Molecular HIV Surveillance, 2013-2015

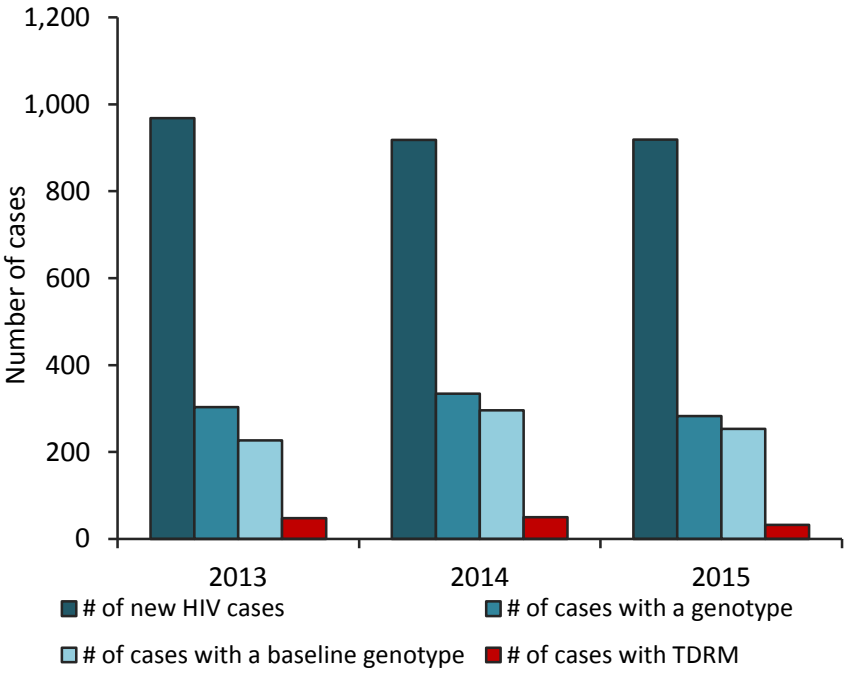
Virginia Department of Health 12.2016

Molecular HIV Surveillance (MHS)
The systematic collection and analysis of HIV genotype data to supplement routine HIV surveillance activities

Objectives

- Collect all **HIV-1 nucleotide sequence data** from laboratories that perform HIV genotype drug resistance testing.
- Use molecular epidemiologic techniques to assess HIV **drug resistance**, evaluate HIV **genetic diversity**, and describe HIV **transmission patterns**.
- Disseminate results of molecular HIV data analyses to assist HIV **treatment**, **prevention**, and **program planning** and **evaluation**.

Figure 1. HIV Genotype Completeness in Virginia, 2013-2015[ab]



A scanning electron microscopic image of HIV-1 virions (green) on a cultured lymphocyte

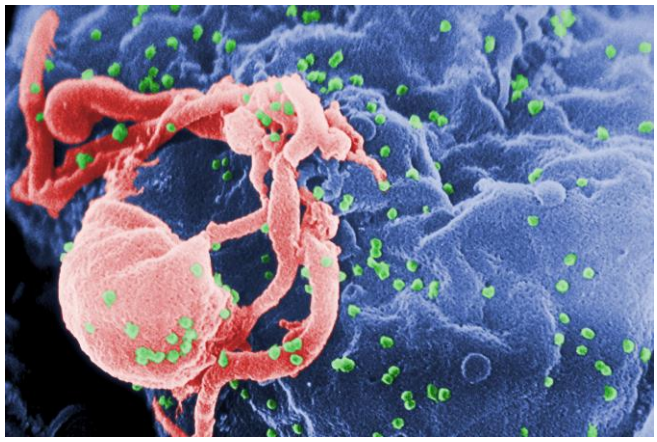


Photo by CDC/C. Goldsmith https://phil.cdc.gov/phil/details.asp?pid=10000

MHS Facts

Antiretroviral drugs (**ARV**) are used to suppress HIV viral loads and lead to better health outcomes when used appropriately and consistently.

MHS collects data regarding four classes of ARVs that target enzymes used in HIV replication: protease inhibitors (**PI**), nucleoside reverse transcriptase inhibitors (**NRTI**), non-nucleoside reverse transcriptase inhibitors (**NNRTI**), and integrase strand transfer inhibitors (**INSTI**).

Cases with **baseline genotypes** have HIV genotype drug-resistance testing performed within 3 months of diagnosis and no prior history of ARV use.

Cases with **transmitted drug resistance mutations** (**TDRM**) have an HIV-1 strain resistant to a class of ARV, potentially limiting ARV effectiveness. The presence of TDRMs in a newly diagnosed case, prior to ARV use, indicates the resistant virus was transmitted at the time of initial infection.

How does HIV genotype drug resistance testing work?

- Viral HIV-1 RNA is extracted from a patient's blood plasma and compared to a wild-type, non-mutated HIV strain to identify mutations associated with drug resistance.
- The level of drug resistance detected is reported to the ordering provider
- This raw HIV-1 nucleotide sequence data is reported electronically to the health department

[a] Limited to persons who resided in Virginia at diagnosis and were reported to CDC through December 2015. Persons with missing diagnosis years were excluded.
[b] For persons with multiple sequences, the earliest and longest was selected. Duplicate and invalid sequences were also excluded. TDRM limited to sequences assigned to the following subtypes: A, B, C, D, F, G, CRF01_AE and CRF02_AG

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Figure 2. Summary of drug resistance of all collected sequences, 2013-2015[ab]

