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Comparing Molecular and Time-Space HIV Cluster Detection Methods in Rural Washington, 2020-2024

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BACKGROUND

As part of the "Response" pillar of the Ending the HIV Epidemic Initiative, the CDC requires jurisdictions to use two methods to detect HIV transmission clusters: time-space (TS) and molecular HIV surveillance (MHS). TS methods use spatiotemporal proximity, and MHS uses genetic distance.

Between 2023 to 2024, the proportion of people newly diagnosed with HIV in Washington State (WA) that had HIV genotype data decreased by 6%. Along with an increasing proportion of diagnoses occurring in rural areas in WA (12% in 2020 to 15% in 2024), these two factors prompted us to evaluate the relative performance of these two cluster detection methods in rural areas.

METHODS

We analyzed HIV surveillance data from WA (2020-2024) to identify TS and MHS clusters that met CDC's cluster definitions:

- **TS**: annual number of cases in a county > 2 standard deviations *and* ≥ 2 cases above the five-year mean
- **MHS**: ≥ 5 diagnoses in 12 months at ≤ 0.5% genetic distance)

We classified each cluster as urban or rural using WA's Office of Financial Management county definition. MHS clusters, which could span multiple counties, were categorized based on the modal value of their individual cluster members. We calculated agreement between methods at the individual level (proportion of individuals detected by one method also detected by the other) and at the cluster level (proportion of clusters occurring in the same county during the same calendar year) by rurality.

Finally, we examined the overall proportion of people newly diagnosed with HIV with genotype results and compared completion of HIV genetic results by rurality using a chi-square test.

In Washington state, molecular HIV surveillance (MHS) cluster detection captured mainly urban clusters, while time-space (TS) captured both urban and rural clusters. In jurisdictions with increasing rural HIV diagnoses, it is vital to use detection methods effective in both settings.

RESULTS

From 2020 to 2024, there were seven TS clusters (n=131) and seven MHS clusters (n=84) in WA. Three TS clusters (43%) were classified as rural and four (57%) were urban. Three MHS clusters (43%) spanned both urban and rural counties but were predominantly urban; the remaining four (57%) were urban.

In rural areas, 20% of new diagnoses were included in clusters (95% TS, 5% MHS) compared with 40% in urban areas (87% TS, 13% MHS). Only 2% of people identified in a TS cluster were also identified in an MHS cluster, and 3% of people identified in MHS clusters were also in TS clusters. Four clusters overlapped at the county level (Figure 1).

Figure 1. Identified Molecular (MHS) and Time-Space (TS) HIV Clusters by Urban and Rural Counties, Washington State 2020-2024

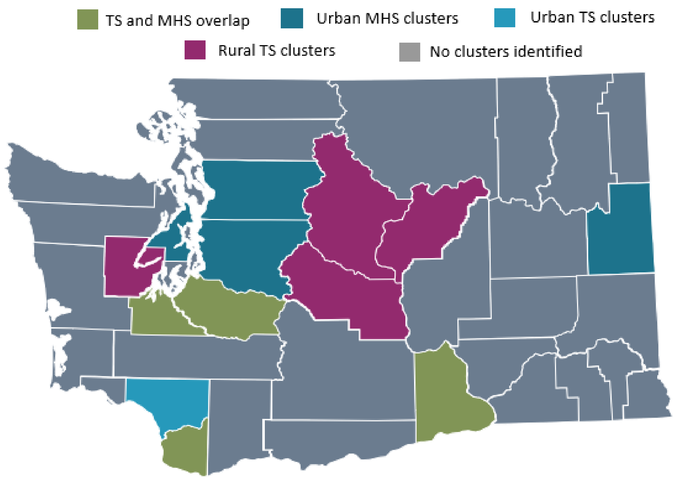
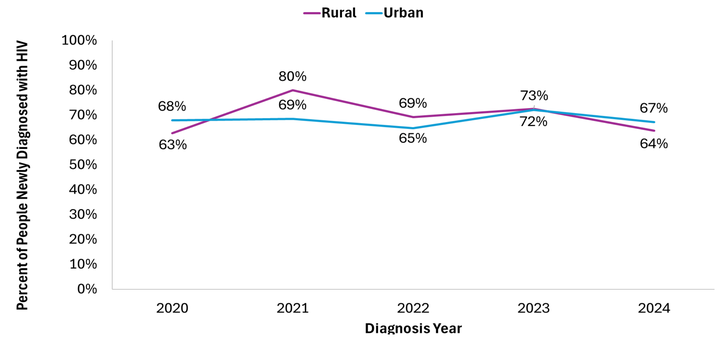


Figure 2 shows the proportion of people newly diagnosed with HIV with complete genotype results. Overall, genotype completion has remained relatively stable since 2020, with a slight decrease from 2023 (72% urban;73% rural) to 2024 (67% urban; 64% rural).

Figure 2. Proportion of People Newly Diagnosed with HIV with Genotype Results by Rurality in Washington State, 2020-2024



There was no difference in the five-year average genetic data completion between urban and rural counties (68% vs. 69%; p=0.64).

DISCUSSION

Each cluster detection method identified distinct clusters in WA. While all MHS clusters were urban, almost half of the TS clusters were in rural counties. While the percentage of people newly diagnosed with HIV with a genotype in WA is higher than the ≥50% threshold CDC recommends, the overall incidence of HIV drug resistance is declining. If this trend continues, it may influence testing priorities and the availability of genotype data used for MHS cluster detection. It is important not to rely solely on one method. Jurisdictions should use both MHS and TS for HIV cluster detection to accurately capture all potential clusters.

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