NATIONAL CENTER FOR HIV/AIDS, VIRAL HEPATITIS, STD, AND TB PREVENTION

Increasing Capacity for Detecting Clusters of Rapid HIV Transmission—United States

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BACKGROUND

- Responding to HIV clusters and outbreaks is a pillar of the U.S. Ending the HIV Epidemic (EHE) initiative
  - EHE is initially focusing on 48 counties; Washington, D.C.; San Juan, Puerto Rico; and 7 states with substantial rural burden
- By using HIV sequence data collected via routine surveillance, clusters of rapid transmission can be identified for public health response
  - In 2015–2016, most persons in U.S. clusters were men who have sex with men (MSM)—only 1% were persons who inject drugs (PWID)[1]
- In 2018, requirements to collect HIV sequence data expanded from 27 to all CDC-funded health departments

Objective: **describe changes in molecular cluster detection capability in the United States, including in EHE areas, and geographic variation in transmission dynamics across states.**

METHODS

- Examined HIV-1 polymerase sequence completeness (percentage of diagnoses in the past 3 years with an HIV sequence available) in quarterly National HIV Surveillance System data sets from December 2015 (first implementation of molecular cluster detection) to December 2019
- For 17 quarterly analyses (December 2015–December 2019), identified clusters of rapid transmission among people with HIV diagnosed in the past 3 years using HIV-TRACE[2,3]
  - Pairwise genetic distance threshold of 0.5%
  - Priority clusters had ≥ 5 diagnoses in the past 12 months
- For people in clusters first detected in 2018–2019, described transmission category and race/ethnicity, overall and for 3 states

RESULTS

- Sequence completeness increased nationwide, in EHE areas, and in areas not previously funded to collect sequences (Figure 1).
- Of 242 clusters detected, 136 were first detected in 2018–2019
- Of 1,212 people in these 136 clusters:
  - 69% were MSM, 11% were PWID, and 5% were MSM who inject drugs
  - 56% resided in EHE areas at diagnosis
- State-by-state analysis showed tremendous variation in risk and racial/ethnic groups included in clusters of rapid transmission (examples shown in Figure 2).

CONCLUSIONS

- Sequence completeness increased nationwide
  - Together with expansion of local cluster analysis capacity, demonstrates increased capacity to detect clusters of rapid transmission
- Molecular cluster analysis can identify recent and rapid transmission in varied populations, which may change over time
  - Has detected increased rapid transmission among PWID in recent years (11% in 2018–2019 compared with 1% in 2015–2016)
- Molecular cluster detection offers a focused, local approach to identify populations experiencing rapid transmission and to tailor response to scale up services for these populations
  - Different populations are experiencing rapid transmission in different states, indicating that different prevention and response approaches are needed
- These results demonstrate that use of molecular cluster detection provides great potential for guiding public health response to clusters and outbreaks

References [1]France AM *et al.* CROI 2018. [2]Oster AM, France AM *et al. JAIDS* 2018. [3]Kosakovsky Pond SL *et al. Mol Biol Evol* 2018.

Molecular HIV cluster detection offers a *focused, local* approach to identify networks experiencing rapid HIV transmission and tailor and scale up services for the populations involved in these networks.

