis because they had no follow-up information. The final sample for the present analysis consisted of 109 participants with confirmed SARS-CoV-2 and at least one day of follow up (Figure 1). Median intervals to enrollment were: 9 days (interquartile range [IQR]: 6–13) from onset of symptoms (99/109 were symptomatic prior to enrollment) and 5.5 days (IQR: 3–7) from the first positive test for participants who were positive prior to enrollment (n=74: 62 source participants and 12 household members). The follow-up period for the 109 participants ranged from 1–38 days from symptom onset (Figure 2).

Investigation Measures

Participants were classified into three categories based on their viral RNA shedding duration: persistent, not persistent, or indeterminant. Persistent viral RNA shedding was defined as a positive rRT-PCR test ≥ 14 days after symptom onset or first positive test. Not persistent viral RNA shedding was defined as a negative rRT-PCR test < 14 days after symptom onset or positive rRT-PCR test. Participants classified as indeterminant were those who withdrew after the first day or were observed for < 14 days after symptom onset at the conclusion of the investigation, and those whose shedding status could not be determined due to testing interval. Because we did not test participants daily, we could not classify some participants as having persistent viral RNA shedding although they tested negative more than 14 days after

symptom onset. This was because some days elapsed between their last positive test and first negative, and it was unclear if they stopped shedding before or after the 14-day cutoff.

We categorized symptom data reported by participants from symptom onset through the last follow-up day as constitutional (fever, chills, myalgia, or fatigue), upper respiratory (runny nose, nasal congestion, or sore throat), lower respiratory (cough, shortness of breath, wheezing, or chest pain), neurologic (headache, loss of taste, or loss of smell), and gastrointestinal (nausea/vomiting, diarrhea, or abdominal pain).

This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy (e.g., 45 C.F.R. part 46, 21 C.F.R. part 56; 42 U.S.C. §241(d); 5 U.S.C. §552a; 44 U.S.C. §3501 et seq). Informed consent was obtained from all adult participants and legal guardians for those <18 years. Child assent was also obtained from all children ≥ 7 years old.

Role of the Funding source

No external funding was received for this study.

Data Analysis

We calculated frequencies and percentages for demographic factors, underlying medical conditions, and symptoms. We used the Kaplan-Meier estimator to calculate probabilities for viral RNA shedding resolution over time. The log-rank test was used to compare viral RNA shedding resolution probabilities over time among categories of demographic and underlying medical condition variables. After confirming that the data met the hazard proportionality assumption in a Cox model ($p > 0.2$ for all covariates) [24], we conducted Cox proportional hazards regression analysis to identify participant characteristics associated with viral RNA shedding resolution. The outcome was viral RNA shedding resolution, defined as first

negative rRT-PCR test, and we included age, sex, race/ethnicity, and any underlying medical condition (yes/no) as covariates.

The number of days to resolution of viral shedding was calculated as: (1) the number of days from date of symptom onset to the date of the last positive NP specimen collection for those who withdrew, or were hospitalized after enrollment, or were still shedding at the conclusion of the investigation; or (2) the number of days from date of symptom onset to the date of first negative NP specimen collection for those who had viral RNA shedding resolution during the investigation; or (3) among four participants who were asymptomatic at the time of first positive test, the number of days from date of the first positive test to date of last positive specimen collection if they were shedding at the end of the investigation, or to date of first negative specimen collection if they had viral RNA shedding resolution during the investigation. Because participants were not swabbed daily, some days elapsed between last positive test and first negative test among participants who had viral RNA shedding resolution. Unlike the persistent shedding determination described under *Investigation Measures*, in both the Kaplan-Meier analysis and Cox proportional hazards regression model, participants who had viral RNA shedding resolution were assumed to be positive until the date of negative specimen collection.

To account for clustering of participants within households and study sites, we used the robust sandwich estimator to adjust the standard errors of the hazard ratios (HR).[25] A two-tailed statistical significance level of 0.05 was set *a priori*.

Results

Of the 109 participants included in the analysis, 52% were male, 61% were non-Hispanic White, and 15% were non-Hispanic Black. The participants were 3–90 years of age (median: 33; IQR: 21–52 years). Forty-three percent of the participants reported at least one underlying medical condition. Participants reported neurologic (92%), upper respiratory (90%), lower respiratory (87%), constitutional (84%), and gastrointestinal (64%) symptoms. One participant who was classified as not persistent was asymptomatic through resolution (Table 1). One participant was hospitalized for three days and discharged prior to enrollment, and another was hospitalized after enrollment and was still in hospital at the conclusion of the investigation.

A total of 35 rRT-PCR-positive NP specimens (Ct values 26.3–38.4) collected ≥ 10 days after symptom onset from 34 participants were placed in viral culture to attempt virus isolation. The characteristics of participants whose specimens were submitted for viral culture were similar to the total sample, except that they were slightly older (47% vs 30% were aged ≥ 50 years) (Table 1). Replication-competent virus was not recovered from any of the specimens in culture (Figure 3).

Among 109 participants, 51 (47%) had indeterminant viral RNA shedding status. Among the remaining 58 (53%) with adequate information for categorization, 51 (88%) met the criteria for persistent viral RNA shedding (i.e., shedding ≥ 14 days from symptom onset) and 7 (12%) met the criteria for not persistent viral RNA shedding. The Ct values of N1 primer positive specimens collected during the investigation ranged from 14.4 to 38.4.

