






# Module 2.1 – SARS-CoV-2 sequencing in Arizona



**Overview:** This module provides insight into how SARS-CoV-2 sequencing is used to describe the genomic epidemiology of a state and as an investigative tool in COVID-19 outbreak settings. You can read more about this work: [An Early Pandemic Analysis of SARS-CoV-2 Population Structure and Dynamics in Arizona](http://mbio.asm.org/content/11/5/e02107-20)  (<http://mbio.asm.org/content/11/5/e02107-20>)

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View Presentation [Full Version]  (<https://nextstrain.org/community/narratives/tgennorth/arizona-covid-19>)  
[Short Version]  (<https://nextstrain.org/community/narratives/tgennorth/arizona-covid-19/short>)

## Further Reading:

1. An early pandemic analysis of SARS-CoV-2 population structure and dynamics in Arizona.  (<https://mbio.asm.org/content/11/5/e02107-20>) Ladner, et al. *mBio*, 2020.
2. AZ-Strain: Genomic epidemiology of SARS-CoV-2 in Arizona.  (<https://nextstrain.org/community/narratives/tgennorth/arizona-covid-19>) Arizona COVID Genomics Union (ACGU).

## Additional Resources:

1. *Communicating results using narratives.*  (<https://docs.nextstrain.org/en/latest/guides/communicate/narratives-intro.html>) Nextstrain.org (documentation).
2. Coast-to-coast spread of SARS-CoV-2 during the early epidemic in the United States.  (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7204677/>) Fauver, et al. *Cell*, 2020.
3. Large-scale sequencing of SARS-CoV-2 genomes from one region allows detailed epidemiology and enables local outbreak management.  (<https://www.microbiologyresearch.org/content/journal/mgen/10.1099/mgen.0.000589>) Page, et al. *Microb Genom*, 2021.
4. Viral genomes reveal patterns of the SARS-CoV-2 outbreak in Washington State.  (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8158963/>) Mueller, et al. *Sci Transl Med*, 2021.
5. Revealing fine-scale spatiotemporal differences in SARS-CoV-2 introduction and spread.  (<https://www.nature.com/articles/s41467-020-19346-z>) Moreno, et al. *Nat Commun*, 2020.



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## Further Reading for Case Studies

1. Presymptomatic SARS-CoV-2 infections and transmission in a skilled nursing facility.  (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7200056/>) Arons et al. 2020 *NEJM*.

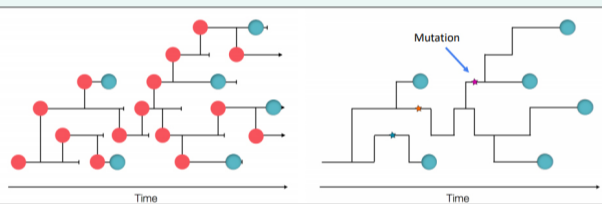
2. COVID-19 outbreak associated with a 10-day motorcycle rally in a neighboring state. ([/mmwr/volumes/69/wr/mm6947e1.htm?s\\_cid=mm6947e1\\_w](https://mmwr.volumes/69/wr/mm6947e1.htm?s_cid=mm6947e1_w)) Firestone *et al.* 2020 *MMWR*.
3. The emergence of SARS-CoV-2 in Europe and North America. [🔗](https://science.sciencemag.org/content/370/6516/564) (<https://science.sciencemag.org/content/370/6516/564>) Worobey *et al.* 2020 *Science*.
4. Interregional SARS-CoV-2 spread from a single introduction outbreak in a meat-packing plant in northeast Iowa. [🔗](https://www.medrxiv.org/content/10.1101/2020.10.12.20210294v1) (<https://www.medrxiv.org/content/10.1101/2020.10.12.20210294v1>) Richmond *et al.* 2020 *MedRxiv*.
5. SARS-CoV-2 sequencing reveals rapid transmission from college student clusters resulting in morbidity and deaths in vulnerable populations. [🔗](https://www.medrxiv.org/content/10.1101/2020.10.12.20210294v1) (<https://www.medrxiv.org/content/10.1101/2020.10.12.20210294v1>) Richmond *et al.* 2020 *MedRxiv*.

## Related Videos

### Module 1.3

#### How to read a phylogenetic tree

Interpreting phylogenetic trees in the context of transmission

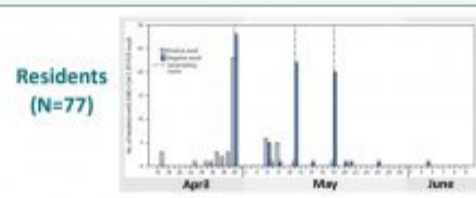


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### Module 2.2

#### Healthcare cluster transmission

Investigating outbreaks in two skilled nursing facilities

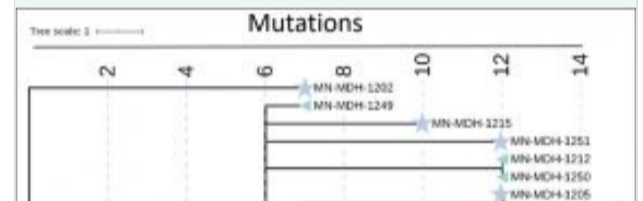


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### Module 2.3

#### Investigating workplace-community transmission

How sequencing helped distinguish between workplace and community transmission



[\(/amd/training/covid-toolkit/module2-3.html\)](/amd/training/covid-toolkit/module2-3.html)