

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

- mRNA vaccination boosts cross-variant neutralizing antibodies elicited by SARS-CoV-2 infection (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=979)
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We examined whether sera from recovered and naïve donors collected prior to, and following immunizations with existing mRNA vaccines, could neutralize the Wuhan-Hu-1 and B.1.351 variants. Pre-vaccination sera from recovered donors neutralized Wuhan-Hu-1 and sporadically neutralized B.1.351, but a single immunization boosted neutralizing titers against all variants and SARS-CoV-1 by up to 1000-fold.

- SARS-CoV-2 infection of the oral cavity and saliva. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=989)
Huang Ni et al. Nature medicine 2021 3

Matched nasopharyngeal and saliva samples displayed distinct viral shedding dynamics, and salivary viral burden correlated with COVID-19 symptoms, including taste loss. Upon recovery, this asymptomatic cohort exhibited sustained salivary IgG antibodies against SARS-CoV-2. Collectively, these data show that the oral cavity is an important site for SARS-CoV-2 infection and implicate saliva as a potential route of SARS-CoV-2 transmission.

- Monozygotic twins discordant for severe clinical recurrence of COVID-19 show drastically distinct T cell responses to SARS-CoV-2 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=992)
MV Castro et al, MEDRXIV, March 28, 2021
- Emergence of a SARS-CoV-2 E484K variant of interest in Arizona (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=994)
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In contrast to other instances when the E484K mutation was acquired independently in the parental lineage, genomic surveillance indicates that the B.1.243.1 variant of interest is in the process of being established in Arizona and beginning to cross state borders to New Mexico and Texas.

- Escape of SARS-CoV-2 501Y.V2 from neutralization by convalescent plasma (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1000)
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Using a live virus neutralization assay, we compared neutralization of a non-VOC variant versus the 501Y.V2 variant using plasma collected from adults hospitalized with COVID-19 from two South African infection waves, with the second wave dominated by 501Y.V2 infections. The observed effective neutralization of first wave virus by 501Y.V2 infection elicited plasma provides evidence that vaccines based on VOC sequences could retain activity against other circulating lineages.

- Initial report of decreased SARS-CoV-2 viral load after inoculation with the BNT162b2 vaccine (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1002)
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In this analysis of a real-world dataset of positive severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) test results after inoculation with the BNT162b2 messenger RNA vaccine, we found that the viral load was substantially reduced for infections occurring 12–37d after the first dose of vaccine. These reduced viral loads hint at a potentially lower infectiousness, further contributing to vaccine effect on virus spread.

- Viral genomic, metagenomic and human transcriptomic characterization and prediction of the clinical forms of COVID-19. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1007)
Rodriguez Christophe et al. PLoS pathogens 2021 3 (3) e1009416

Shotgun metagenomics from nasopharyngeal swabs were used to characterize the genomic, metagenomic and transcriptomic features of patients from the first pandemic wave with various forms of COVID-19, including outpatients, patients hospitalized not requiring intensive care, and patients in the intensive care unit, to identify viral and/or host factors associated with the most severe forms of the disease. Neither the genetic characteristics of SARS-CoV-2, nor the detection of bacteria, viruses, fungi or parasites were associated with the severity of pulmonary disease

- Phylogenetic analyses of SARS-CoV-2 B.1.1.7 lineage suggest a single origin followed by multiple exportation events versus convergent evolution. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1011)
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"The emergence of new variants of SARS-CoV-2 herald a new phase of the pandemic. This study used state-of-the-art phylodynamic methods to ascertain that the rapid rise of B.1.1.7 "Variant of Concern" most likely occurred by global dispersal rather than convergent evolution from multiple sources."

- Innate immune deficiencies in patients with COVID-19 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1014)
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We investigated the links between innate phagocyte phenotype and functions and severity in COVID-19 patients. 84 consecutive patients were included, 44 were in intensive care units (ICU). ICU patients were characterized by increased CD10low CD13low immature neutrophils, LOX-1+ and CCR5+ immunosuppressive neutrophils, and HLA-DRlow CD14low downregulated monocytes. Markers of immature and immunosuppressive neutrophils were strongly associated with severity and poor outcome.

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