

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

- Effect of an Inactivated Vaccine Against SARS-CoV-2 on Safety and Immunogenicity Outcomes Interim Analysis of 2 Randomized Clinical Trials (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=65)
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- Geographic and Genomic Distribution of SARS-CoV-2 Mutations. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=71)
Mercatelli Daniele et al. Frontiers in microbiology 2020 1800

We analyzed and annotated all SARS-CoV-2 mutations compared with the reference Wuhan genome NC_045512.2, observing an average of 7.23 mutations per sample. Our analysis shows the prevalence of single nucleotide transitions as the major mutational type across the world. There exist at least three clades characterized by geographic and genomic specificity.

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- Sequencing identifies multiple early introductions of SARS-CoV-2 to the New York City Region (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=92)

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Analysis of 864 SARS-CoV-2 sequences from cases in the New York City metropolitan area shows that the majority of cases had no recent travel history or known exposure, and genetically linked cases were spread throughout the region. Comparison to global viral sequences showed that early transmission was most linked to cases from Europe.

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