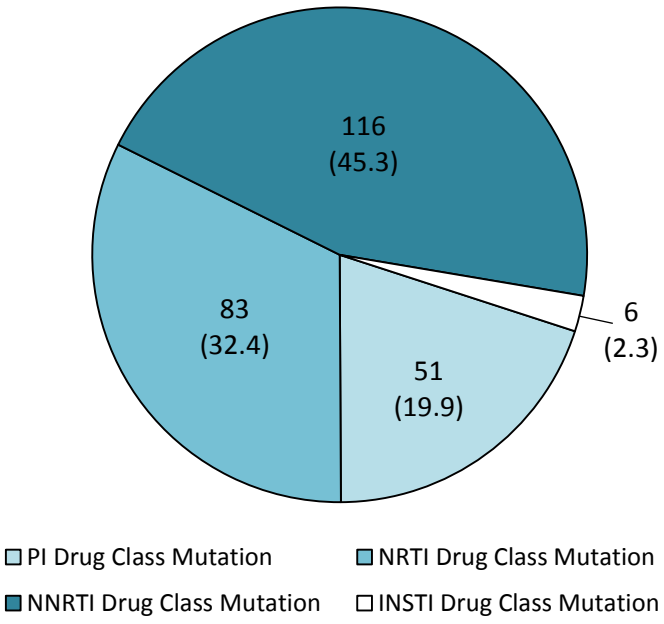

Figure 3. Number and percent of diagnoses by subtypes, 2013-2015[ac]

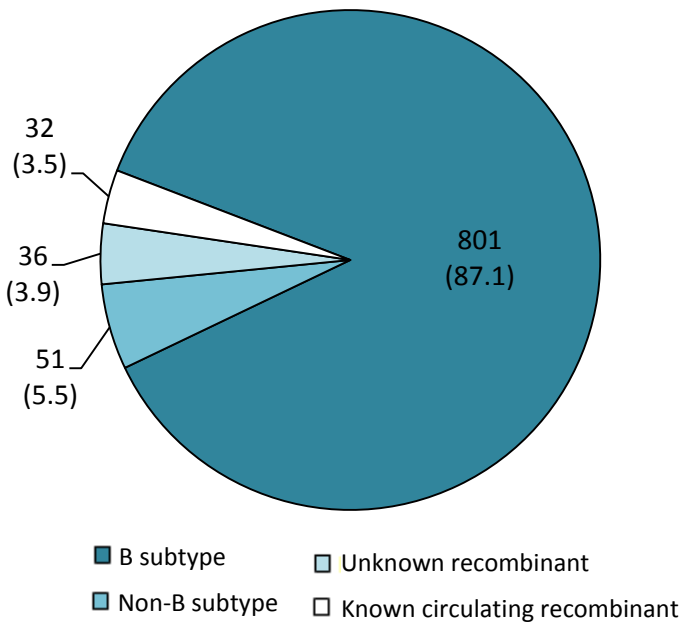

Table 1. Frequency and percentage of drug susceptibility of all collected sequences by ARV, 2013-2015[abde]

ARV[f]	Susceptible	Potential low level resistance	Low level resistance	Intermediate resistance	High level resistance
Nevirapine (NVP)	807 (84.0)	33 (3.4)	6 (0.6)	8 (0.8)	107 (11.1)
Efavirenz (EFV)	808 (84.1)	37 (3.9)	8 (0.8)	13 (1.4)	95 (9.9)
Elvitegravir (EVG)	167 (88.8)	12 (6.4)	3 (1.6)	0	6 (3.2)
Raltegravir (RAL)	167 (88.8)	12 (6.4)	4 (2.1)	0	5 (2.7)
Etravirine (ETR)	866 (90.1)	71 (7.4)	8 (0.8)	13 (1.4)	3 (0.3)
Rilpivirine (RPV)	866 (90.1)	29 (3.0)	37 (3.9)	7 (0.7)	22 (2.3)
Didanosine (DDI)	883 (91.9)	40 (4.2)	16 (1.7)	8 (0.8)	14 (1.5)
Stavudine (D4T)	893 (92.9)	13 (1.4)	29 (3.0)	19 (2.0)	7 (0.7)
Nelfinavir (NFV)	904 (94.1)	17 (1.8)	17 (1.8)	5 (0.5)	18 (1.9)
Zidovudine (AZT)	905 (94.2)	9 (0.9)	32 (3.3)	9 (0.9)	6 (0.6)
Abacavir (ABC)	913 (95.0)	2 (0.2)	29 (3.0)	19 (0.7)	7 (1.0)
Fosamprenavir (FPV)	914 (95.1)	28 (2.9)	16 (1.7)	3 (0.3)	0
Emtricitabine (FTC)	924 (96.1)	8 (0.8)	0	2 (0.2)	27 (2.8)
Lamivudine (3TC)	924 (96.1)	8 (0.8)	0	2 (0.2)	27 (2.8)

[a] Limited to persons who resided in Virginia at diagnosis and were reported to CDC through December 2015. Persons with missing diagnosis years were excluded.
[b] Includes all sequences, not limited to one sequence per person or to baseline sequences or people without evidence of ARV use. Excludes duplicate and invalid sequences.
[c] For persons with multiple sequences, the earliest and longest was selected. Duplicate and invalid sequences were also excluded
[d] Susceptibility results were ascertained using the Stanford University HIV Drug Resistance Database algorithm. For more information, including definitions and interpretations of drug susceptibility levels, go to https://hivdb.stanford.edu/page/release-notes/
[e] Darker shades of color indicate a larger proportion
[f] ARV not included due to low frequency of any type of resistance (% resistant): tenofovir (2.9) dolutegravir (2.7) atazanavir (3.3) darunavir (0.1) indinavir (3.2) lopinavir (2.7) saquinavir (3.1) tipranavir (3.6)