

SARS-CoV2 Sequencing and Variants: KY Update

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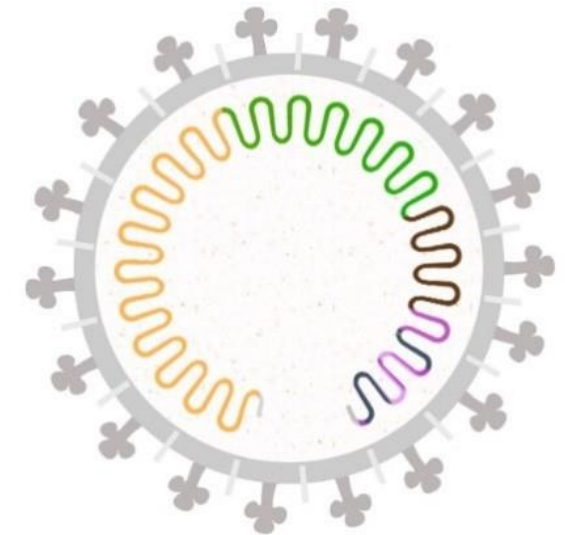
Kentucky Public Health
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Variants

The SARS-CoV-2 Genome



- Viruses are constantly changing, and this includes SARS-CoV-2, the virus that causes COVID-19. These genetic variations occur over time and can lead to the emergence of new variants that may have different characteristics.



Genomic surveillance

- Virus characterization and pathogenesis
- Diagnostics
- Vaccines
- Therapeutics
- Animal-Human interface

Surveillance of emerging variants can help detect variant with:

- Ability to spread more quickly in people
- Ability to cause either milder or more severe disease in people
- Ability to evade detection by specific diagnostic tests
- Decreased susceptibility to therapeutics that employ monoclonal antibodies
- Ability to evade natural or vaccine-induced immunity

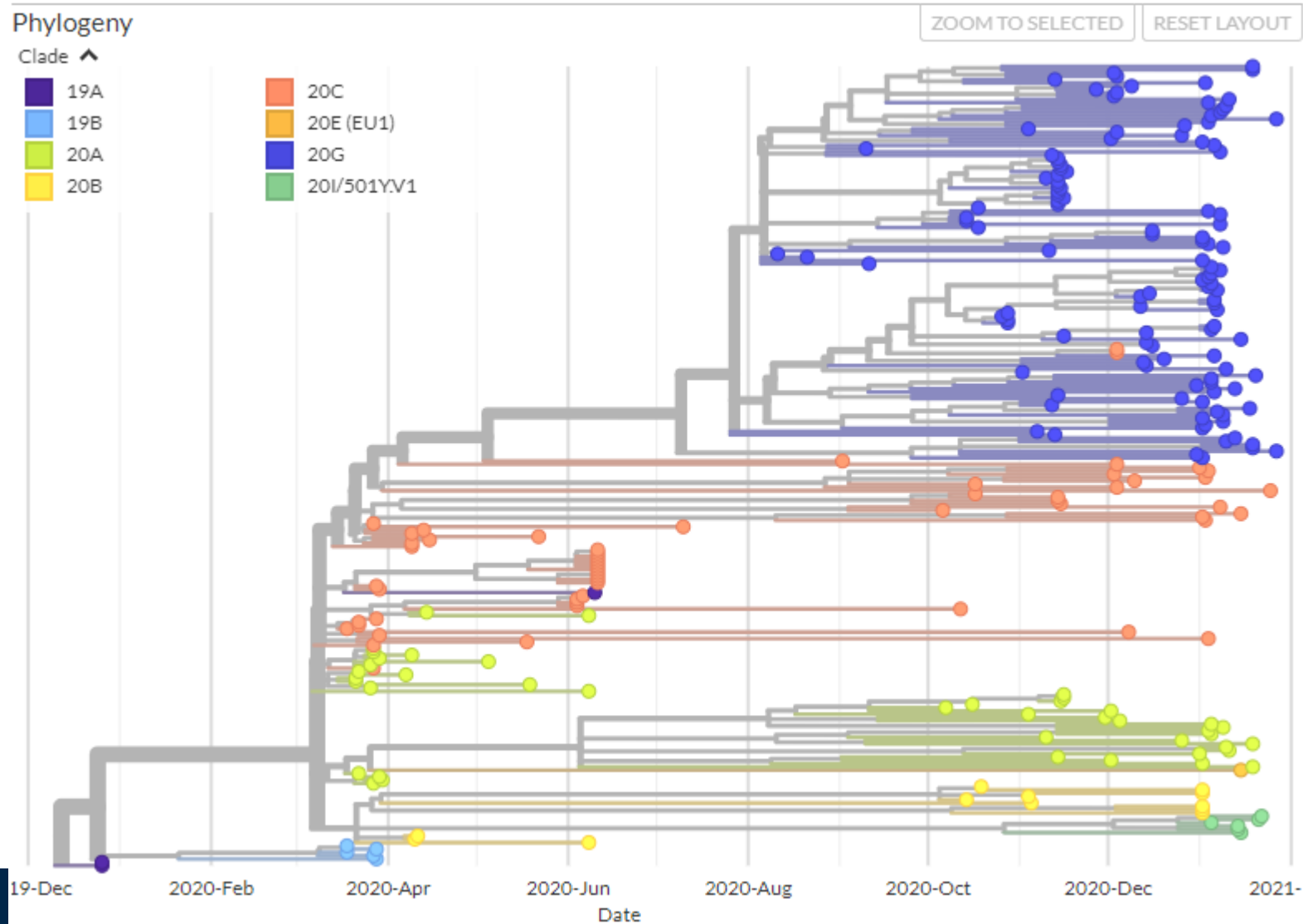
New Variants

- Multiple SARS-CoV-2 variants are circulating globally. Several new variants emerged in the fall of 2020, most notably:
 - United Kingdom (UK)
 - (20I/501Y.V1, VOC 202012/01, or B.1.1.7)
 - First detected in the U.S. at the end of December 2020
 - South Africa,
 - (20H/501Y.V2 or B.1.351) emerged independently of B.1.1.7.
 - First detected in the U.S. at the end of January 2021
 - Brazil
 - (P.1) emerged that was first was identified in four travelers from Brazil, who were tested during routine screening at Haneda airport outside Tokyo, Japan.
 - First detected in the U.S. at the end of January 2021

Public Health/CDC

- National SARS-CoV-2 Strain Surveillance (NS3) system
- Commercial diagnostic laboratories
- Collaborating with universities
- State, territorial, local and tribal health departments
- SARS-CoV-2 Sequencing for Public Health Emergency Response, Epidemiology, and Surveillance (SPHERES) consortium

Phylogeny SARS-CoV2 sequences from KY



Transmissions

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