



Archived Editions (COVID-19 Genomics and Precision Public Health Weekly Update)

Published on 01/07/2021

COVID-19 Genomics and Precision Public Health Weekly Update Content

- Pathogen and Human Genomics Studies
- Non-Genomics Precision Health Studies
- News, Reviews and Commentaries

Pathogen and Human Genomics Studies

- Safety and Efficacy of the BNT162b2 mRNA Covid-19 Vaccine
(/web/20210409033238/https://phgkb.cdc.gov/PHGKB/phgHome.action?
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FP Polack et al, NEJM, December 31, 2020

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- Is sickle cell disease a risk factor for severe COVID-19 : a multicenter national retrospective cohort
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- Report 42 - Transmission of SARS-CoV-2 Lineage B.1.1.7 in England: insights from linking epidemiological and genetic data (/web/20210409033238/https://phgkb.cdc.gov/PHGKB/phgHome.action?
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"We examine epidemiological evidence for this VOC having a transmission advantage from several perspectives. First, whole genome sequence data collected from community-based diagnostic testing

provides an indication of changing prevalence of different genetic variants through time. Phylodynamic modelling additionally indicates that genetic diversity of this lineage has changed in a manner consistent with exponential growth. Second, we find that changes in VOC frequency inferred from genetic data correspond closely to changes inferred by S-gene target failures (SGTF) in community-based diagnostic PCR testing. Third, we examine growth trends in SGTF and non-SGTF case numbers at local area level across England, and show that the VOC has higher transmissibility than non-VOC lineages, even if the VOC has a different latent period or generation time."

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Swadi T, et al. *Emerg Infect Dis*, Jan 5, 2021.

"Among 86 passengers on a flight from Dubai, United Arab Emirates, that arrived in New Zealand on September 29, test results were positive for 7 persons in MIQ [managed isolation and quarantine]. These passengers originated from 5 different countries before a layover in Dubai; 5 had negative predeparture SARS-CoV-2 test results. To assess possible points of infection, we analyzed information about their journeys, disease progression, and virus genomic data. All 7 SARS-CoV-2 genomes were genetically identical, except for a single mutation in 1 sample. Despite predeparture testing, multiple instances of in-flight SARS-CoV-2 transmission are likely."

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Non-Genomics Precision Health Studies

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Page last reviewed: Oct 1, 2020

Page last updated: Apr 08, 2021

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