Assuming that participants remained positive until the date of rRT-PCR-negative specimen collection, the probability of viral RNA shedding resolution among all participants ($n=109$) at 10, 15, 20, and 25 days after symptom onset was approximately 3%, 9%, 32%, and 63%,

respectively (Figure 4). The median day from symptom onset (or first positive test, whichever came first) to viral RNA shedding resolution was 21 days (IQR: 18–24). The viral RNA shedding resolution over time differed by age groups, with younger participants' shedding resolution occurring sooner than that of older participants (Log rank $P < 0.001$) (Figure 5).

Resolution of viral RNA shedding occurred sooner in participants aged < 18 years (aHR: 3.01; 95% CI: 1.6–5.6) and later in those aged ≥ 50 years (aHR: 0.50; 95% CI: 0.3–0.9) than those aged 18–49 years, controlling for sex, race/ethnicity, and underlying medical conditions. There was no statistically significant association with other demographic or clinical factors. The unadjusted and adjusted estimates are reported in Table 2.

Discussion

Many participants in our investigation continued to shed viral RNA beyond 10 days after symptom onset. However, no replication-competent virus was isolated ≥ 10 days after symptom onset, suggesting it was unlikely they would be able to transmit SARS-CoV-2. These findings support the current guidance that people who are positive for SARS-CoV-2 can be released from home isolation 10 days after symptom onset [26,27].

Our results add to our understanding about SARS-CoV-2 viral shedding among community-based individuals with mild or moderate disease. We found prolonged viral RNA shedding among individuals with mild disease. We also found that children aged < 18 years were more likely to have viral RNA shedding resolution and adults aged ≥ 50 years were less likely to have resolution of viral RNA shedding during the observation period compared with adults aged 18–49 years.

Our findings are important because our investigation included predominantly non-hospitalized people with mild to moderate COVID-19 and we observed viral RNA shedding periods similar to those reported for hospitalized patients [2,9,13,28,29]. Previous studies

reported viral RNA shedding duration of a median days of 20–31 in hospitalized patients [2,3,30]. In our investigation, we found that community-based participants infected with SARS-CoV-2 continued to shed virus a median of 21 days after symptom onset. Researchers in China observed that persons aged >45 years experienced delayed resolution of viral RNA shedding among 59 hospitalized patients [29]. Similarly, we found that participants <50 years ceased shedding earlier than older participants. The differences in viral RNA shedding by age may coincide with the difference in clinical syndromes experienced by younger versus older people. These findings can help with developing guidance for how to address scenarios when people with COVID-19 exhibit persistent positive rRT-PCR test results.

In this investigation, we did not recover any replication-competent virus from the 35 rRT-PCR-positive NP specimens collected 10–36 days after symptom onset. Our group has performed virus isolation for numerous other published [22,23,28] and unpublished studies and have found virus recovery of 71% during days (-4) to 0 pre-symptomatic, 47% days 0–4 post symptom onset, and 30% days 5–9 post symptom onset. These data indicate that an absence of culturable virus is not due to the laboratory method, but the time of specimen collection. Previous studies examined whether replication-competent SARS-CoV-2 could be recovered from specimens collected on different days [5,12,14,22]. One study recovered replication-competent viruses from respiratory specimens 1–9 days (median=4) after onset, [28] and in another study, replication-competent viruses were isolated from 31 of 46 rRT-PCR-positive specimens collected from 6 days before to 9 days after onset of classical symptoms [22]. However, replication-competent virus was isolated up to 12 days (median 4 days) in patients with mild to moderate disease [15] and up to 20 days (median 8 days) after symptom onset for severe and critically ill patients [14]. Further studies are still needed to better characterize shedding of replication-competent virus longitudinally from people with infection to better define the timing of infectivity.

When considering the generalizability of our findings, the results are based on a convenience sample of people with COVID-19. The convenience sample approach is subject to potential selection bias, including selection of health-conscious participants who may be healthier than the general population. Also, the probabilities reported in this study were calculated using the Kaplan Meier estimator with no adjustment for the cluster sampling design. Another consideration is that the estimated duration of viral RNA shedding may be longer than the actual duration of shedding for some participants who had viral RNA shedding resolution which we did not detect because we did not conduct testing daily. On the other hand, by limiting viral RNA shedding resolution to first negative, we might have misclassified intermittent shedding as resolution of viral RNA shedding. Despite these limitations, this study is one of the few to describe viral RNA shedding duration in community-based individuals with mild to moderate illness and to include viral culturing of NP rRT-PCR-positive specimens collected at multiple time points.

Based on our data, community-based individuals with confirmed COVID-19 may shed viral RNA beyond 21 days after symptom onset, particularly older adults. While the majority of people diagnosed with COVID-19 will likely remain rRT-PCR positive after the recommended 10-day isolation period [26,27,31], shedding of replication-competent virus appears to be rare ≥ 10 after symptom onset. Our findings provide further evidence that people with mild to moderate COVID-19 are unlikely to be infectious ≥ 10 days after symptom as long as they do not have any risk factors for prolonged infectivity, such as immunocompromising conditions [14]. Our findings support a time-based/symptom-based strategy, versus a test-based approach for decisions about discontinuation of isolation to limit the spread of SARS-CoV-2.

Conflict of Interest

Authors declare they have no conflict of interest.

