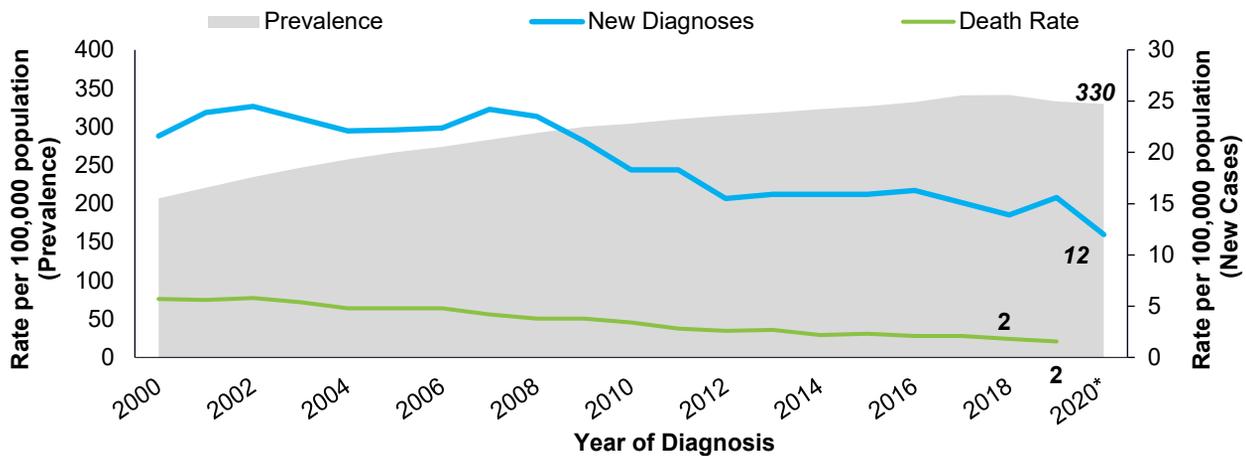




HIV Genotyping and Molecular Clusters, 2020



HIV rates in North Carolina: New diagnoses, people living with HIV (prevalence), and death rate 2000-2020*



- 1,079 adults/adolescents were newly diagnosed with HIV/AIDS in 2020 (rate of 12.0 cases per 100,000).
- Since 2012, there has been a plateau in the rate of new HIV diagnoses among adults/adolescents living in NC.

To continue to decrease new HIV infections in NC, the Division of Public Health is beginning to use HIV genotypes to identify molecular clusters

What is a genotype?

- An HIV genotype is a string of DNA, the genetic sequence of the virus in a person’s body.
- HIV genotypes are extracted from blood samples and used for HIV drug-resistance testing, which helps healthcare providers choose the best antiretroviral drugs for their patients.
- HIV sequence data is collected in the form of consensus sequences when next generation sequencing (NGS) has been conducted. Raw NGS data is not collected or reported.

How are genotypes used to control HIV?

- HIV genotypes are currently being reported to the North Carolina HIV Surveillance Unit from labs that conduct drug-resistance testing.
- HIV genotypes that are similar enough can be linked into molecular clusters, or groups of people with similar HIV genotypes.
- If people newly diagnosed with HIV are linked into a molecular cluster, it can indicate that there is HIV transmission occurring within that cluster.

However

- A molecular cluster link does not indicate HIV transmission between two people, just that their viruses are genetically similar.
- A molecular cluster can never show who is transmitting HIV to whom, since information is always incomplete.

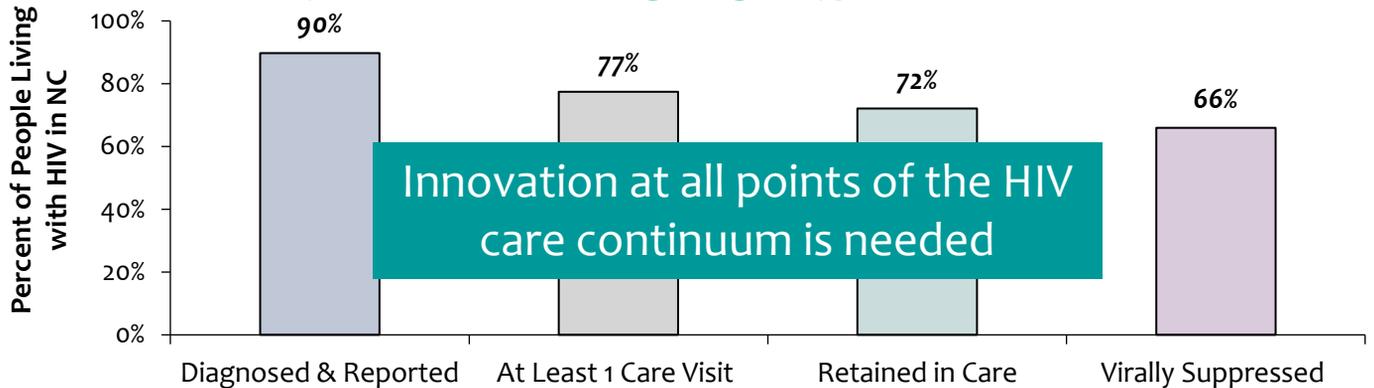
*Note: 2020 data should be treated with caution due to reduced availability of testing caused by the COVID-19 pandemic. Data is italicized for this reason.



HIV Genotyping and Molecular Clusters, 2020



Why is North Carolina using HIV genotype information?



We need to innovate to improve our responses to HIV

- Identifying HIV molecular clusters helps NC Surveillance and Prevention staff assign linkage to care, education, and testing resources where they are most needed.

How is North Carolina using HIV genotype information?

- The HIV/STD/Viral Hepatitis Surveillance Unit is beginning to conduct HIV molecular cluster analyses.
- HIV Field Services staff will include cluster information in information used to identify people who are not in care and who are the highest priority for help in linking to care, finding pre-exposure prophylaxis (PrEP), and other support services.

How will North Carolina protect this information?

- Cluster information will remain confidential; while example clusters may be shared with the public, identifying information will never be released and clusters will only be shown with anonymous indicators.
- The Centers for Disease Control and Prevention (CDC) is requiring states to report cluster link information. NC never sends and the CDC does not accept names or other personally identifying information as part of HIV reporting.

What can COMMUNITY MEMBERS do?

- Learn more about HIV genetic sequencing and molecular clusters (resource in sidebar).
- Provide feedback on the DPH's use of HIV genotypes and this factsheet at this meeting.
- Educate yourself about HIV in NC, as well as PrEP and other HIV prevention methods (resources in sidebar).
- If you have HIV, seek treatment, as it is not only important for maintaining your own good health, but also for preventing further transmission of HIV. If you can't afford treatment, see the HIV Medical Assistance Program (HMAP) resource in sidebar.

What can HEALTHCARE PROVIDERS do?

- Request recommended HIV drug-resistance testing once a patient is first diagnosed with HIV or experiences virologic failure.
- Inform patients that HIV genotype data is currently being reported to the NC HIV/STD/Viral Hepatitis Surveillance Unit.

Data Sources: enhanced HIV/AIDS Reporting System (eHARS) (data as of June 28, 2021).