

[Emergence in Late 2020 of Multiple Lineages of SARS-CoV-2 Spike Protein Variants Affecting Amino Acid Position 677 \(medRxiv – pre-print\)](#)

Bottom Line: In this pre-print study, genomic sequencing of SARS-CoV-2 samples in the US over the past few months identified 7 lineages that independently gained a mutation in one spot on the Spike protein, suggesting convergent evolution.

Details: This pre-print study reports on findings from two SARS-CoV-2 genomic surveillance programs in the US that independently detected an increase in variants with mutations on the Spike (S) protein affecting a particular amino acid (677) in late 2020 (S:677H/P). First detected at the end of October, from 12/20 to mid 1/21 it grew to represent 11.3% and 27.8% of all SARS-CoV-2 genomes sequenced from New Mexico and Louisiana. Further analyses identified 6 additional independent mutations on the same part of the Spike protein (Q677H sub-lineages), the earliest detected in August 2020. By early February 2021, they accounted for 2,327/102,462 genomes sequenced. The authors note that while sampling bias and founder effects may contribute to the rise of these variants, the fact that this amino acid position is in close proximity to a boundary on the S protein that may facilitate cell entry suggests parallel evolution of a trait that may confer an advantage. Moreover, the fact that these variants were detected in the under-sampled US population, which sequences <1% of all SARS-CoV-2 samples, suggests that these lineages may be more common.

Key Takeaways:

- It is not known where these mutations first arose, or whether they have increased due to greater transmissibility of the virus; however, their independent rise and spread suggests some fitness advantage.
- Findings underscore the need for more genomic sequencing to monitor variants over time and examine differences in transmissibility.

[Viral Load of SARS-CoV-2 in Adults during the First and Second Wave of COVID-19 Pandemic in Houston, TX: The Potential of the Super-Spreader \(Journal of Infectious Diseases\)](#)

Bottom Line: This study characterized individuals with extremely high/high SARS-CoV-2 viral load and/or prolonged viral shedding in order to contribute to what is known about super-spreading.

Details: In order to better understand the phenomenon of super-spreading during the COVID-19 pandemic, this study sought to identify phenotypic (observable) characteristics of individuals with extremely high/high viral load and/or prolonged viral shedding. Data from people tested for SARS-CoV-2 between 3/18 and 8/15 were analyzed: hospitalized patients, patients attending medical/surgical clinics, patients requiring clearance for an outpatient surgical or aerosol generating procedure, and symptomatic employees visiting occupational health services. 1,319 of 11,564 samples (11.4%) were positive for SARS-CoV-2. Weekly median viral loads increased during the second pandemic wave, and in both waves, preceded the highest positivity rates. Positive individuals in wave 2 were significantly more likely to be women, attend outpatient settings, have high to extremely

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high viral loads, and be symptomatic. Analyzing the sample by 4 viral load categories based on cycle threshold distribution, individuals in the extremely high viral load group often presented with symptomatic illness, whereas those in the high viral load group were more often asymptomatic at diagnosis, tested positive by RT-PCR 2+ times, and were seen at the occupational health clinic. Of those who had several consecutive polymerase chain reaction (PCR) positive tests, viral shedding duration was similar regardless of disease severity.

Key Takeaways:

- This study observed a substantial increase in weekly median viral load of individuals infected with SARS-CoV-2 during wave 2; weekly median viral loads preceded the highest positivity rates in each wave.
- Patients in the extremely high to high viral load groups were often asymptomatic or had mild symptoms at diagnosis, necessitating appropriate viral detection, physical distancing, and quarantine to mitigate SARS-CoV-2 transmission.
- More research about the social dynamics of individuals with extremely high/high viral load and/or prolonged viral shedding is needed.

COVID-19 Vaccination Intent, Perceptions, and Reasons for Not Vaccinating Among Groups Prioritized for Early Vaccination — United States, September and December 2020 (MMWR)

Bottom Line: Intent to receive the COVID-19 vaccine increased from September to December in the US; however, non-intent is still highest among Black individuals, those without insurance, and adults who live in non-metropolitan areas, have less education, and less income.

Details: From September to December 2020, adults who intended to receive the vaccine increased from 39% to 49% while non-intent decreased from 38% to 32%. Though non-intent decreased among all groups, rates of non-intent remain much higher among Black individuals, women, young adults, those living in nonmetropolitan areas, and adults with lower education, lower income, and no health insurance. Non-intent among Black individuals decreased from 56% to 47% compared to 36% to 30% among White individuals and 36% to 32% among Hispanic individuals. Non-intent decreased 8% among those with a high school education or lower and 11% among those with an annual income of \$35,000–\$49,999. Non-intent was highest among those without health insurance (45%), compared to those with private health insurance (31%) and public health insurance (29%) - with numbers similar in September and December. The largest increase in intent to receive the vaccine was among older adults aged ≥ 65 years (49% to 66%). Intent to get vaccinated also increased among essential workers (37% to 46%) and among adults with underlying conditions between the ages of 18 and 64 years (37% to 42%). Concern for the safety of the vaccine increased from September to December (23% to 30%) while concern for the vaccine being developed too quickly decreased (22% to 10%).

Key Takeaways:

- Addressing reasons for why people do not intend to receive the COVID-19 vaccination, particularly side effects, is critical given hesitancy is still high.

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- Strategies to tailor messages for specific populations are needed to increase people's confidence in the COVID-19 vaccine and decrease hesitancy.

Effect of the New SARS-CoV-2 Variant B.1.1.7 on Children and Young People (The Lancet – Child & Adolescent Health)

Bottom Line: While more children and young people were admitted to a London hospital with COVID-19 in wave 2 (11/1-1/19) than wave 1 (3/1-5/31), there were no significant differences by patient comorbidity, age, proportion of Black, Asian, and minority ethnicity background, or deprivation score between children/young adult patients in wave 1 vs wave 2, and severe disease was infrequent in both waves.

Details: This study adds to the growing literature on the clinical impact of the B.1.1.7 variant on children and adolescents. The authors report that as of January 2021, this variant is estimated to account for over 2/3rds of infections in the London region. Comparing data on patient characteristics and clinical outcomes among children/young people admitted to a south London hospital with COVID-19 in wave 1 (3/1-5/31) and wave 2 (11/1-1/19), the authors report that 20 vs 60 people <18 were admitted. There were no significant differences by patient comorbidity, age, proportion of Black, Asian, and minority ethnicity background, or deprivation score between children/young adult patients in wave 1 vs wave 2. Severe disease requiring oxygen or ventilation support was infrequent in both waves, and proportionally higher in wave 1.

Key Takeaways:

- The number of children, young people, and adult patients admitted to Kings' College Hospital increased by 1/3rd between wave 1 and wave 2.
- Severe disease in children/young adults was not more common in wave 2 vs wave 1, indicating that infection with the B.1.1.7 variant does not change the course of disease significantly in this population.