

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 and healthcare dynamics of nosocomial SARS-CoV-2 transmission.

(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=947)

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- induced immunity may be retained against the B.1.1.7 variant.
- Sequence Analysis of 20,453 SARS-CoV-2 Genomes from the Houston Metropolitan Area Identifies the Emergence and Widespread Distribution of Multiple Isolates of All Major Variants of Concern. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=961)
Long S Wesley et al. The American journal of pathology 2021 3

Based on our extensive genome sequencing program involving 20,453 COVID-19 patient samples collected from March 2020 to February 2021, we report identification of all six of these SARS-CoV-2 variants among Houston Methodist Hospital patients residing in the greater metropolitan area. Although these variants are currently at relatively low frequency (aggregate of 1.1%) in the population, they are geographically widespread. Houston is the first city in the United States in which active circulation of all six current variants of concern has been documented by genome sequencing.
- Common variants at 21q22.3 locus influence MX1 and TMPRSS2 gene expression and susceptibility to severe COVID-19 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=963)
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- Emergence of the E484K Mutation in SARS-CoV-2 Lineage B.1.1.220 in Upstate New York (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=968)
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