

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
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Pathogen and Human Genomics Studies

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In this study, we investigated the emergence and spread of SARS-CoV-2 genetic variants in Missouri, examined viral shedding over time, and analyzed the associations among emerging genetic variants, viral shedding, and disease severity. We found that COVID-positive individuals that presented with increased viral shedding had less severe disease by several measures.

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We sequenced 212 B.1.1.7 SARS-CoV-2 genomes collected from testing facilities in the U.S. from December 2020 to January 2021. We found that while the fraction of B.1.1.7 among SGTF samples varied by state, is on a similar trajectory as other countries where B.1.1.7 rapidly became the dominant SARS-CoV-2 variant.

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potent mAbs tested was reduced or abolished by either K417N, or E484K, or N501Y mutations.

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