MOLECULAR HIV SURVEILLANCE

CONNECTICUT 2010-2015

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Report prepared by Rory Angulo MD, MBA, Epidemiologist, MHS Program Coordinator. Collaborators: Lynn Sosa MD, TB/STD Control Programs Coordinator. Suzanne Speers MPH, Epidemiologist/Data Manager, HIV Surveillance Program.

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Molecular HIV Surveillance, Connecticut 2010–2015

Connecticut (CT) Molecular HIV Surveillance (MHS), a CDC-sponsored project, has been operating since 2008 under the umbrella of HIV Surveillance. The goal of the project is to characterize the resistance pattern in people newly diagnosed with HIV, monitor trends in HIV drug resistance and provide information to stakeholders that can be used for strategic prevention efforts.

In 2009, CT Department of Public Health (DPH) mandated the electronic laboratory reporting of HIV nucleotide sequences. MHS collects all HIV genotype sequences. De-identified HIV sequences are transmitted to CDC for data cleaning and processing. In turn, CDC provides a dataset utilized for local data analysis. Analysis includes the first genotype result from a specimen taken within three months of the date of diagnosis, the case-patient is a Connecticut resident at time of diagnosis and the case-patient has not taken anti-retrovirals (ARV) at the time of HIV genotype specimen collection.

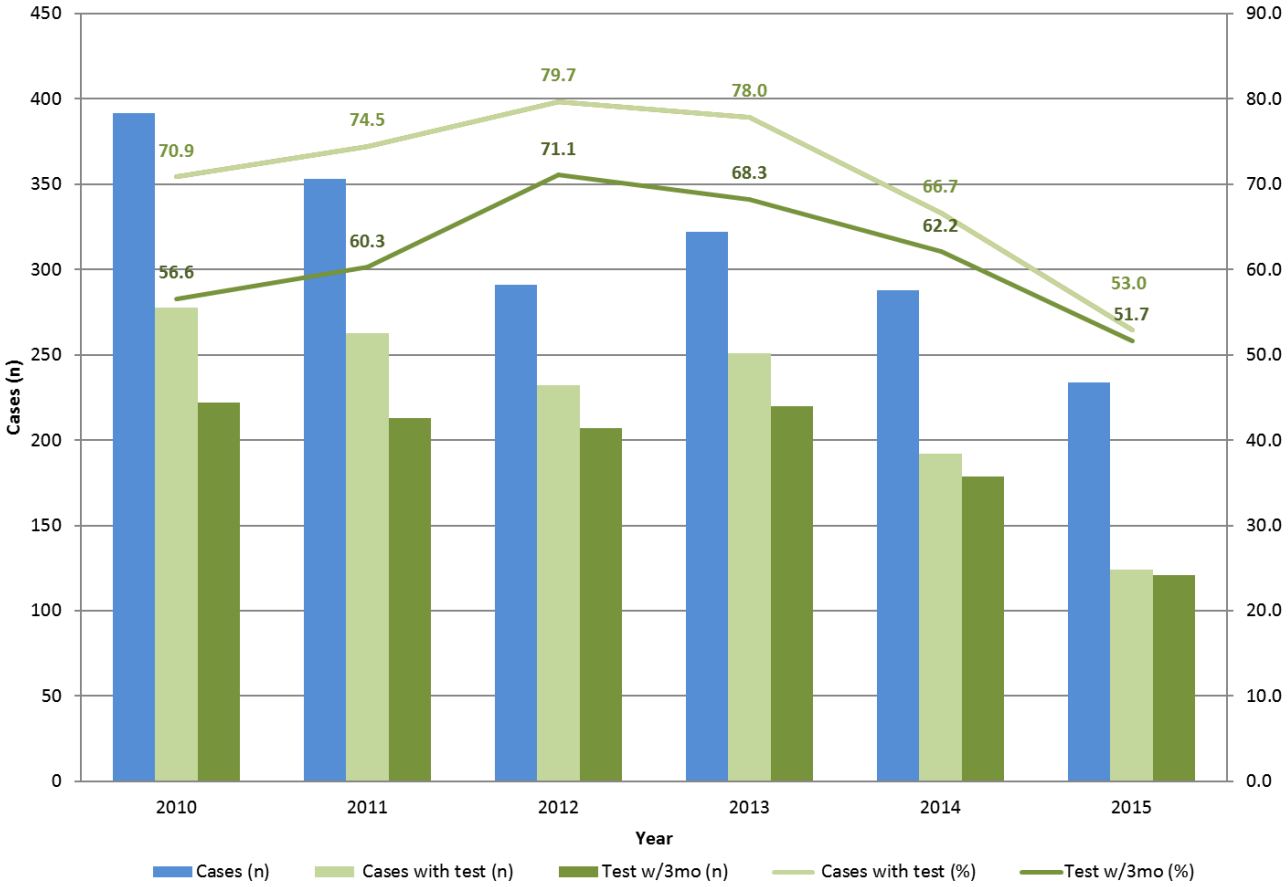
After de-duplication and selecting for eligibility, 3,651 nucleotide sequences were analyzed. This report focuses on protease (PR) and reverse transcriptase (RT) mutations of the HIV nucleotide sequence from specimens collected during 2010–2015.

