

Association between Upper Respiratory Tract Viral Load, Comorbidities, Disease Severity and Outcome of Patients with SARS-CoV-2 Infection (JID)

Bottom Line: In this study, patients with comorbidities often had high viral load of SARS-CoV-2 in the upper respiratory tract, and patients with high viral load developed COVID-19 more often, were intubated, or died.

Details: This study explored associations between upper respiratory tract (URT) SARS-CoV-2 viral loads, patient characteristics, and disease severity in 1,122 patients with both symptomatic and asymptomatic infection diagnosed by polymerase chain reaction (PCR). PCR cycle threshold was used to categorize URT viral load as low, moderate, or high. Among this sample, the average age was 46, and 29.9% had at least 1 comorbidity. 24.4% of the sample had an asymptomatic infection and 75.6% developed COVID-19. 44.3%, 28.2%, and 27.5% of patients had low, moderate, and high URT viral load, respectively. Children <18 and adults 18-64 had similar viral load levels (29.3% vs 26.3%, 26.8% vs 29.2%, and 43.9% vs 46.1% for high, moderate, and low viral load, respectively). Compared to patients with low/moderate viral load, patients with high viral load tended to be older, had more comorbidities, developed COVID-19, were intubated, and died. Patients with asymptomatic infection had a low viral load more often than a moderate/high viral load. Compared to patients with low viral load, those with high viral load had longer ICU stays and longer intubation. Comorbidities associated with high viral load at diagnosis were hypertension, chronic cardiovascular, pulmonary, or neurological disease, obesity, and immunosuppression. In multivariate analyses, high viral load was independently associated with developing COVID-19.

Key Takeaways:

- Viral load in the upper respiratory tract could be used to screen patients for high risk of COVID-19 associated morbidity and severe outcomes.

Implications of Shortened Quarantine Among Household Contacts of Index Patients with Confirmed SARS-CoV-2 Infection — Tennessee and Wisconsin, April–September 2020 (MMWR)

Bottom Line: Among people exposed to a household contact with COVID-19 (“index” patient) who remained asymptomatic and had negative tests 7 days after the start of an index patient’s symptoms, 19% had a positive test result or symptoms of COVID-19 in the following week.

Details: CDC recently made changes to guidance regarding a shorter (<14 day) quarantine period for close contacts of individuals infected with SARS-CoV-2 based on testing availability and local epidemiological context in order to improve compliance: 1) ending quarantine on day 10 post exposure without a test or 2) ending quarantine on day 7 post exposure after receiving a negative test. This analysis used data from a household transmission study to explore potential risk for onward transmission from individuals who may develop symptoms or become infected toward the end of the recommended 14-day period. Household contacts of individuals infected with SARS-

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CoV-2 (index patients) self-collected respiratory samples and completed a daily symptom diary for 14 days; samples were tested using reverse transcription-polymerase chain reaction (RT-PCR). 109 of 185 enrolled household contacts had detectable SARS-CoV-2 at any time during the study period; 83/109 and 94/109 received positive test results within 7 and 10 days following the date of the index patient's illness onset. Among household contacts who were negative for SARS-CoV-2 and remained asymptomatic through day 7 and 10, there was an 81% and 93% chance, respectively, of remaining asymptomatic and receiving negative test results through day 14, indicating some risk of onward transmission after a shorter quarantine period.

Key Takeaways:

- Findings from this study suggest that a shorter quarantine period (e.g., 10 days) after household exposure to SARS-CoV-2, though perhaps easier to complete, may pose some risk for onward transmission.
- CDC recommends that people who stop quarantining before 14 days continue to avoid close contact and wear masks until 14 days post-exposure.

S Gene Dropout Patterns in SARS-CoV-2 Tests Suggest Spread of the H69del/V70del Mutation in the US (MedRxiv – pre-print)

Bottom Line: An analysis of 2 million SARS-CoV-2 tests revealed that strains with amino acid deletions in the virus S gene have been observed in the U.S. since early October, though it is unknown if these samples represent the more infectious B.1.1.7 strain.

Details: Several novel strains of SARS-CoV-2, including the more infectious B.1.1.7 variant, share the same mutation – a deletion of amino acids (H69 and V70) in the virus S gene. Using 2 million reverse transcription-polymerase chain reaction (RT-PCR) SARS-CoV-2 tests performed in the U.S., the DNA testing company Helix sought to assess the prevalence of S gene dropout, a phenomenon occurring in tests from individuals infected with SARS-CoV-2 strains with the aforementioned mutation. In early October, 0.25% of daily SARS-CoV-2 tests exhibited S gene dropout; this has increased over time, to up to 0.5% most recently. S gene dropout positive samples were found in 19 states. In 14 states with adequate sample sizes, SARS-CoV-2 tests with S gene dropout have increased in MA, FL, and OH, with 1.85% of MA samples exhibiting the mutation. Analyses could not determine if the S gene dropout samples represented the B.1.1.7 strain.

Key Takeaways:

- S gene dropout among SARS-CoV-2 samples included in this study increased from 0.25% to 0.5% since October, with the highest number of samples found in Massachusetts.
- Expanded genomic sequencing is needed to determine the extent to which S gene drop out identified in this study represents B.1.1.7, and estimate its prevalence.