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Disclaimer

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References

1. CDC. Coronavirus Disease 2019 (COVID-19): Cases in the U.S. [Internet]. 2020 [cited 2020 Oct 16]. Available from: <https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/cases-in-us.html>
2. Zhou B, She J, Wang Y, Ma X. The duration of viral shedding of discharged patients with severe COVID-19. *Clin Infect Dis* [Internet]. NLM (Medline); **2020** [cited 2020 Jun 22]; . Available from: <http://www.ncbi.nlm.nih.gov/pubmed/32302000>
3. 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* [Internet]. **2020** [cited 2020 Jun 22]; 395(10229):1054–1062. Available from: <http://www.ncbi.nlm.nih.gov/pubmed/32171076>
4. Liu W-D, Chang S-Y, Wang J-T, et al. Prolonged virus shedding even after seroconversion in a patient with COVID-19. *J Infect* [Internet]. **2020**; 81(2):318–356. Available from: <http://www.ncbi.nlm.nih.gov/pubmed/32283147>
5. Wölfel R, Corman VM, Guggemos W, et al. Virological assessment of hospitalized patients with COVID-2019. *Nature* [Internet]. **2020** [cited 2020 Jul 4]; 581(7809):465–469. Available from: <https://www.nature.com/articles/s41586-020-2196-x?fbclid=IwAR0dxTczGh6zOK3e0mvBEtNPOIdO5rK9na6RNpd2LPS5cCorbiViL8a9XIU>
6. Bustin SA, Nolan T. Pitfalls of quantitative real-time reverse-transcription polymerase chain reaction. *J Biomol Tech* [Internet]. **2004**; 15(3):155–66. Available from: <http://www.ncbi.nlm.nih.gov/pubmed/15331581>
7. He X, Lau EHY, Wu P, et al. Temporal dynamics in viral shedding and

- transmissibility of COVID-19. *Nat Med* [Internet]. **2020** [cited 2020 Jun 22]; 26(5):672–675. Available from: <https://www.nature.com/articles/s41591-020-0869-5?fbclid=IwAR3x2cKnIDqZfFIpOn6R04KCFDkD7y2Fn1jVIQHC1G8Uq9iCt0w8H7OXmpk>
8. Scola B La, Bideau M Le, Andreani J, et al. Viral RNA load as determined by cell culture as a management tool for discharge of SARS-CoV-2 patients from infectious disease wards. *Eur J Clin Microbiol Infect Dis* [Internet]. **2020** [cited 2020 Jul 4]; 39(6):1059–1061. Available from: <https://doi.org/10.1007/s10096-020-03913-9>
 9. 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* [Internet]. BMJ Publishing Group; **2020** [cited 2020 Jul 4]; 369:m1443. Available from: <https://www.bmj.com/lookup/doi/10.1136/bmj.m1443>
 10. To KK-W, Tsang OT-Y, Leung W-S, et al. Temporal profiles of viral load in posterior oropharyngeal saliva samples and serum antibody responses during infection by SARS-CoV-2: an observational cohort study. *Lancet Infect Dis* [Internet]. **2020**; 20(5):565–574. Available from: [http://dx.doi.org/10.1016/S1473-3099\(20\)30196-1](http://dx.doi.org/10.1016/S1473-3099(20)30196-1)
 11. Zou L, Ruan F, Huang M, et al. SARS-CoV-2 Viral Load in Upper Respiratory Specimens of Infected Patients. *N Engl J Med* [Internet]. Massachusetts Medical Society; **2020** [cited 2020 Jul 15]; 382(12):1177–1179. Available from: <http://www.nejm.org/doi/10.1056/NEJMc2001737>
 12. Bullard J, Dust K, Funk D, et al. Predicting Infectious Severe Acute Respiratory Syndrome Coronavirus 2 From Diagnostic Samples. *Clin Infect Dis* [Internet]. **2020**

- [cited 2020 Jul 4]; . Available from:
<http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC7314198>
13. Walsh KA, Jordan K, Clyne B, et al. SARS-CoV-2 detection, viral load and infectivity over the course of an infection. *J Infect* [Internet]. *J Infect*; **2020** [cited 2020 Jul 4]; 81(3):357–371. Available from: <http://www.ncbi.nlm.nih.gov/pubmed/32615199>
 14. Kampen J van, Vijver D van de, Fraaij PLAF, et al. Shedding of infectious virus in hospitalized patients with coronavirus disease-2019 (COVID-19): duration and key determinants. *medrxiv.org* [Internet]. **2020** [cited 2020 Jul 4]; . Available from: <https://www.medrxiv.org/content/10.1101/2020.06.08.20125310v1?rss=1%22>
 15. Singanayagam A, Patel M, Charlett A, et al. Duration of infectiousness and correlation with RT-PCR cycle threshold values in cases of COVID-19, England, January to May 2020. *Eurosurveillance* [Internet]. NLM (Medline); **2020** [cited 2020 Sep 4]; 25(32). Available from: <http://www.ncbi.nlm.nih.gov/pubmed/32794447>
 16. Yousaf AR, Duca LM, Chu V, et al. A prospective cohort study in non-hospitalized household contacts with SARS-CoV-2 infection: symptom profiles and symptom change over time. *Clin Infect Dis* [Internet]. **2020** [cited 2020 Aug 11]; . Available from: <https://academic.oup.com/cid/advance-article/doi/10.1093/cid/ciaa1072/5877084>
 17. Lewis NM, Chu VT, Ye D, et al. Household Transmission of SARS-CoV-2 in the United States. *Clin Infect Dis* [Internet]. **2020** [cited 2020 Aug 17]; . Available from: <https://academic.oup.com/cid/advance-article/doi/10.1093/cid/ciaa1166/5893024>
 18. CDC. Real-time RT-PCR Primers and Probes for COVID-19 | CDC [Internet]. 2020 [cited 2020 Jul 10]. Available from: <https://www.cdc.gov/coronavirus/2019-ncov/lab/rt-pcr-panel-primer-probes.html>

