

# Genomic epidemiology strengthens public health outbreak response in healthcare settings

Utilizing genomic epidemiology to explore SARS CoV-2 transmission patterns and support outbreak investigations in long term care facilities, Washington State, April-October 2021

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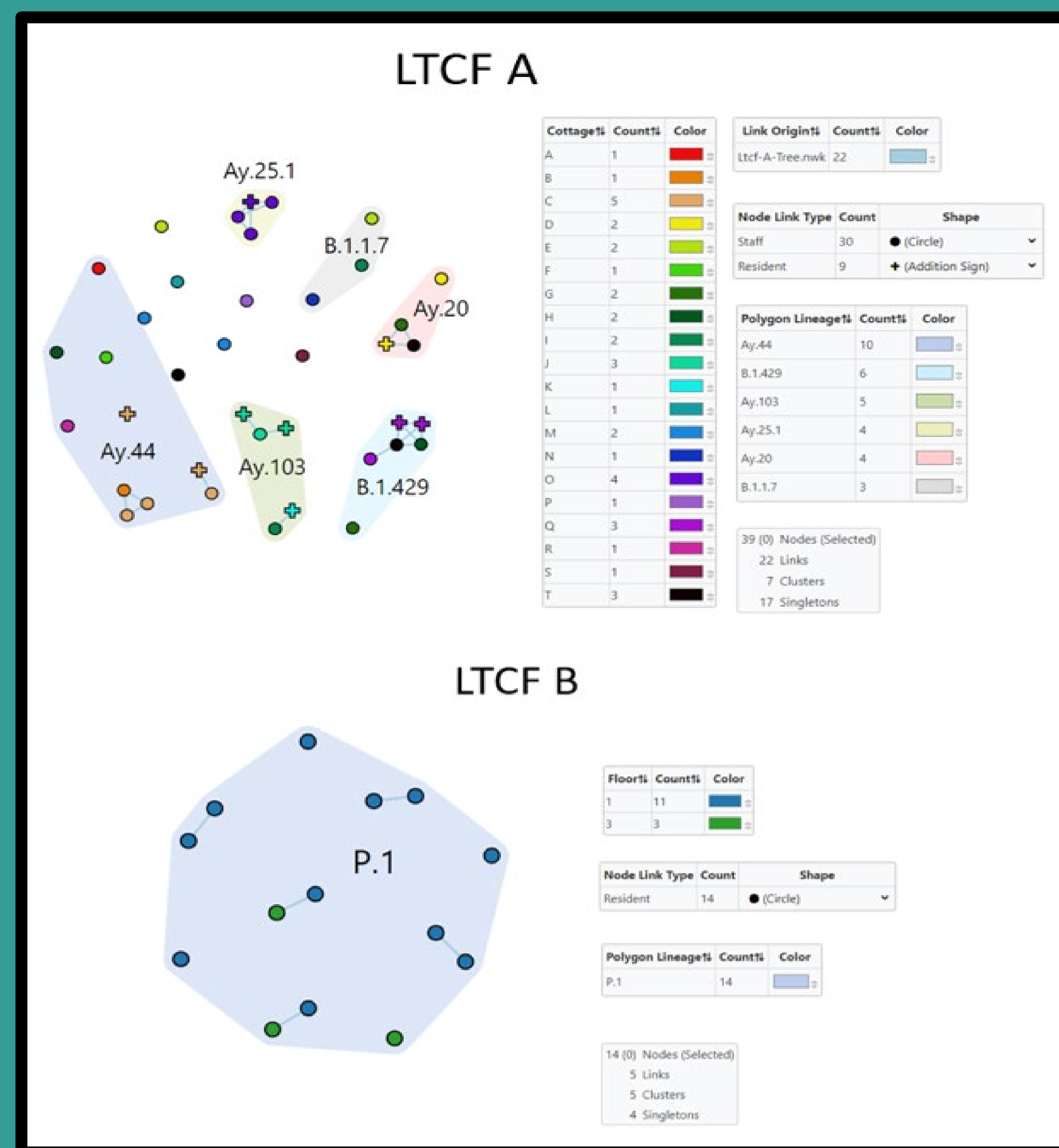
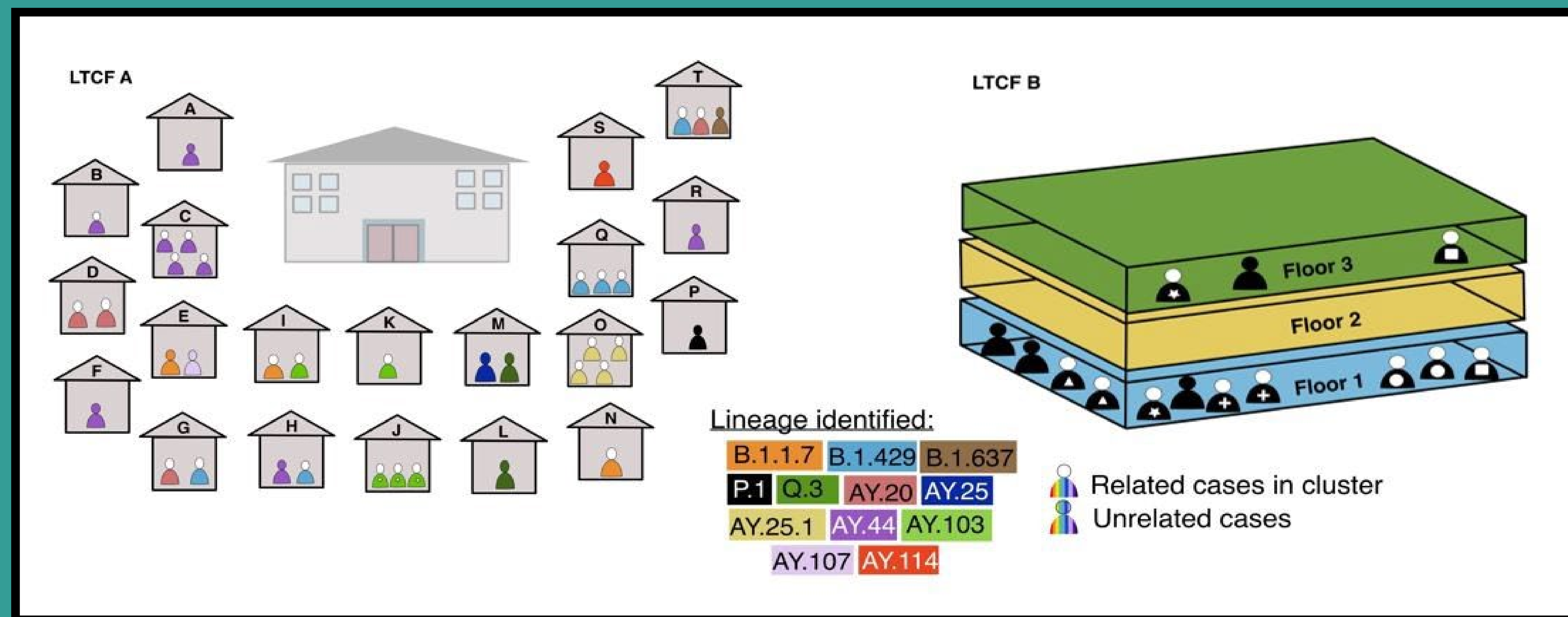
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## INTRODUCTION

