Variant, Atypical, and Resistant HIV Surveillance (VARHS)

Variant, atypical, and resistant HIV surveillance is an extension of HIV case surveillance activities funded by the Centers for Disease Control and Prevention (CDC). The Colorado Department of Public Health and Environment has been funded since 2004 to collect HIV genetic sequence data.

Data from VARHS are used to monitor the frequency of transmitted antiretroviral (ARV) drug-resistance-associated mutations and HIV subtypes among persons for whom HIV is newly diagnosed in Colorado. These data are analyzed to determine the variance among transmitted strains of HIV and the emergence of resistant strains.

The following tables summarize the CDC analyzed genetic sequence data obtained from genotype testing when a person newly diagnosed with HIV enters care for HIV Infection. Transmitted drug resistance-associated mutations (TDRM) are monitored in three antiretroviral drug classes: the protease inhibitor (PI) class, the nucleoside reverse transcriptase inhibitor (NRTI) class and the non-nucleoside reverse transcriptase inhibitor (NNRTI) class.

From 2006 through 2010, 686 genetic sequences were obtained for analysis. Mutations associated with transmitted drug resistance occurred in 97 (14%) persons. TDRM associated specifically with the PI drug class occurred in 18 (2.6 %) sequences. TDRM associated specifically with the NRTI drug class occurred in 36 (5.5%) sequences. TDRM associated specifically with the NNRTI drug class occurred in 57 (8.3%) sequences. HIV-1 subtype B was the most prevalent occurring in 95.4 percent of 686 sequences. Data in Colorado is similar to the national trends.

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Table 1.
Prevalence of Mutations Associated With Transmitted Resistance to PI Drug Class (N = 18), 2006-2010

AA*	Mutation†	Exclusions	Total Prevalence		Only Mutation	
			N	%‡	N§	%¶
V11	I	CRF01-AE CRF02-AG G	1	5.6	1	100
L24	I		3	16.7	0	0
D30	N		1	5.6	0	0
M46	I		2	11.1	1	50
	L		3	16.7	1	33.3
I47	V		1	5.6	1	100
I54	V		2	11.1	0	0
Q58	E	D	2	11.1	2	100
T74	S	A CRF01-AE CRF02-AG C F G	1	5.6	0	0
V82	A		3	16.7	0	0
I85	V		3	16.7	2	66.7
N88	D		1	5.6	0	0
L90	M		5	27.8	2	40

[1]Limited to cases with sequences that can be assessed using CDC mutation list, i.e., those that include all positions on CDC list and belong to subtypes A, B, C, D, F, and G and circulating recombinant forms CRF01-AE and CRF02-AG
**Total no. of sequences with ≥1 PI TDRM (Transmitted Drug Resistance-associated Mutation)*
*[2]*Amino Acid*
†Some TDRM excluded from analysis of specifc subtypes (see Exclusions column) due to possible naturally-occurring polymorphisms in drug-naïve HIV-infected persons
‡Denominator = No. of sequences with ≥1 PI TDRM
**No. of sequences for which identifed mutation is only TDRM present*
¶Denominator = No. of sequences with TDRM at specified AA position

Table 2.
Prevalence of Mutations Associated With Transmitted Resistance to NRTI Drug Class (N = 36) 2006-2010

AA*	Mutation†	Exclusions	Total Prevalence		Only Mutation	
			N	%‡	N§	%¶
M41	L		4	11.1	1	25
E44	D	D F	1	2.8	0	0
A62	V	A	2	5.6	1	50
D67	N		6	16.7	1	16.7
T69	A	D F	7	19.4	7	100
	D		1	2.8	0	0
	N		5	13.9	3	60
V75	A		2	5.6	1	50

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Table 2.
Prevalence of Mutations Associated With Transmitted Resistance to NRTI Drug Class (N = 36) 2006-2010