19. CDC. CDC 2019-Novel Coronavirus (2019-nCoV) Real-Time RT-PCR Diagnostic Panel [Internet]. 2020 [cited 2020 Nov 8]. Available from:
<https://www.fda.gov/media/134922/download>
20. Lu X, Wang L, Sakthivel SK, et al. US CDC Real-Time Reverse Transcription PCR Panel for Detection of Severe Acute Respiratory Syndrome Coronavirus 2. *Emerg Infect Dis* [Internet]. **2020**; 26(8):1654–1665. Available from:
<http://www.ncbi.nlm.nih.gov/pubmed/32396505>
21. Ravi N, Cortade DL, Ng E, Wang SX. Diagnostics for SARS-CoV-2 detection: A comprehensive review of the FDA-EUA COVID-19 testing landscape. *Biosens Bioelectron* [Internet]. **2020**; 165:112454. Available from:
<https://linkinghub.elsevier.com/retrieve/pii/S0956566320304486>
22. Arons MM, Hatfield KM, Reddy SC, et al. Presymptomatic SARS-CoV-2 infections and transmission in a skilled nursing facility. *N Engl J Med. Massachusetts Medical Society*; **2020**; 382(22):2081–2090.
23. Harcourt J, Tamin A, Lu X, et al. Severe Acute Respiratory Syndrome Coronavirus 2 from Patient with Coronavirus Disease, United States. *Emerg Infect Dis* [Internet]. Centers for Disease Control and Prevention (CDC); **2020** [cited 2020 Jul 10]; 26(6):1266–1273. Available from: http://wwwnc.cdc.gov/eid/article/26/6/20-0516_article.htm
24. UCLA Statistical Consulting. Testing the proportional hazard assumption in Cox models [Internet]. 2020 [cited 2020 Aug 11]. Available from:
<https://stats.idre.ucla.edu/other/examples/asa2/testing-the-proportional-hazard-assumption-in-cox-models/>

25. Knox KL, Bajorska A, Feng C, Tang W, Wu P, Tu XM. Survival analysis for observational and clustered data: an application for assessing individual and environmental risk factors for suicide. *Shanghai Arch psychiatry* [Internet]. **2013**; 25(3):183–94. Available from:
<http://ci.nii.ac.jp/lognavi?name=nels&lang=jp&type=pdf&id=ART0004852131>
26. WHO. Criteria for releasing COVID-19 patients from isolation [Internet]. 2020 [cited 2020 Jul 4]. Available from: <https://www.who.int/publications/i/item/criteria-for-releasing-covid-19-patients-from-isolation>
27. CDC. Disposition of Non-Hospitalized Patients with COVID-19 [Internet]. 2020 [cited 2020 Jul 15]. Available from: <https://www.cdc.gov/coronavirus/2019-ncov/hcp/disposition-in-home-patients.html>
28. The COVID-19 Investigation Team. Clinical and virologic characteristics of the first 12 patients with coronavirus disease 2019 (COVID-19) in the United States. *Nat Med* [Internet]. **2020**; 26(6):861–868. Available from:
<http://www.nature.com/articles/s41591-020-0877-5>
29. Hu X, Xing Y, Jia J, et al. Factors associated with negative conversion of viral RNA in patients hospitalized with COVID-19. *Sci Total Environ* [Internet]. Elsevier B.V.; **2020** [cited 2020 Jun 22]; 728:138812. Available from:
<https://linkinghub.elsevier.com/retrieve/pii/S0048969720323299>
30. Xiao AT, Tong YX, Zhang S. Profile of RT-PCR for SARS-CoV-2: a preliminary study from 56 COVID-19 patients. *Clin Infect Dis* [Internet]. **2020**; 53(9):1689–1699. Available from: <https://academic.oup.com/cid/advance-article/doi/10.1093/cid/ciaa460/5822175>

31. Gombar S, Chang M, Hogan CA, et al. Persistent detection of SARS-CoV-2 RNA in patients and healthcare workers with COVID-19. *J Clin Virol* [Internet]. **2020** [cited 2020 Sep 4]; 129:104477. Available from: <https://www.sciencedirect.com/science/article/pii/S1386653220302195>

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Table 1. Demographic and clinical characteristics of rRT-PCR-confirmed COVID-19 participants in Utah and Wisconsin in the household transmission investigation (n=109) — March–May, 2020

Characteristics	Total (n=109)	Individual classification by viral RNA shedding status			Participants whose specimens were submitted for viral culture (n=34)
		Persistent ^a (n=51)	Not persistent (n=7)	Indeterminant ^b (n=51)	
	n (%)	n (%)	n (%)	n (%)	n (%)
State					
Utah	67 (61.5%)	34 (66.7%)	6 (85.7%)	27 (52.9%)	27 (79.4%)
Wisconsin	42 (38.5%)	17 (33.3%)	1 (14.3%)	24 (47.1%)	7 (20.6%)
Age					
<18	15 (13.8%)	3 (5.9%)	2 (28.6%)	10 (19.6%)	4 (11.8%)
18–49	61 (56.0%)	26 (51.0%)	4 (57.1%)	31 (60.8%)	14 (41.2%)
≥50	33 (30.3%)	22 (43.1%)	1 (14.3%)	10 (19.6%)	16 (47.1%)
Sex					
Male	57 (52.3%)	25 (49.0%)	4 (66.7%)	5 (71.4%)	18 (52.9%)
Female	52 (47.7%)	26 (51.0%)	2 (33.3%)	2 (28.6%)	16 (47.1%)
Race/Ethnicity					
Non-Hispanic White	66 (60.6%)	31 (60.8%)	4 (57.1%)	31 (60.8%)	22 (64.7%)
Non-Hispanic Black	16 (14.7%)	10 (19.6%)	0 (0.0%)	6 (11.8%)	4 (11.8%)

