

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

- Increased viral variants in children and young adults with impaired humoral immunity and persistent SARS-CoV-2 infection: A consecutive case series (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1137)
TT Truong et al, EBiomedicine, April 26, 2021

We found compelling evidence of ongoing replication and infectivity for up to 162 days from initial positive by subgenomic RNA, single-stranded RNA, and viral culture analysis. Our results reveal a broad spectrum of infectivity, host immune responses, and accumulation of mutations, some with the potential for immune escape.

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Respiratory failure is the leading cause of death in patients with severe SARS-CoV-2 infection^{1,2}, yet the host response at the lung tissue-level is poorly understood. Here, we performed single-nucleus RNA-sequencing of ~116,000 nuclei of lungs from 19 COVID-19 decedents who underwent rapid autopsy and 7 control lungs. Integrated analyses revealed significant alterations in cellular composition, transcriptional cell states, and cell-to-cell interactions, providing insights into the biology of lethal COVID-19.

- Prior SARS-CoV-2 infection rescues B and T cell responses to variants after first vaccine dose (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1139)
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We analyzed T and B cell responses after first dose vaccination with the Pfizer/BioNTech mRNA vaccine BNT162b2 in healthcare workers (HCW) followed longitudinally, with or without prior Wuhan-Hu-1 SARS-CoV-2 infection. After one dose, individuals with prior infection showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 and B.1.351. By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants. B.1.1.7 and B.1.351 spike mutations resulted in increased, abrogated or unchanged T cell responses depending on human leukocyte antigen (HLA) polymorphisms

- A urinary peptidomic profile predicts outcome in SARS-CoV-2-infected patients (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1141)
R Wendt et al, E Clinical Medicine, May 3, 2021

This multicentre (six European study sites) Prospective Validation of a Proteomic Urine Test for Early and Accurate Prognosis of Critical Course Complications in Patients with SARS-CoV-2 Infection Study (Crit-COV-U) is recruiting consecutive patients (= 18 years) with PCR-confirmed SARS-CoV-2 infection. A urinary proteomic biomarker (COV50) developed by capillary-electrophoresis-mass spectrometry (CE-MS) technology, comprising 50 sequenced peptides and identifying the parental proteins, was evaluated in 228 patients (derivation cohort) with replication in 99 patients (validation cohort).

- In South Africa, a 2-dose Oxford/AZ vaccine did not prevent mild to moderate COVID-19 (cases mainly B.1.351 variant).

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Irfan Neal et al. Annals of internal medicine 2021 5

2026 persons aged 18 to <65 years (median age, 30 y; 57% men; 70% Black Africans; 83% seronegative at baseline) who had no or well-controlled chronic medical conditions. In adults in South Africa, a 2-dose Oxford/AstraZeneca vaccine regimen did not prevent mild to moderate COVID-19. >90% of incident cases were B.1.351 variant.

- Accelerated vaccine rollout is imperative to mitigate highly transmissible COVID-19 variants. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1147)

Sah Pratha et al. EclinicalMedicine 2021 5 100865

We used an agent-based model of SARS-CoV-2 transmission and vaccination to simulate the spread of novel variants with S-Gene Target Failure (SGTF) in addition to the original strain. We incorporated age-specific risk and contact patterns and implemented a two-dose vaccination campaign in accord with CDC-recommended prioritization.

- Prevalent, protective, and convergent IgG recognition of SARS-CoV-2 non-RBD spike epitopes in COVID-19 convalescent plasma. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1151)

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The molecular composition and binding epitopes of the immunoglobulin G (IgG) antibodies that circulate in blood plasma following SARS-CoV-2 infection are unknown. Proteomic deconvolution of the IgG repertoire to the spike glycoprotein in convalescent subjects revealed that the response is directed predominantly (>80%) against epitopes residing outside the receptor-binding domain (RBD). In one subject, just four IgG lineages accounted for 93.5% of the response

- Rapid Emergence and Epidemiologic Characteristics of the SARS-CoV-2 B.1.526 Variant — New York City, New York, January 1–April 5, 2021 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1153)

CN THompson et al, CDC MMWR, May 5, 2021

The NYC Department of Health and Mental Hygiene analyzed laboratory and epidemiologic data to characterize cases of B.1.526 infection and the associated potential for breakthrough infection and reinfection. Preliminary evidence suggests that, to date, B.1.526 does not lead to more severe disease or increased risk for infection after vaccination. Rapid integration of whole genome sequencing and population-based surveillance data is critical to characterizing new SARS-CoV-2 variants.

- Effectiveness of the BNT162b2 Covid-19 Vaccine against the B.1.1.7 and B.1.351 Variants. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1156)

Abu-Raddad Laith J et al. The New England journal of medicine 2021 5

The estimated effectiveness of the vaccine against any documented infection with the B.1.1.7 variant was 89.5% (95% confidence interval [CI], 85.9 to 92.3) at 14 or more days after the second dose (Table 1 and Table S2). The effectiveness against any documented infection with the B.1.351 variant was 75.0% (95% CI, 70.5 to 78.9). Vaccine effectiveness against severe, critical, or fatal disease due to infection with any SARS-CoV-2 (with the B.1.1.7 and B.1.351 variants being predominant within Qatar) was very high, at 97.4% (95% CI, 92.2 to 99.5).

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Vaccine efficacy among HIV-negative participants was 60.1% (95% CI, 19.9 to 80.1). Of 41 sequenced isolates, 38 (92.7%) were the B.1.351 variant. Post hoc vaccine efficacy against B.1.351 was 51.0% (95% CI, -0.6 to 76.2) among the HIV-negative participants. Preliminary local and systemic reactogenicity events were more common in the vaccine group; serious adverse events were rare in both groups.

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Disclaimer: Articles listed in COVID-19 Genomics and Precision Public Health Weekly Update are selected by the CDC Office of Public Health Genomics to provide current awareness of the scientific literature and news. Inclusion in the update does not necessarily represent the views of the Centers for Disease Control and Prevention nor does it imply endorsement of the article's methods or findings. CDC and DHHS assume no responsibility for the factual accuracy of the items presented. The selection, omission, or content of items does not imply any endorsement or other position taken by CDC or DHHS. Opinion, findings and conclusions expressed by the original authors of items included in the Clips, or persons quoted therein, are strictly their own and are in no way meant to represent the opinion or views of CDC or DHHS. References to publications, news sources, and non-CDC Websites are provided solely for informational purposes and do not imply endorsement by CDC or DHHS.

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