

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

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Sindelar Miriam et al. medRxiv : the preprint server for health sciences 2021 Feb

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Based on SARS-CoV-2 genomes, we reconstruct a partial transmission tree of the early pandemic and coinfer the geographic location of ancestral lineages as well as the number of migration events into and between European regions. We find that the predominant lineage spreading in Europe during this time has a most recent common ancestor in Italy and was probably seeded by a transmission event in either Hubei, China or Germany.

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For this cohort study, a total of 1808 asymptomatic participants were screened for SARS-CoV-2 using a CRISPR-based assay and a point-of-reference reverse transcriptase-quantitative polymerase chain reaction (RT-qPCR). The concordance between CRISPR-based and RT-qPCR testing suggests that CRISPR-based assays are reliable and offer alternative options for surveillance testing and detection of SARS-CoV-2 outbreaks, as is required to resume operations in higher-education institutions.

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Among the 23 specimens collected during December 16–23, 22 (96%) were the B.1.351 variant. None of the 245 previously sequenced genomes was from this lineage. Among the 22 specimens containing the variant strain, 21 (95%) contained all nine B.1.351 lineage-defining mutations. Thirteen (57%) were from males, and the median patient age was 32 years.

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