Asian	5 (4.6%)	4 (7.8%)	0 (0.0%)	1 (2%)	3 (8.8%)
American Indian/Alaska Native	2 (1.8%)	0 (0.0%)	1 (14.3%)	1 (2%)	0 (0.0%)
Native	1 (0.9%)	1 (2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Hawaiian/Other Pacific Islander					
Multiracial	4 (3.7%)	0 (0.0%)	0 (0.0%)	4 (7.8%)	
Hispanic or Latino	12 (11%)	4 (7.8%)	1 (14.3%)	7 (13.7%)	4 (11.8%)
Unknown race/ethnicity	3 (2.8%)	1 (2%)	1 (14.3%)	1 (2%)	1 (2.9%)
Underlying medical conditions					
Any underlying medical conditions	47 (43.1%)	26 (51.0%)	2 (28.6%)	19 (37.3%)	17 (50.0%)
Any chronic lung disease	19 (17.4%)	9 (17.7%)	1 (14.3%)	9 (17.7%)	6 (17.7%)
Any cardiovascular disease	14 (12.8%)	9 (17.7%)	0 (0.0%)	5 (9.8%)	6 (17.7%)
Diabetes mellitus	8 (7.3%)	3 (5.9%)	0 (0.0%)	5 (9.8%)	1 (2.9%)
Any chronic renal disease	3 (2.8%)	2 (3.9%)	0 (0.0%)	1 (2.0%)	1 (2.9%)
Any neurological conditions	3 (2.8%)	2 (4.0%)	0 (0.0%)	1 (2.0%)	1 (2.9%)
Any immunocompromised condition	4 (3.7%)	1 (2.0%)	0 (0.0%)	3 (5.9%)	1 (2.9%)
Smoking Status^c					
Never smoker	87 (80.6%)	40 (80.0%)	6 (100%)	40 (78.4%)	26 (78.8%)

Former smoker	18 (16.7%)	8 (16.0%)	0 (0.0%)	10 (19.6.6%)	6 (18.2%)
Current smoker	3 (2.8%)	2 (4.0%)	0 (0.0%)	1 (2.0%)	1 (3.0%)
Symptoms^d					
Asymptomatic	1 (0.9%)	0 (0.0%)	1 (14.3%)	0 (0.0%)	0 (0.0%)
Constitutional	91 (83.5%)	40 (78.4%)	6 (85.7%)	45 (88.2%)	28 (82.4%)
Upper respiratory	98 (89.9%)	44 (86.3%)	5 (71.4%)	49 (96.1%)	29 (85.3%)
Lower respiratory	95 (87.2%)	45 (88.2%)	6 (85.7%)	44 (86.3%)	29 (85.3%)
Neurologic	100 (91.7%)	48 (94.1%)	6 (85.7%)	46 (90.2%)	33 (97.1%)
Gastrointestinal	70 (64.2%)	31 (60.8%)	4 (57.1%)	35 (68.6%)	21 (61.8%)

^a rRT-PCR positive after ≥ 14 days of symptom onset or first rRT-PCR positive test; ^b This includes participants who withdrew or were still positive at the end of the study but were observed for < 14 days after symptom onset, and those who could not be classified due to testing interval. ^c There was one participant with no information on current smoking. ^d Symptoms reported any time from onset to the end of study follow up. Symptoms were classified as constitutional (fever, chills, myalgia, or fatigue), upper respiratory (runny nose, nasal congestion, or sore throat), lower respiratory (cough, difficulty breathing, shortness of breath, wheezing, or chest pain), neurologic (headache, loss of taste, or loss of smell), and gastrointestinal (nausea/vomiting, diarrhea, or abdominal pain).

Table 2: Predictors of SARS-CoV-2 RNA shedding resolution during 1–38 days after symptom onset/positive test among a cohort of rRT-PCR-confirmed COVID-19 participants in Utah and Wisconsin in the household transmission investigation (n=109) — March–May, 2020

Variable	unHR ^a (95% CI ^b)	P-value	aHR ^c (95% CI ^b)	P-value
Age				
<18 years	3.01 (1.8–5.0)	<0.001	3.01 (1.6–5.6)	<0.001
18–49 years	Ref		Ref	
≥50 years	0.49 (0.3–0.8)	0.010	0.50 (0.3–0.9)	0.01
Sex				
Male	Ref		Ref	
Female	0.92 (0.6–1.4)	0.69	0.88 (0.6–1.4)	0.60
Race/Ethnicity				
Non-Hispanic White	Ref	0.13	Ref	
Non-Hispanic Black	0.62 (0.3–1.1)	0.97	0.66 (0.3–1.4)	0.27
Other ^d	0.99 (0.5–2.1)		0.88 (0.4–1.8)	0.72
Any underlying medical condition				
No	Ref		Ref	
Yes	0.96 (0.6–1.5)	0.86	1.20 (0.7–2.0)	0.54

Note: ^aunHR, unadjusted hazard ratios; ^bCI, confidence interval; ^caHR, adjusted hazard ratios. Outcome is resolution of viral RNA shedding. aHR and 95% CI were estimated using Cox proportional hazard regression model. ^dThis includes Asian (n=4), American Indian/Alaska Native (n=2), Native Hawaiian/Other Pacific Islander (n=1), Native Hawaiian/Other Pacific Islander (n=1), multiracial (n=4), Hispanic or Latino (n=12), and unknown race/ethnicity (n=3).