AA*	Mutation†	Exclusions	Total Prevalence		Only Mutation	
	T		1	2.8	0	0
M184	I		1	2.8	1	100
	V		2	5.6	1	50
L210	W		1	2.8	0	0
T215	C		3	8.3	0	0
	D		2	5.6	0	0
	E		2	5.6	2	100
	S		6	16.7	4	66.7
K219	E		1	2.8	0	0
	N		1	2.8	0	0
	Q		4	11.1	0	0

[1]Limited to cases with sequences that can be assessed using CDC mutation list, i.e., those that include all positions on CDC list and belong to subtypes A, B, C, D, F, and G and circulating recombinant forms CRF01-AE and CRF02-AG
[2]Total no. of sequences with ≥1 NRTI TDRM (Transmitted Drug Resistance-associated Mutation)
**Amino Acid*
[†]Some TDRM excluded from analysis of specific subtypes (see Exclusions column) due to possible naturally-occurring polymorphisms in drug-naïve HIV-infected persons
[‡]Denominator = No. of sequences with ≥1 NRTI TDRM
[§]No. of sequences for which identified mutation is only TDRM present
[¶]Denominator = No. of sequences with TDRM at specified AA position

Table 3.
Prevalence of Mutations Associated With Transmitted Resistance to NNRTI Drug Class (N = 57), 2006-2010

AA*	Mutation	Total Prevalence		Only Mutation	
		N	%‡	N§	%¶
K101	E	2	3.5	0	0
K103	N	47	82.5	37	78.7
	S	3	5.3	2	66.7
Y181	C	3	5.3	0	0
Y188	L	1	1.8	0	0
G190	A	6	10.5	3	50
	E	1	1.8	1	100
P225	H	2	3.5	0	0

[1]Limited to cases with sequences that can be assessed using CDC mutation list, i.e., those that include all positions on CDC list and belong to subtypes A, B, C, D, F, and G and circulating recombinant forms CRF01-AE and CRF02-AG
[2]Total no. of sequences with ≥1 NNRTI TDRM (Transmitted Drug Resistance-associated Mutation)
**Amino Acid*
[‡]Denominator = No. of sequences with ≥1 NNRTI TDRM
[§]No. of sequences for which identified mutation is only TDRM present

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¶*Denominator = No. of sequences with TDRM at specified AA position*

Table 4.
Number and Percent of New Diagnoses of HIV Disease with VARHS Genotyping Results[1], by TDRM[2] Content and Selected Demographic Characteristics, 2006-2010

		Any TDRM		1-Class TDRM		2-Class TDRM		3-Class TDRM		PI TDRM		NRTI TDRM		NNRTI TDRM	
	Total	N	%	N	%	N	%	N	%	N	%	N	%	N	%
	686	97	14	87	12.7	6	0.9	4	0.6	18	2.6	36	5.2	57	8.3
Sex															
Male	611	86	14	78	12.8	5	0.8	3	0.5	15	2.5	32	5.2	50	8.2
Female	75	11	15	9	12	1	1.3	1	1.3	3	4	4	5.3	7	9.3
Age at Diagnosis															
13–19	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20–29	228	38	17	35	15.4	1	0.4	2	0.9	11	4.8	14	6.1	18	7.9
30–39	206	29	14	26	12.6	2	1	1	0.5	3	1.5	10	4.9	20	9.7
40–49	165	24	15	22	13.3	1	0.6	1	0.6	2	1.2	10	6.1	15	9.1
50–59	58	5	8.6	4	6.9	1	1.7	0	0	2	3.4	1	1.7	3	5.2
≥60	13	1	7.7	0	0	1	7.7	0	0	0	0	1	7.7	1	7.7
Race/Ethnicity															
American Indian/Alaska Native	9	2	22	2	22.2	0	0	0	0	1	11.1	1	11.1	0	0
Asian	13	1	7.7	1	7.7	0	0	0	0	0	0	0	0	1	7.7
Black/African American	97	13	13	10	10.3	2	2.1	1	1	3	3.1	6	6.2	8	8.2
Hispanic/Latino	201	23	11	21	10.4	2	1	0	0	3	1.5	10	5	12	6
Multiple Races	6	2	33	1	16.7	1	16.7	0	0	0	0	2	33.3	1	16.7
White	360	56	16	52	14.4	1	0.3	3	0.8	11	3.1	17	4.7	35	9.7
Transmission Category															
MSM	492	70	14	63	12.8	4	0.8	3	0.6	13	2.6	26	5.3	41	8.3
MALE IDU	11	1	9.1	0	0	1	9.1	0	0	0	0	1	9.1	1	9.1
MSM & IDU	48	9	19	9	18.8	0	0	0	0	2	4.2	2	4.2	5	10.4
Male Heterosexual Contact	28	2	7.1	2	7.1	0	0	0	0	0	0	0	0	2	7.1
Male Other/Unknown	32	4	13	4	12.5	0	0	0	0	0	0	3	9.4	1	3.1
Female IDU	4	2	50	2	50	0	0	0	0	0	0	0	0	2	50
Female Heterosexual Contact	60	9	15	7	11.7	1	1.7	1	1.7	3	5	4	6.7	5	8.3
Female Other/Unknown	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Facility of Diagnosis															
Other	26	6	23	5	19.2	1	3.8	0	0	2	7.7	1	3.8	4	15.4
Unknown	16	1	6.3	1	6.3	0	0	0	0	0	0	0	0	1	6.3

