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HIV SEQUENCING AT DIAGNOSIS ENHANCES DETECTION OF CLUSTERS AND POTENTIAL CARE GAPS

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BACKGROUND

Status quo

HIV diagnosis

Linkage to care

Drug resistance testing
- Includes **HIV genetic sequencing**

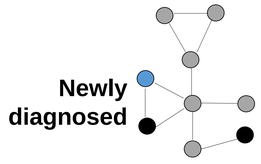
Viral load & CD4 count measurement

Data reported to public health

Sequences used to identify growing transmission clusters

Antiretroviral therapy adherence

Viral suppression



Can HIV genetic sequencing at time of diagnosis improve our understanding of transmission clusters and potential gaps in care?

METHODS

Population: 847 persons aged ≥13 years old, diagnosed with HIV in North Carolina between 2018-2021, alive within one year of HIV diagnosis, with an HIV test processed by the North Carolina State Laboratory for Public Health (NC-SLPH) (~25% of all new HIV diagnoses), and with HIV sequencing conducted within one year of HIV diagnosis and reported by January 18, 2023.

- **Routine clinical sequencing:** collected during drug resistance testing at antiretroviral therapy (ART) initiation, and reported to state public health by commercial laboratories or the NC-SLPH
- **Next-generation sequencing (NGS):** from 2018-2021, conducted additional sequencing on **remnant diagnostic specimens** from persons testing newly positive for HIV at the NC-SLPH (Zhou, 2020)

Cluster analysis: Clusters were defined at <1.5% genetic distance threshold between ≥2 sequences using the TN-93 model. Analysis used >20,000 sequences, including those from persons diagnosed prior to 2018 and at commercial laboratories.

Clinical outcomes:
- **Never received care:** no reported HIV viral load or CD4 cell count within one year of HIV diagnosis
- **Most recent viral load unsuppressed or missing:** no reported viral load, or latest viral load within one year of HIV diagnosis >200 copies of HIV /mL blood

HIV sequencing from diagnostic samples overcomes reporting gaps and incorporates persons unengaged in care into cluster analysis

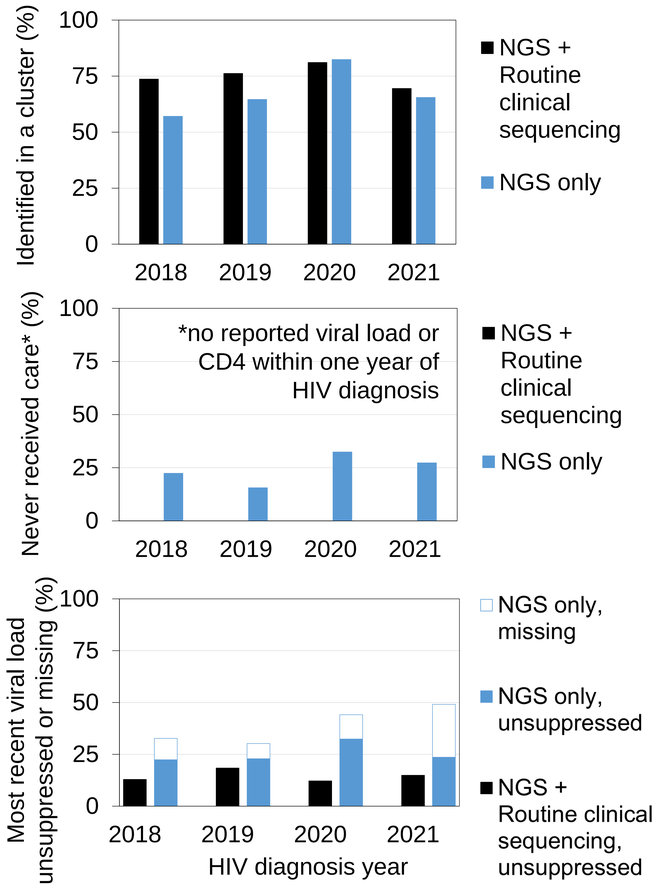
CONCLUSIONS

- 33% of persons diagnosed with HIV through NC-SLPH did not receive routine clinical sequencing within one year. These persons were frequently identified in a cluster, but less likely to receive timely HIV care.
- Many persons without a routine clinical sequence did access care, indicating underreporting.
- HIV sequencing of diagnostic samples can overcome reporting shortfalls, incorporate persons unengaged or more difficult to engage in care into cluster analysis, and accelerate cluster identification and response.

RESULTS – clinical and cluster characteristics

Within one year of HIV diagnosis…

564 persons (67%)	Had a sequence from NGS at diagnosis + Routine clinical sequencing
283 persons (33%)	Had a sequence from NGS at diagnosis only



322 clusters
of persons living with HIV in North Carolina in which ≥1 newly diagnosed† member had a sequence from NGS

135 clusters
in which ≥1 newly diagnosed† member had a sequence from NGS only

22 clusters (•)
in which ALL newly diagnosed† members had a sequence from NGS only

† diagnosed between 2018-2021, ≥1 HIV sequence reported within one year of diagnosis