Figure 1: Follow-up period of participants from the COVID-19 household transmission investigation in Utah and Wisconsin (n=109) — March–May, 2020

Note: ^aIQR, Interquartile range. Among the 109 participants, 99 developed symptoms a median of 9 days (IQR: 6–13) prior to enrollment and 74 (62 source participants and 12 household members) had their first positive test a median of 5.5 days (IQR: 3–7) prior to enrollment. The follow-up period for the 109 participants ranged from 1–38 days from symptom onset.

Figure 2: Selection of the final sample from the COVID-19 household transmission investigation in Utah and Wisconsin — March–May, 2020

Note: SARS-CoV-2, the virus that causes COVID-19; rRT-PCR, real-time reverse transcription polymerase chain reaction. Source individuals were individual who were first diagnosed of COVID-19 in the household. Data from CDC COVID-19 Household Transmission Investigation conducted in Utah and Wisconsin from March 22 through May 22, 2020. A total of 261 participants (62 source individuals and 199 contacts) from 62 households (26 in Wisconsin and 36 in Utah) were enrolled in the investigation. In addition to the source individuals (n=62), 50 household contacts had at least one rRT-PCR positive test for SARS-CoV-2. Among the 112 people with confirmed COVID-19, three (2.7%) withdrew on the same day of their symptom onset and first rRT-PCR positive specimen collection. These participants were excluded from the investigation because they had no follow-up information. The final sample for the analysis consisted of 109 participants with confirmed COVID-19 with at least one day of follow up after date of symptom onset.

Figure 3: Cycle threshold values by days since symptom onset of rRT-PCR-positive nasopharyngeal specimens showing those submitted for viral culture among individuals in Utah and Wisconsin in the household transmission investigation —March–May, 2020

Note: Diagnosis of COVID-19 was performed using the CDC 2019–Novel Coronavirus (2019-nCoV) Real-Time RT-PCR Diagnostic Panel.[18] rRT-PCR tests amplify and detect viral genetic sequences from 2 regions of the nucleocapsid protein, N1 and N2. The rRT-PCR results were reported positive if amplification was seen for both N1 and N2 probes. Here, we plot cycle threshold values of the N1 probe against the time elapsed between initial symptom onset and NP specimen. No replication-competent virus was recovered from the 35 specimens collected days 10–36 after symptom onset, submitted for culture.

Figure 4: Probability of SARS-CoV-2 RNA shedding resolution over time among participants in Utah and Wisconsin in the household transmission investigation (n=109) — March–May, 2020

Note: These results were derived from Kaplan-Meier Estimator.

Figure 5: Probability of SARS-CoV-2 RNA shedding resolution over time stratified by age groups among participants in Utah and Wisconsin in the household transmission investigation (n=109) — March–May, 2020

Note: These results were derived from Kaplan-Meier Estimator.

