

Viral genomes reveal patterns of the SARS-CoV-2 outbreak in Washington State

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Spiking variants

Understanding the impact of emerging SARS-CoV-2 variants is essential to inform the development of effective antiviral measures. Studies have indicated that the D614G substitution in the SARS-CoV-2 Spike protein may increase transmissibility, but to what extent this variant has propelled the pandemic is debated. Analyzing thousands of viral genomes together with clinical data, Müller *et al.* found no evidence that the 614G variant rose in frequency in Washington State mid-2020 due to increased transmissibility or virulence. Instead, the data provided a stronger signal that the surge in 614G was explainable by its repeated introduction into the state as well as local differences in lockdown measures—both human-catalyzed factors.

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