I. Genotype Testing Patterns – Healthcare Providers

The 'Guidelines for the Use of Antiretroviral Agents in HIV-1-Infected Adults and Adolescents', published by the Department of Health and Human Services (DHHS) recommends, among other tests/procedures, HIV drug resistance testing for persons with HIV infection at entry into care, genotypic testing being the preferred resistance testing.

A complete baseline evaluation at entry into care, in addition to laboratory test results, provides clinicians with the necessary information to assess initial HIV staging, guide management goals and plans and to achieve viral suppression as the ultimate goal.

Figure 1. HIV Cases and MHS-qualifying Genotype Testing, Connecticut, 2010–2015



Source: eHARS through 2015.

Figure 1 displays, on a yearly basis, the number of new HIV diagnoses, the number of cases with a genotype test and the number of cases with a genotype test within 3 months of initial diagnosis. Figure shows an upward trend in providers requesting a genotype test during years 2010–2012. In this upward trend, the 8.6 percentage point gap between cases with test and cases with test within 3 months is narrowest for year 2012, indicating the peak year when most providers were requesting the test at, or near, the time of initial diagnosis as part of a baseline evaluation. Also, this is the year with the greatest percentage of providers requesting the test overall.

After 2012, total percentage of cases with a test at any time follows a downward trend, reaching all-time lowest point of 51.7% in 2015. Reasons for this trend could be a declining number of care providers not ordering the test at entry into care, no virologic failure that would require a genotype test to support change of ARV medication given current (standard) treatment, clinicians not requesting a genotype test as part of HIV management, patient's compliance to laboratory request, patient's lack of insurance or insufficient coverage.

II. Resistance Profile.

Figure 2. Cases with Genotype Testing and Resistant Patterns, by Drug-resistance Mutation, Connecticut 2010–2015

In total, 1,162 nucleotide sequences were collected for cases diagnosed during 2010–2015; of these, 947 (81.5%) met eligibility for sequence analysis and were reported to CDC through December 2015. Persons with missing diagnosis years were excluded.

Figure 2 shows that approximately 17% of new diagnoses present with an HIV variant that may be resistant to an ARV. Among these cases, 140 (85.4%) had a mutation associated with one class of ARV and 24 (14.6%) had a mutation associated with two or more classes of ARV. Nucleotide mutations resulted in HIV variants most commonly resistant to Non-nucleoside Reverse Transcriptase Inhibitor (NNRTI) drugs.

HIV genotyping showed that transmission occurred with a B-type strain in 90% of the cases.

Table 1. Number and Percent of Diagnoses with PR and RT sequences[1], by TDRM[2] and Selected Demographic Characteristics. Connecticut 2009–2015.