Figure 1

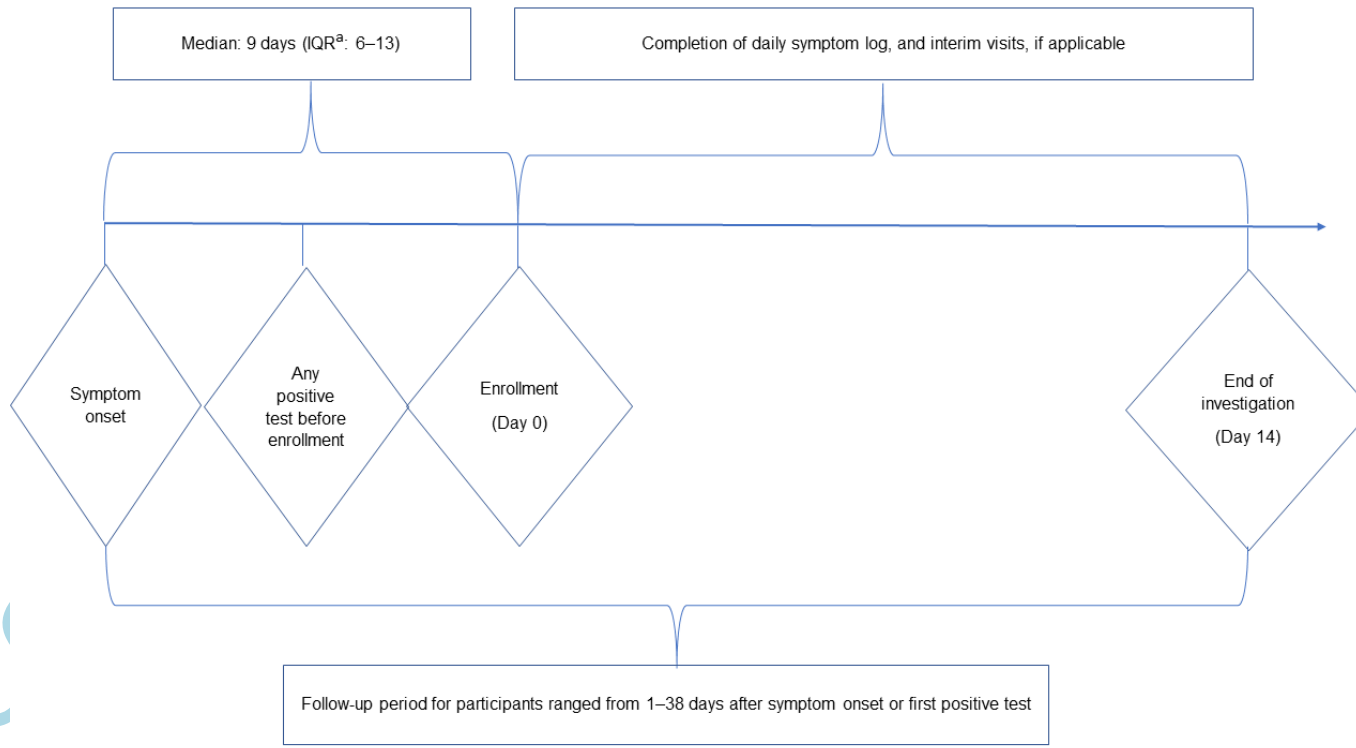
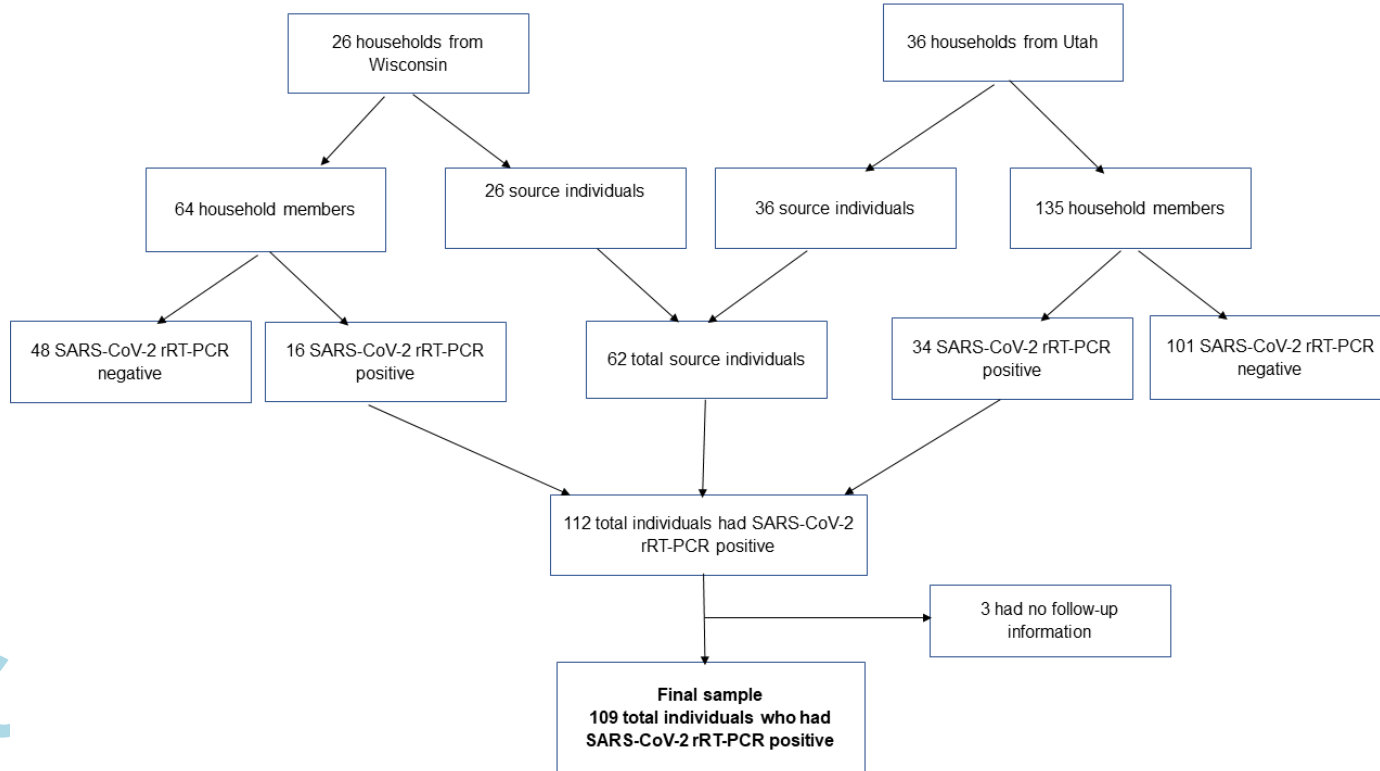
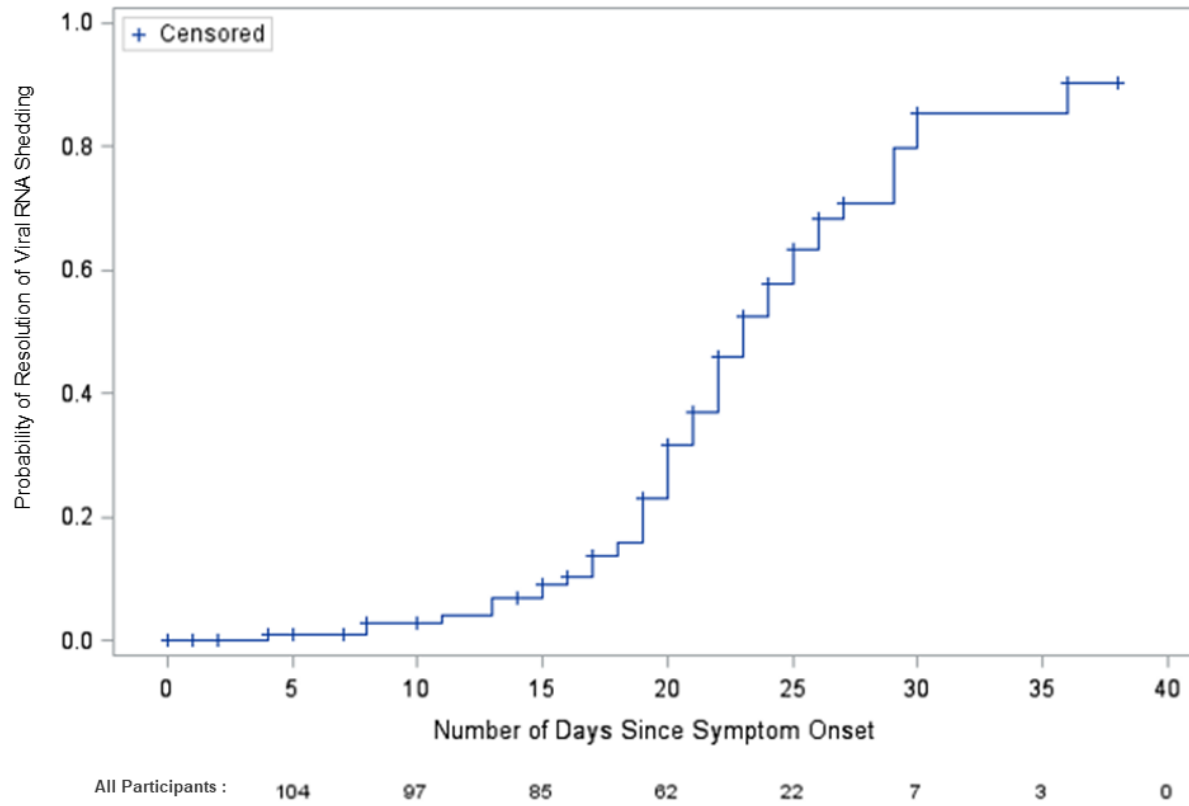


