Poster
1504

HIV Antiretroviral Drug Resistance in Virginia:

a Descriptive Analysis Comparing Genotype Data from Two Different Time Periods

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Introduction

- Antiretroviral drug (ARV) resistance is conferred via mutations in the HIV genome
- Major mutations, by themselves, may reduce susceptibility to one or more ARVs[2]
- Minor mutations have little to no effect on susceptibility unless combined with a major mutation or may increase the replication fitness of viruses with major mutations[2]
- These mutations can be spread through transmitted drug resistant mutations (TDRMs) and are associated with treatment failure[1]
- Evaluating TDRMs and ARV resistance patterns can help guide treatment and direct public health interventions

Background

TDRMs and ARV resistance patterns in circulating HIV strains have been monitored in Virginia by two similar surveillance programs:

•Variant, Atypical, and Resistant HIV Surveillance (VARHS) program from 2004-2007, which used aliquots of remnant specimens drawn for HIV diagnostic testing of newly diagnosed individuals

•Molecular HIV Surveillance (MHS) program from 2013-2015, which uses eligible baseline genotypes reported to VDH from laboratories and healthcare providers

Purpose

The aim of this study was to compare circulating TDRMs and ARV resistance patterns seen in Virginia across two different timeframes.

Methods

- Data were collected from VARHS between 2004-2007 and from MHS between 2013-2015.
- Only eligible baseline HIV genotypes were included; eligible baseline HIV genotypes were defined as genotypes collected within 3 months of initial HIV diagnosis
- The Stanford University HIV Drug Resistance Database's genotypic resistance interpretation algorithm was used to identify ARV-resistant mutations and predict resistance patterns[2]
- Genotype completeness was reviewed and common mutations and ARV resistance patterns were compared between the two timeframes

Results

Completeness of Variant, Atypical, and Resistant HIV Surveillance (VARHS) Data in Virginia*

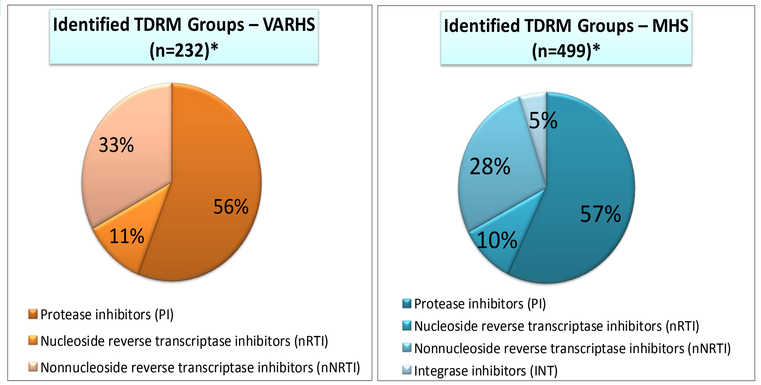
	2004		2005		2006		2007		Total	
	No.	%	No.	%	No.	%	No.	%	No.	%
Total genotypes collected	20	--	116	--	216	--	207	--	559	--
Total eligible baseline genotypes collected[a]	17	85	103	89	193	89	180	87	493	88
Total eligible baseline genotypes with transmitted drug resistant mutations[b]	9	53	40	39	75	39	66	37	190	39

* Based on specimen collection date
a Defined as total number of genotype tests conducted within three months of HIV diagnosis
b Defined as the total number of eligible genotypes with a major, minor, or accessory mutation

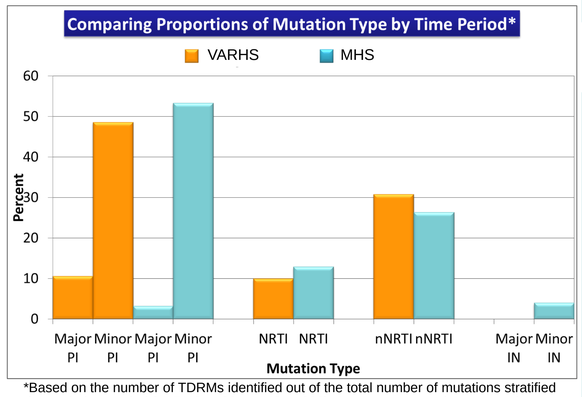
Completeness of Molecular HIV Surveillance (MHS) Data in Virginia*

	2013		2014		2015		Total	
	No.	%	No.	%	No.	%	No.	%
Total genotypes collected	970	--	1065	--	1182	--	3217	--
Total eligible baseline genotypes collected[a]	230	24	304	29	333	28	867	27
Total eligible baseline genotypes with transmitted drug resistant mutations[b]	106	46	135	44	152	46	393	45

