



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

Published on 11/05/2020

### 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

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Ramos-Lopez Omar et al. International journal of genomics 2020 6901217

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Employing phylogenetic methods on Danish genome sequences of SARS-CoV-2, we exemplify how genetic data can be used to trace the introduction of a virus to a country. Our analysis supports the hypothesis that the virus was brought to Denmark by skiers returning from Ischgl. On the other hand, we identify transmission routes which suggest that Denmark was part of a network of countries among which the virus was being transmitted.

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Du Pengcheng et al. Nature communications 2020 10 (1) 5503

Here we present genomic surveillance data on 102 imported cases, which account for 17.2% of the total cases in Beijing. Our data suggest that all of the cases can be broadly classified into one of three groups: Wuhan exposure, local transmission and overseas imports. We classify all genomes into 7 clusters. Comparisons reveal higher genomic diversity in the imported group compared to the Wuhan exposure and local transmission, indicating continuous evolution during global transmission.

- SARS-CoV-2 viral load is associated with increased disease severity and mortality. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=319)

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- Revealing fine-scale spatiotemporal differences in SARS-CoV-2 introduction and spread (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=322)

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Evidence-based public health approaches that minimize the introduction and spread of new SARS-CoV-2 transmission clusters are urgently needed in the United States and other countries struggling with expanding epidemics. Here we analyze 247 full-genome sequences from two nearby communities in Wisconsin, and find surprisingly distinct patterns of viral spread.

- Quick COVID-19 Healers Sustain Anti-SARS-CoV-2 Antibody Production (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=323)

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76 subjects followed to ~100 days demonstrated marked heterogeneity in antibody duration. Virus-specific IgG decayed substantially in most individuals, but a subset had stable or increasing antibody levels despite similar initial antibody magnitudes. Individuals with increasing responses recovered rapidly from COVID-19 disease, had increased somatic mutations in virus-specific memory B cell antibody genes, and had persistent higher frequencies of previously activated CD4+ T cells.

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Page last reviewed: Oct 1, 2020

Page last updated: Jan 15, 2021

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