Figure 2



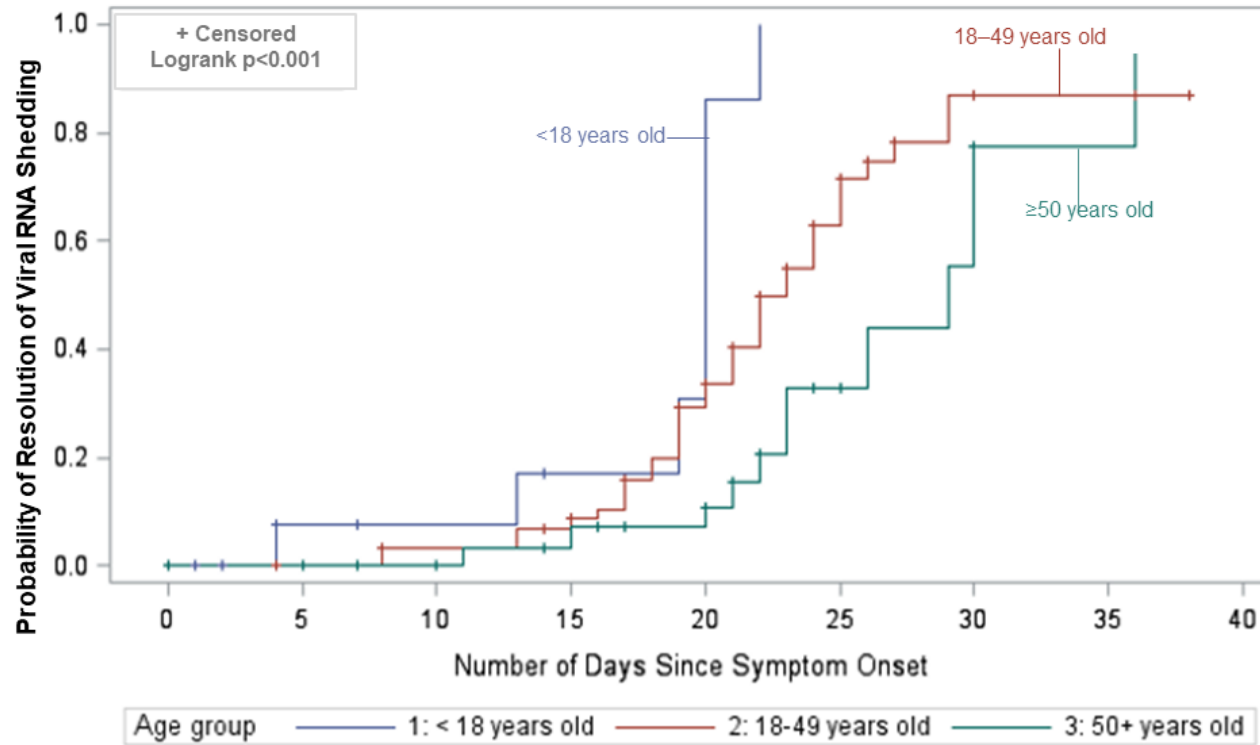
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Figure 4



Note: The numbers beneath the x-axis label are the number of participants still positive

Figure 5



Note: The numbers beneath the x-axis label are the number of participants still positive in each age group.