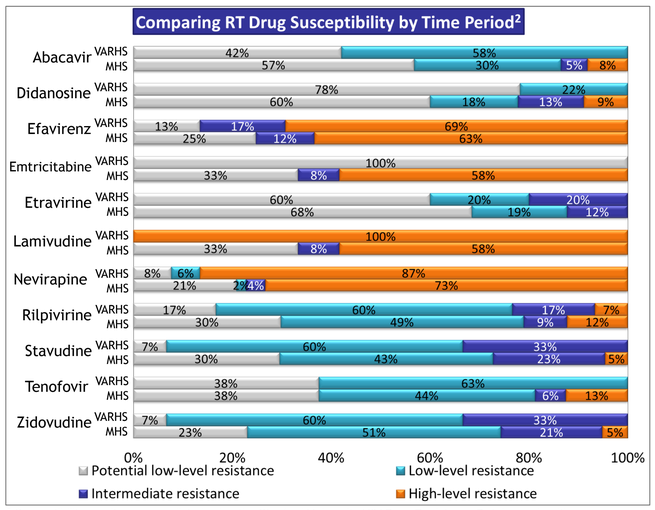
* Based on specimen collection date
a Defined as total number of genotype tests conducted within three months of HIV diagnosis
b Defined as the total number of eligible genotypes with a major, minor, or accessory mutation



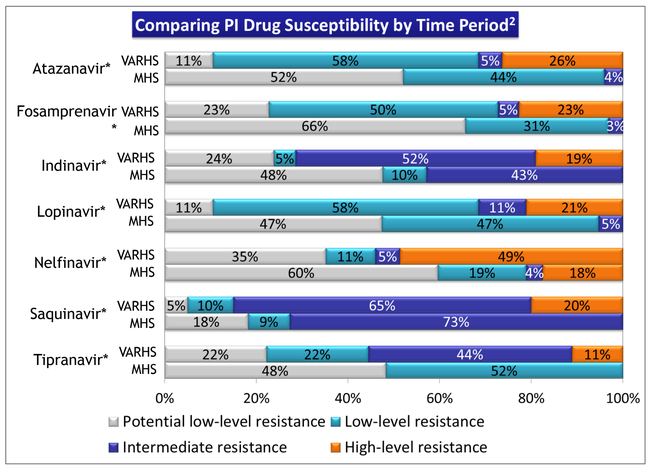
*Based on the total number of TDRMs identified in eligible baseline genotypes per TDRM group for each time period. A sequence may be included in more than one TDRM group. INT tests were not performed during the VARHS time period.



*Based on the number of TDRMs identified out of the total number of mutations stratified for each time period (VARHS n=321; MHS n=622). A sequence may have more than one mutation within a TDRM group and may have mutations in multiple groups.



[2] Susceptibility results were predicted using the Stanford University HIV Drug Resistance Database algorithm



*Coupled with a low dose of ritonavir
[2] Susceptibility results were predicted using the Stanford University HIV Drug Resistance Database algorithm
Note: Darunavir excluded due to low numbers: potential low-level (1) and low-level resistance were seen in VARHS data and low-level resistance (1) was seen in MHS.

Conclusion

- Overall, the mutation and resistance patterns observed across the two time frames appear to be similar
- There was a higher percentage of high-level resistance to PI ARVs identified in the VARHS time period compared to the MHS time period
- The MHS time period had an overall higher proportion of TDRMs, but VARHS had a higher proportion of major mutations
- The increased high-level resistance observed in VARHS genotypes may be attributable to a higher frequency of major mutations that was not observed in MHS
- The overall similarities between the VARHS and MHS time periods show that there has been consistency in the TDRMs circulating in Virginia.

Limitations and Next Steps

- INT testing was not performed during the VARHS time period, thus comparisons with MHS data could not be made
- HIV nucleotide sequence data reporting was not mandated during these two time periods, leading to low and incomplete numbers of genotypes reported to VDH.
- Of the 9 laboratories conducting HIV nucleotide genotyping on VA residents, only 7 were submitting data at some point during the MHS time period. At least 1 of the 7 were only able to submit data for 2015, leaving 2013 and 2014 underreported
- Complete reporting of all baseline genotypes is critical to continue tracking the evolution and transmission of TDRMs and ARV resistance patterns

References

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2. Liu, T.F., Shafer, R.W. (2006). Web Resources for HIV type 1 Genotypic-Resistance Test Interpretation. *Clin Infect Dis*, 42(11):1608-18. Epub 2006 Apr 28.
3. Shafer, R.W., and Schapiro, J.M. (2008). HIV-1 Drug Resistance Mutations: an Updated Framework for the Second Decade of HAART. *AIDS Reviews*, 10:67-84.

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