Variant, Atypical, and Resistant HIV Surveillance (VARHS)

Table 4.
Number and Percent of New Diagnoses of HIV Disease with VARHS Genotyping Results[1], by TDRM[2] Content and Selected Demographic Characteristics, 2006-2010

		Any TDRM		1-Class TDRM		2-Class TDRM		3-Class TDRM		PI TDRM		NRTI TDRM		NNRTI TDRM	
	Total	N	%	N	%	N	%	N	%	N	%	N	%	N	%
	686	97	14	87	12.7	6	0.9	4	0.6	18	2.6	36	5.2	57	8.3
Hospital	27	3	11	3	11.1	0	0	0	0	0	0	2	7.4	1	3.7
HMO Clinic	51	5	9.8	4	7.8	0	0	1	2	1	2	3	5.9	3	5.9
Private Physician's Office	118	16	14	13	11	2	1.7	1	0.8	5	4.2	6	5.1	9	7.6
Adult HIV Clinic	9	2	22	2	22.2	0	0	0	0	1	11.1	0	0	1	11.1
Infectious Disease Clinic	6	2	33	2	33.3	0	0	0	0	0	0	1	16.7	1	16.7
Pediatric HIV Specialty Clinic	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OB-GYN Clinic	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Other Clinic	25	4	16	3	12	0	0	1	4	2	8	1	4	3	12
Community Health Center	8	1	13	1	12.5	0	0	0	0	0	0	1	12.5	0	0
Primary Care Clinic, Not Specified	15	3	20	3	20	0	0	0	0	0	0	0	0	3	20
School or University Clinic	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Emergency Room	13	3	23	3	23.1	0	0	0	0	1	7.7	1	7.7	1	7.7
Blood Bank or Plasma Center	5	1	20	1	20	0	0	0	0	0	0	0	0	1	20
Family Planning Clinic	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HIV Case Management Agency	50	4	8	3	6	1	2	0	0	4	8	0	0	1	2
HIV Counseling and Testing Site	47	6	13	6	12.8	0	0	0	0	0	0	2	4.3	4	8.5
Insurance Screening	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
STD Clinic	210	34	16	32	15.2	1	0.5	1	0.5	2	1	16	7.6	19	9
Other	14	1	7.1	1	7.1	0	0	0	0	0	0	0	0	1	7.1
Correctional Facility	36	5	14	4	11.1	1	2.8	0	0	0	0	2	5.6	4	11.1
Country of Birth															
United States	605	90	15	81	13.4	5	0.8	4	0.7	17	2.8	32	5.3	54	8.9
Other (non-U.S.)	78	7	9	6	7.7	1	1.3	0	0	1	1.3	4	5.1	3	3.8
Unknown/Missing	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0