	Total	Any TDRM		1-Class TDRM		2-Class TDRM		3-Class TDRM		PI TDRM		NRTI TDRM		NNRTI TDRM	
	N	N	Row %	N	Row %	N	Row %	N	Row %	N	Row %	N	Row %	N	Row %
Total	**1,053**	**179**	**17.0**	**152**	**14.4**	**20**	**1.9**	**7**	**0.7**	**45**	**4.3**	**71**	**6.7**	**97**	**9.2**
Sex															
Male	815	131	16.1	112	13.7	13	1.6	6	0.7	35	4.3	51	6.3	70	8.6
Female	238	48	20.2	40	16.8	7	2.9	1	0.4	10	4.2	20	8.4	27	11.3
Age at diagnosis (yr)															
<13	1	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
13–19	43	8	18.6	6	14.0	1	2.3	1	2.3	3	7.0	3	7.0	5	11.6
20–29	282	40	14.2	37	13.1	2	0.7	1	0.4	11	3.9	9	3.2	24	8.5
30–39	243	46	18.9	38	15.6	6	2.5	2	0.8	6	2.5	22	9.1	28	11.5
40–49	257	46	17.9	40	15.6	5	1.9	1	0.4	12	4.7	19	7.4	22	8.6
50–59	164	27	16.5	20	12.2	6	3.7	1	0.6	12	7.3	12	7.3	11	6.7
≥60	63	12	19.0	11	17.5	0	0.0	1	1.6	1	1.6	6	9.5	7	11.1
Race/ethnicity															
Black/African American	392	81	20.7	68	17.3	9	2.3	4	1.0	20	5.1	30	7.7	48	12.2
Hispanic/Latino	279	47	16.8	39	14.0	6	2.2	2	0.7	12	4.3	17	6.1	28	10.0
White	359	51	14.2	45	12.5	5	1.4	1	0.3	13	3.6	24	6.7	21	5.8
Unknown	23	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
Transmission category															
MSM	502	77	15.3	73	14.5	1	0.2	3	0.6	19	3.8	23	4.6	42	8.4
Male IDU	59	9	15.3	5	8.5	3	5.1	1	1.7	3	5.1	5	8.5	6	10.2
Male MSM & IDU	22	6	27.3	5	22.7	1	4.5	0	0.0	2	9.1	3	13.6	2	9.1
Male Heterosexual	143	24	16.8	18	12.6	5	3.5	1	0.7	6	4.2	10	7.0	15	10.5
Male Other/Unknown	89	15	16.9	11	12.4	3	3.4	1	1.1	5	5.6	10	11.2	5	5.6
Female IDU	32	9	28.1	8	25.0	1	3.1	0	0.0	2	6.3	4	12.5	4	12.5
Female Heterosexual	150	33	22.0	26	17.3	6	4.0	1	0.7	7	4.7	14	9.3	20	13.3
Female Other/Unknown	55	6	10.9	6	10.9	0	0.0	0	0.0	1	1.8	2	3.6	3	5.5

1 Sequences with no evidence of prior ARV drug use, collected within 3 months of diagnosis and able to be assessed for presence of transmitted drug-resistance–associated mutations using the CDC mutation list, included sequence with PR and RT segments and able to be interpreted for the presence of drug class mutations by Sierra.

2 TDRM=Transmitted Drug Resistant mutation

Females were proportionally the more affected sex group with a TDRM strain, with 20.2% females compared to 16.1% of males.

Nineteen percent of cases ≥60 years were affected by a TDRM strain, followed by those 30–39 years old (18.9%) and 13–19 years old (18.6%).

Among black/African American cases with an eligible nucleotide sequence, 20.7% had any TDRM, followed by Hispanic/Latinos (16.8%) and whites (14.2%).

Among males, men who have sex with men (MSM) with a history of intravenous drug use (IDU) was the group most affected with a TDRM strain, about one-third of the cases in that group, followed by the Other/Unknown risk factor with 16.9%.

Among females, those with a history of IDU were the most affected with a resistant strain at 28.1%, followed for those with heterosexual contact, 22%.