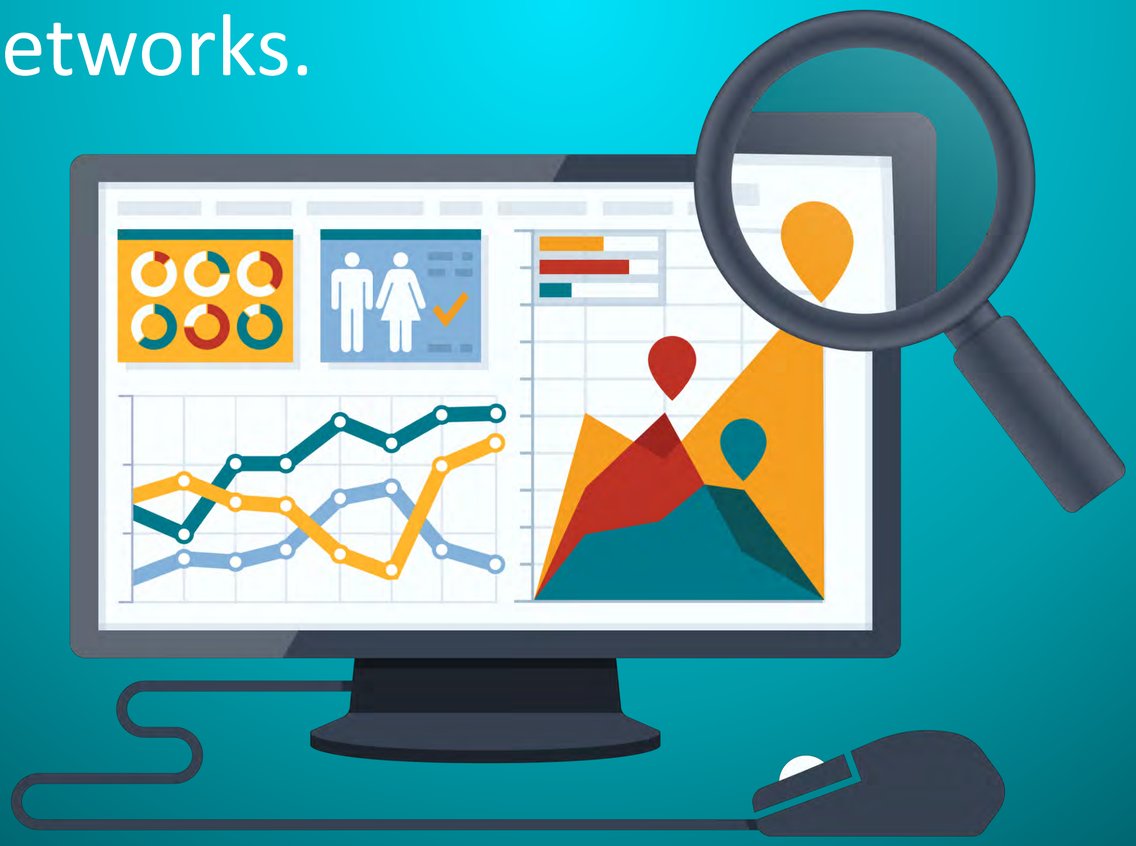


Figure 1. Sequence completeness (percentage of diagnoses in the past 3 years with an HIV sequence available), by quarterly dataset

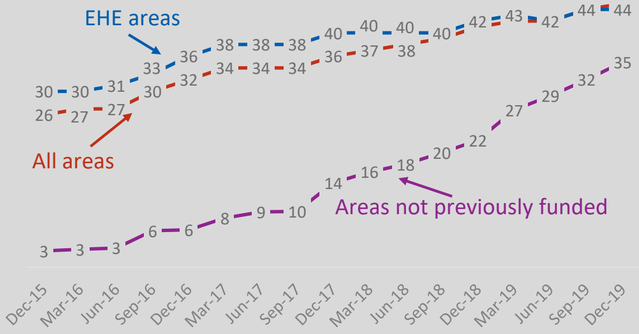
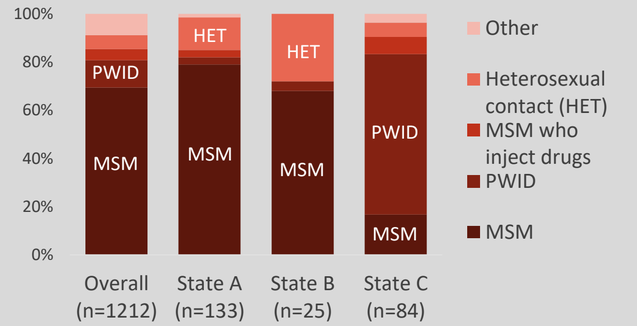
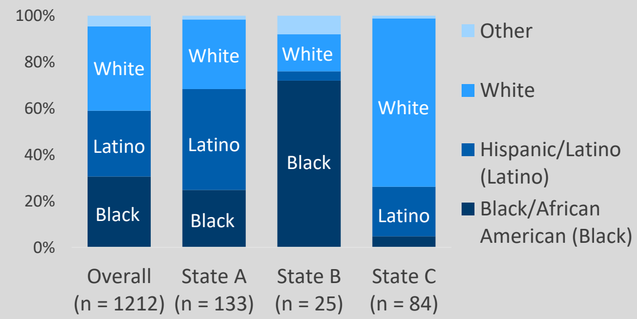


Figure 2. Characteristics of people in clusters of rapid transmission first detected during 2018–2019, overall and in selected states

A. Transmission category



B. Race/ethnicity



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