

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

- Phylogenetic estimates of SARS-CoV-2 introductions into Washington State. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1102)

Tordoff Diana M et al. medRxiv : the preprint server for health sciences 2021 4

We estimated a minimum 287 separate introductions (median, range 244-320) into Washington and 204 exported lineages (range 188-227) of SARS-CoV-2 out of Washington. Introductions began in mid-January and peaked on March 29, 2020. Lineages with the Spike D614G variant accounted for the majority (88%) of introductions. Overall, 61% (range 55-65%) of introductions into Washington likely originated from a source elsewhere within the US.

- Real World Effectiveness of COVID-19 mRNA Vaccines against Hospitalizations and Deaths in the United States (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1107)

FS Vahidy et al. MEDRXIV< April 23, 2021

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- Trans-ancestry analysis reveals genetic and nongenetic associations with COVID-19 susceptibility and severity (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1114)

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Giovanetti Marta et al. Communications biology 2021 4 (1) 489

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eventually catalyzed the coalescence of such clusters, thus driving up the number of infections and initiating a new epidemic wave. Our results suggest that the efficacy of public health interventions is, ultimately, limited by the size and structure of epidemic reservoirs, which may warrant prioritization during vaccine deployment.

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Peripheral blood samples were obtained from 407 confirmed COVID-19 patients = 61 years of age and without comorbidities, 194 (47.7%) of whom had mild symptomatology that did not involve hospitalization and 213 (52.3%) had a severe clinical course that required respiratory support. We analysed the DNA methylation status of 850,000 CpG sites in these patients. The DNA methylation status of 44 CpG sites was associated with the clinical severity of COVID-19. Of these loci, 23 (52.3%) were located in 20 annotated coding genes. These genes, such as the inflammasome component Absent in Melanoma 2 (AIM2) and the Major Histocompatibility Complex, class I C (HLA-C) candidates, were mainly involved in the response of interferon to viral infection.

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In this study, we investigated 224 SARS-CoV-2 genome sequences from the Global Initiative on Sharing Avian Influenza Data (GISAID) in the early part of the outbreak, of which 69 were from Africa. We analyzed a total of 550 mutations by comparing them with the reference SARS-CoV-2 sequence from Wuhan. We classified the mutations observed based on country and

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We analyze data from ~300,000 RT-PCR samples collected from December 6th 2020 to February 10th 2021. We reveal that the B.1.1.7 is 45% (95% CI:20-60%) more transmissible than the wild-type strain, and become the dominant in Israel within 3.5 weeks. Despite the rapid increase in viral spread, focused RT-PCR testing and prioritized vaccination programs are capable of preventing the spread of the B.1.1.7 variant in the elderly.

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