

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

- Genomic epidemiology reveals transmission patterns and dynamics of SARS-CoV-2 in Aotearoa New Zealand ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=97](#))
JL Geoghegan et al, MEDRXIV, August 20, 2020

We generated 649 SARS-CoV-2 genome sequences from infected patients in New Zealand representing 56% of all confirmed cases in this time period. The proportion of D614G variants in the virus spike protein increased over time due to an increase in their importation frequency, rather than selection within New Zealand. These data also helped to quantify the effectiveness of public health interventions.

- Genomic Diversity of SARS-CoV-2 During Early Introduction into the United States National Capital Region ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=101](#))
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We established a pipeline for SARS-CoV-2 sequencing which enabled us to capture the significant viral diversity present in the region as early as March 2020. Efforts to control local spread of the virus were likely confounded by the number of introductions into the region early in the epidemic and interconnectedness of the region as a whole.

- An inflammatory cytokine signature predicts COVID-19 severity and survival ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=105](#))
DM Del Valle et al, Nature Medicine, August 24, 2020

We implemented a rapid multiplex cytokine assay to measure serum interleukin (IL)-6, IL-8, tumor necrosis factor (TNF)- α and IL-1 β in hospitalized patients with COVID-19 upon admission. Patients ($n=1,484$) were followed up to 41 d after admission. We found that high serum IL-6, IL-8 and TNF- α levels at the time of hospitalization were strong and independent predictors of patient survival.

- Phylogenetic analysis of SARS-CoV-2 in the Boston area highlights the role of recurrent importation and superspreading events ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=112](#))
J Lemieux et al, MEDRXIV, August 25, 2020

To investigate the introduction, spread, and epidemiology of COVID-19 in the Boston area, we sequenced and analyzed 772 complete SARS-CoV-2 genomes from the region, including nearly all confirmed cases within the first week of the epidemic and hundreds of cases from major outbreaks at a conference, a nursing facility, and among homeless shelter guests and staff. The data reveal over 80 introductions into the Boston area, predominantly from elsewhere in the United States and Europe.

Non-Genomics Precision Health Studies

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