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

Published on 11/24/2020

COVID-19 Genomics and Precision Public Health Weekly Update Content

Pathogen and Human Genomics Studies

- Safety and immunogenicity of ChAdOx1 nCoV-19 vaccine administered in a prime-boost regimen in young and old adults (COV002): a single-blind, randomised, controlled, phase 2/3 trial (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=392)
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- Stability of SARS-CoV-2 phylogenies. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=395)
  Turakhia Yatish et al. PLoS genetics 2020 Nov (11) e1009175

  SARS-CoV-2 genome sequences have been produced by hundreds of labs across the world. Idiosyncratic data generation or processing has the potential to inject non-random errors into genome sequences provided by individual lab groups. Here we show that these sites can be detected and removed by identifying variants that appear to reoccur many times across a phylogeny and are associated with specific lab groups.

- A simple direct RT-LAMP SARS-CoV-2 saliva diagnostic (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=398)
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  We report an optimized RT-LAMP-based SARS-CoV-2 diagnostic protocol for saliva and swab samples. When tested on clinical swab and saliva samples, this assay achieves a limit of detection of 105 viral genomes per ml, with sensitivity close to 90% and specificity close to 100%, and takes 45 minutes from sample collection to result, making it well suited for a COVID-19 surveillance program.

- Coagulation factors and COVID-19 severity: Mendelian randomization analyses and supporting evidence (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=400)
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  We assessed causal relationship between 12 coagulation factors and severe COVID-19 illness based on Mendelian randomization (MR) analyses. We then curated clinical evidence supporting causal associations between COVID-19 severity and particular coagulation factors which showed significant results in MR analyses. We validated our results in an independent cohort from UK Biobank (UKBB) using polygenic risk score (PRS) analysis and logistic regression model.

- Flight-Associated Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 Corroborated by Whole-Genome Sequencing. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=401)
  Speake Hollie et al. Emerging infectious diseases 2020 Dec (12) 2872-2880

  To investigate potential transmission of SARS-CoV-2 during a domestic flight, we performed epidemiologic analyses with whole-genome sequencing. Eleven passengers with PCR-confirmed infection and symptom onset within 48 hours of the flight were considered infectious during travel; 9 had recently disembarked from a cruise ship with a retrospectively identified outbreak. The virus strain of those on the cruise and the flight was linked (A2-RP) and had not been previously identified in Australia. For 11 passengers, none of whom had traveled on the cruise ship, PCR-confirmed SARS-CoV-2 illness developed between 48 hours and 14 days after the flight. Eight cases were considered flight associated with the distinct SARS-CoV-2 A2-RP strain; the remaining 3 cases (1 with A2-RP) were possibly flight associated. All 11 passengers had been in the same cabin with symptomatic persons who had culture-positive A2-RP virus strain.
- On-site rapid molecular testing, mobile sampling teams and eHealth to support primary care physicians during the COVID-19 pandemic (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=402)
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Non-Genomics Precision Health Studies

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News, Reviews and Commentaries

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Page last reviewed: Oct 1, 2020

Page last updated: Jan 16, 2021

Content source: Office of Genomics and Precision Public Health (http://www.cdc.gov/genomics/), CDC Office of Science (https://www.cdc.gov/od/science/index.htm)