[1]Limited to cases with sequences that can be assessed using CDC mutation list, i.e., those that include all positions on CDC list and belong to subtypes A, B, C, D, F, and G and circulating recombinant forms CRF01-AE and CRF02-AG
[2]Transmitted Drug Resistance-associated Mutation(s)

Variant, Atypical, and Resistant HIV Surveillance (VARHS)

Table 5.
Number and Percent of New Diagnoses of HIV Disease with VARHS Genotyping Results[1], by Subtype or Circulating Recombinant Form and Selected Demographic Characteristics, 2006-2010

		A		B		C		CRF01-AE		CRF02-AG		CRF06		F		UNIQUE RECOMBINANT	
	Tot	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%
	691	4	0.6	659	95.4	13	1.9	3	0.4	6	0.9	4	0.6	1	0.1	1	0.1
Sex																	
Male	612	4	0.7	600	98	2	0.3	3	0.5	2	0.3	1	0.2	.	.	.	.
Female	79	.	.	59	74.7	11	13.9	.	.	4	5.1	3	3.8	1	1.3	1	1.3
Age at Diagnosis																	
13–19	16	.	.	16	100	.	.	.	.	.	.	.	.	.	.	.	.
20–29	230	1	0.4	221	96.1	4	1.7	1	0.4	1	0.4	1	0.4	.	.	1	0.4
30–39	209	.	.	197	94.3	5	2.4	.	.	3	1.4	3	1.4	1	0.5	.	.
40–49	165	3	1.8	157	95.2	3	1.8	1	0.6	1	0.6	.	.	.	.	.	.
50–59	58	.	.	56	96.6	.	.	1	1.7	1	1.7	.	.	.	.	.	.
≥60	13	.	.	12	92.3	1	7.7	.	.	.	.	.	.	.	.	.	.
Race/Ethnicity																	
American Indian/Alaska Native	9	.	.	9	100	.	.	.	.	.	.	.	.	.	.	.	.
Asian	13	.	.	11	84.6	.	.	2	15.4	.	.	.	.	.	.	.	.
Black/African American	102	4	3.9	76	74.5	12	11.8	.	.	4	3.9	4	3.9	1	1	1	1
Hispanic/ Latino	201	.	.	199	99	.	.	1	0.5	1	0.5	.	.	.	.	.	.
Multiple Races	6	.	.	6	100	.	.	.	.	.	.	.	.	.	.	.	.
White	360	.	.	358	99.4	1	0.3	.	.	1	0.3	.	.	.	.	.	.
Transmission Category																	
MSM	492	1	0.2	489	99.4	1	0.2	1	0.2	.	.	.	.	.	.	.	.
Male IDU	11	.	.	11	100	.	.	.	.	.	.	.	.	.	.	.	.
MSM & IDU	48	.	.	48	100	.	.	.	.	.	.	.	.	.	.	.	.
Male Heterosexual Contact	29	3	10	20	69	1	3.4	2	6.9	2	6.9	1	3.4	.	.	.	.
Male Unknown	32	.	.	32	100	.	.	.	.	.	.	.	.	.	.	.	.

Variant, Atypical, and Resistant HIV Surveillance (VARHS)

Table 5.
Number and Percent of New Diagnoses of HIV Disease with VARHS Genotyping Results[1], by Subtype or Circulating Recombinant Form and Selected Demographic Characteristics, 2006-2010

		A		B		C		CRF01-AE		CRF02-AG		CRF06		F		UNIQUE RECOMBINANT	
	Tot	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%
Female IDU	4	.	.	4	100	.	.	.	.	.	.	.	.	.	.	.	.
Female Heterosexual Contact	64	.	.	44	68.8	11	17.2	.	.	4	6.3	3	4.7	1	1.6	1	1.6
Female Adult Unknown	11	.	.	11	100	.	.	.	.	.	.	.	.	.	.	.	.

[1]Limited to cases with sequences that can be assessed using CDC mutation list, i.e., those that include all positions on CDC list and belong to subtypes A, B, C, D, F, and G and circulating recombinant forms CRF01-AE and CRF02-AG
[2]Transmitted Drug Resistance-associated Mutation(s)