

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

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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

- Association Between Vaccination With BNT162b2 and Incidence of Symptomatic and Asymptomatic SARS-CoV-2 Infections Among Health Care Workers. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1158)
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In this retrospective cohort study conducted in Tel Aviv, Israel, that included 6710 health care workers who underwent periodic testing for SARS-CoV-2 infection, vaccination with the BNT162b2 vaccine was associated with an adjusted incidence rate ratio of 0.03 for symptomatic infection and 0.14 for asymptomatic infection more than 7 days after the second dose. Both incidence rate ratios were statistically significant.

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In this study of the humoral response to 2 doses of mRNA SARS-CoV-2 vaccine among solid organ transplant recipients, the majority had detectable antibody responses after the second dose, although participants without a response after dose 1 had generally low antibody levels. Poor humoral response was persistently associated with use of antimetabolite immunosuppression.

- Precision Health Diagnostic and Surveillance Network uses S Gene Target Failure (SGTF) combined

with sequencing technologies to identify emerging SARS-CoV-2 variants. ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1163](#))

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Several genomic epidemiology tools have been developed to track the public and population health impact of SARS-CoV-2 community spread worldwide. A SARS-CoV-2 Variant of Concern (VOC) B.1.1.7, known as 501Y.V1, which shows increased transmissibility, has rapidly become the dominant VOC in the United States (US). Our objective was to develop an evidenced-based genomic surveillance algorithm that combines RT-PCR and sequencing technologies to identify VOCs.

- Multi-site Evaluation of SARS-CoV-2 Spike Mutation Detection Using a Multiplex Real-time RT-PCR Assay ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1164](#))
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- Association between ACE2 and TMPRSS2 nasopharyngeal expression and COVID-19 respiratory distress. ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1168](#))
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ACE2 and TMPRSS2 levels positively correlated with age, which was also strongly associated with respiratory distress. Increased nasopharyngeal ACE2 levels showed a protective effect against this outcome (adjOR = 0.30; 95% CI 0.09-0.91), while TMPRSS2/ACE2 ratio was associated with risk (adjOR = 4.28; 95% CI 1.36-13.48).

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Testing of 1475 individual clinical samples pooled in 374 pools of 4 revealed 0.8% false positive pools and no false negative pools. In weekly prophylactic testing of 113 people within 6 months, a two-tier testing approach enabled the detection of 18 infected individuals, including several asymptomatic individuals, with a fraction of the costs of individual RT-PCR testing.

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- "It seems like COVID-19 now is the only disease present on Earth": living with a rare or undiagnosed disease during the COVID-19 pandemic. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1175)
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Respondents (n=?413), including 274 RUD patients and 139 family members, were predominantly female and white, though income varied. Impacts of the pandemic included (1) barriers to accessing essential health care, (2) specific impacts of restrictive COVID-19 visitation policies on ability to advocate in health-care settings, (3) uncertainty and fear regarding COVID-19 risk, (4) exacerbated physical and mental health challenges, (5) magnified impacts of reduced educational and therapeutic services, and (6) unexpected positive changes due to the pandemic.

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To determine whether variants that have emerged more recently are also susceptible to BNT162b2-elicited neutralization, we engineered the complete S genes of the variant viruses into the genetic background of USA-WA1/2020 (isolated in January 2020). Our results suggest that, as compared with the previously reported neutralization of B.1.1.7-spike, the additional E484K mutation, which is also found in the B.1.351 and B.1.526 lineages, caused little compromise to neutralization

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