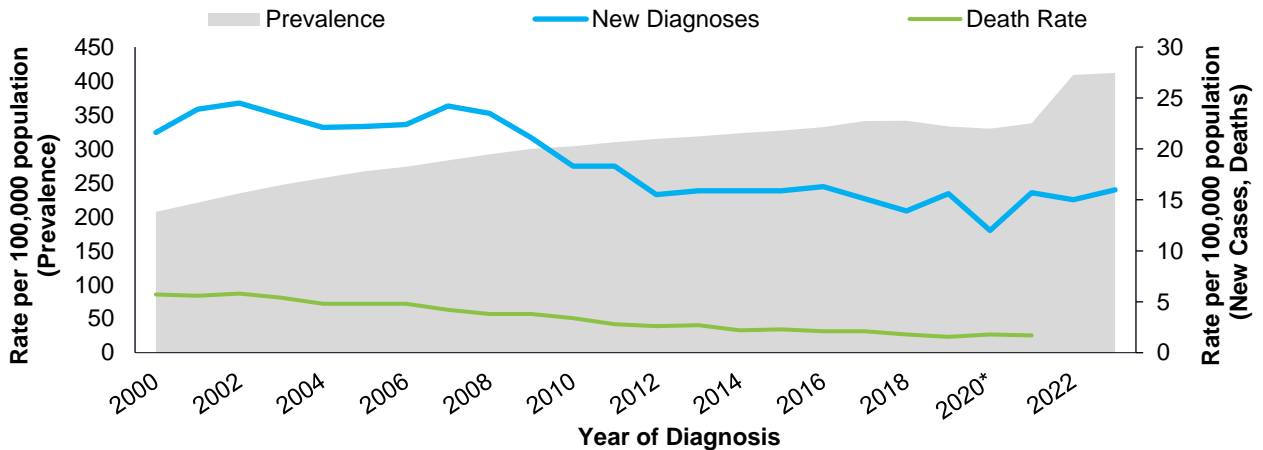




HIV Genotyping and Molecular Clusters, 2023



HIV Rates in North Carolina: New Diagnoses, People Living With HIV (Prevalence), and Death Rates 2000-2023

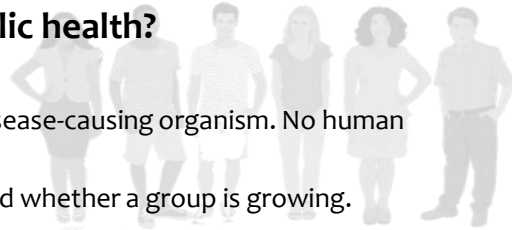


- 1,410 adults/adolescents were newly diagnosed with HIV/AIDS in 2023 (rate of 15.5 per 100,000).
- Since 2012, HIV rates in North Carolina have remained roughly the same.

To End HIV in North Carolina, we need to find new tools.

How are genotypes used for public health?

- A genotype is the genetic sequence of a disease-causing organism.
- For public health use, we only collect genetic information from the disease-causing organism. No human genetic information is collected.
- Organism genotypes are compared to understand how they group and whether a group is growing.
- Genotype information is used to understand many diseases, including COVID-19 (variants), E. coli and salmonella (outbreaks) and HIV (linkage to care and program development as described below).



How are genotypes used to control HIV?

- HIV genotypes that are similar enough can be linked into shared HIV networks.
- If people newly diagnosed with HIV are joined in a shared network, it can indicate that there is HIV transmission occurring within that network. Public health staff can reach out to people who are linked and who are not in care or have other needs, and a community can work to make access to testing, care and other services more available.

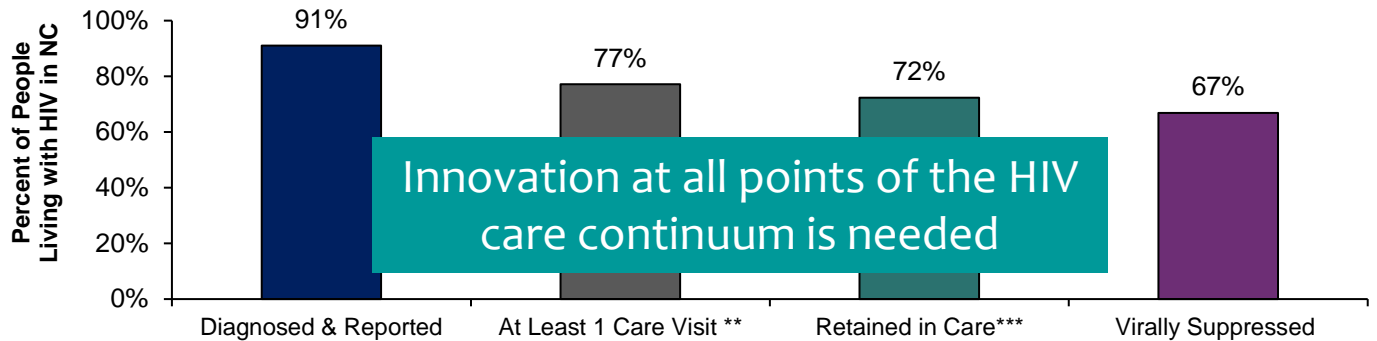
How is North Carolina using HIV genotype information?

- Monthly, growth in shared HIV networks is evaluated.
- Outreach staff will use network information to prioritize outreach to people who are not in care, to provide help in linking to care and other support services.

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



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Can genotypes be used to demonstrate transmission between people?

- A shared HIV network link does not indicate HIV transmission between two people, just that their viruses are genetically similar.
- A shared network can never show who is transmitting HIV to whom, since information is always incomplete; there may always be missing people between linked people.

How will North Carolina protect this information?

- Genotype information will remain confidential; identifying information will never be released.
- While information about growing shared genotype networks may be shared with the community working to End HIV, it will be general information; no identifiers will be shared.

What can COMMUNITY MEMBERS do?

- Learn more about HIV genetic sequencing and how it is used here: <https://www.cdc.gov/hiv/programresources/guidance/cluster-outbreak/index.html>
- Access PrEP and HIV treatment services:
 - HIV treatment: <https://epi.dph.ncdhhs.gov/cd/hiv/hmap.html>
 - PreP: <https://www.med.unc.edu/ncaidstraining/prep/PrEP-for-consumers> or <https://pleaseprepme.org>

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 genotype information for communicable diseases, including HIV genotypes, is reportable to the NC Division of Public Health and is used for communicable disease response and patient support.

Data Sources: enhanced HIV/AIDS Reporting System (eHARS) (data as of July 1, 2024).