Changing Clustering Rates in the Rhode Island HIV-1 Epidemic

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BACKGROUND

Tracking changes over time in proportions and characteristics of persons living with HIV who are part of molecular clusters (clustering rates), has potential to provide valuable insights into HIV transmission dynamics and help guide targeted public health interventions for prevention.

METHODS

We monitored clustering rates patterns and changes among key populations in the statewide HIV-1 epidemic in Rhode Island from 1991 to 2024. Partial HIV-1 *pol* sequences were grouped by year of HIV diagnosis, and molecular clusters were identified in cumulative annual phylogenies (RAxML; bootstrap support ≥80%; mean pairwise TN93 distance 0.045 substitutions/site). Mann-Kendall statistics were used to estimate clustering rates trends over time in newly diagnosed and prevalent HIV infections, and among key populations defined by selected socio-demographic characteristics and transmission risk factors.

Monitoring HIV clustering rates over three decades in a statewide epidemic revealed evolving trends among key populations, suggesting a gradual shift toward a more localized HIV-1 epidemic in Rhode Island.

RESULTS

By the end of 2024, 2,709 persons with sequences represented the statewide Rhode Island HIV-1 epidemic. Overall, clustering rates increased from 8% in 1991 to 47% in 2024, correlating with cumulative sequence increase.

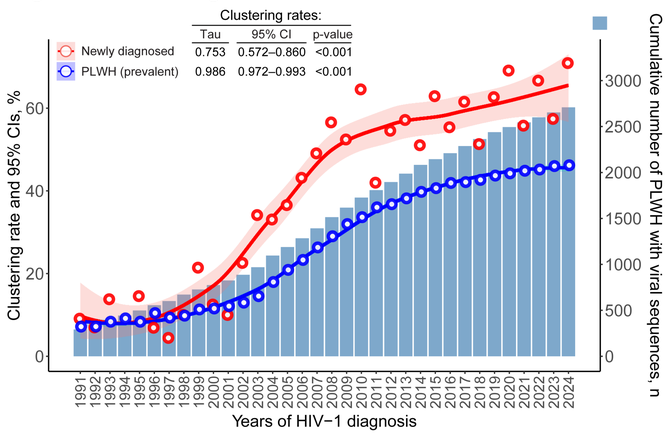
Clustering rates of both newly diagnosed and prevalent infections demonstrated a statistically significant increase over time (Figure 1). In the early phase of the epidemic in Rhode Island, the clustering rates among newly diagnosed individuals and prevalent HIV-1 infections were relatively low and intertwined. From 1991 and 1996, we found no significant difference in clustering rates between these groups. However, since the late 1990s, clustering rates among newly diagnosed individuals increased more rapidly than among prevalent infections, suggesting a divergence between these two groups. Since 1998, the mean clustering rate among newly diagnosed individuals has been significantly higher than among prevalent infections. Since 2010, both clustering rates seemed to plateau.

Clustering rates increased significantly over time more among MSM (Figures 2 and 3), males versus others since 2009 (Figure 4), people >40 years at HIV diagnosis (Figure 5), Whites versus others since 2005 (Figure 6), persons with mental illness versus those without it since 2013 (Figure 7), persons with HIV-1 subtype B versus non-B since 2013 (Figure 8), and US-born versus foreign-born persons since 2007 (Figure 9). Crossovers and divergence patterns in clustering rates identified over time among some groups (dashed vertical lines in Figures 2-9) further characterized clustering trend dynamics.

CONCLUSIONS

Monitoring HIV-1 clustering rates over three decades in a statewide epidemic revealed evolving trends and diverse patterns among key populations over time, suggesting a gradual shift toward a more localized epidemic in Rhode Island. Findings emphasize the importance of tracking clustering rates to guide targeted interventions and prevent new transmissions.

Figure 1*: Clustering rates in Rhode Island over three decades



* Clustering rate trends (left Y-axis) among newly diagnosed (red) and prevalent (blue) HIV-1 infections over time (X-axis). Dots = estimated annual proportions of clustered individuals. Blue bars = cumulative available genotypes (right Y axis).

Figure 2
Primary transmission risk factors

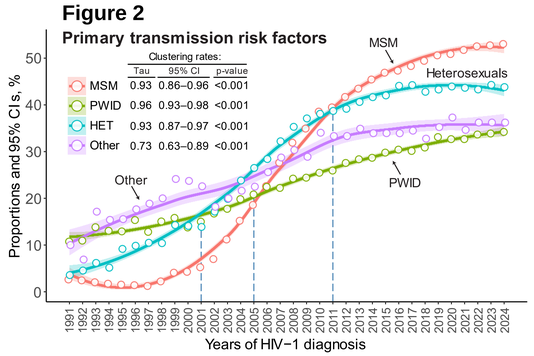


Figure 3
MSM status

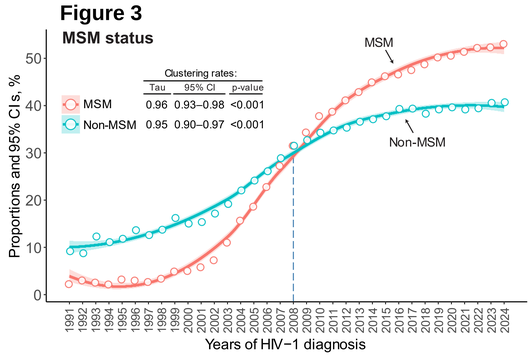


Figure 4
Gender

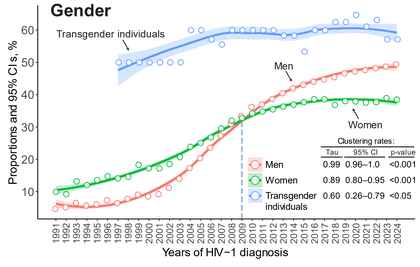


Figure 5
Age at HIV-1 diagnosis

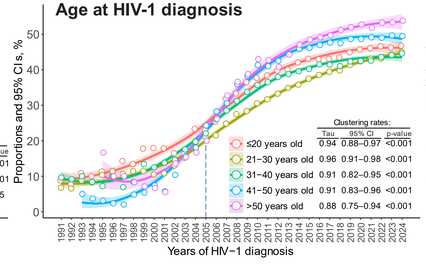


Figure 6
Race

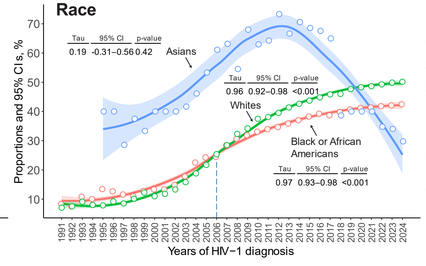


Figure 7
Mental illness

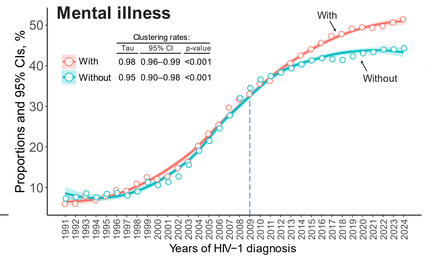


Figure 8
HIV-1 subtypes

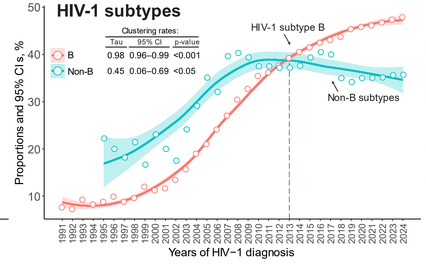


Figure 9
Country of birth