- 30% of Washington State COVID-19 deaths have been among residents of long-term care facilities (LTCF).
- Understanding transmission patterns in healthcare facilities guides outbreak response.
- Outbreak sequencing data analyzed from two large LTCF in Washington State.

## METHODS

- Outbreak data: Washington Disease Reporting System (WDRS).
- Sequencing: Nextalign; SNP distance matrices calculated using Snp-Dists; phylogenetic analysis with IQ-Tree. TreeTime for time-resolving trees.
- Visualizations: MicrobeTrace and Vectornator.



	LTCF A, 234 beds (N=119)	LTCF B, 150 beds (N=36)	Total (N=155)
<b>Age (years)</b>			
Mean (SD)	45.4 (15.2)	79.4 (22.4)	53.3 (22.3)
Median [Min, Max]	45.0 [23.0, 82.0]	88.5 [18.0, 101]	52.0 [18.0, 101]
<b>Staff or Resident</b>			
Resident	27 (22.7%)	29 (80.6%)	56 (36.1%)
Staff	92 (77.3%)	7 (19.4%)	99 (63.9%)
<b>Sex</b>			
Female	67 (56.3%)	29 (80.6%)	96 (61.9%)
Male	52 (43.7%)	7 (19.4%)	59 (38.1%)



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## RESULTS

- LTCF A: multiple independent introductions of SARS-CoV-2, indicating **minimal** intra-facility transmission.
- LTCF B: fewer independent introductions of SARS CoV-2, indicating **more** intra-facility transmission.

## DISCUSSION

- Disease transmission pathways in congregate healthcare settings are diverse.
- Understanding transmission allows for swift risk mitigation, resource prioritization, and improved public health response.
- Useful in all healthcare settings; can be prioritized for vulnerable populations.
- Additional uses
  - Variant identification and impact on disease severity.
  - Cluster identification.
  - Analysis of repeat infections and co-infections.



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