Molecular HIV Surveillance (MHS) in Michigan – technical guidance

Background

The HIV genotype (characterization of HIV nucleotide sequence) is an important laboratory test that the American Medical Association (AMA), World Health Organization (WHO), and IAS (International AIDS Society) recommends be run promptly on all individuals newly diagnosed with HIV infection. This establishes a baseline assessment of HIV strain prior to the initiation of anti-retrovirals. Baseline HIV genotypes are covered by Medicaid, Medicare, Ryan White and private insurance.

HIV genotype testing for the purpose of variant, atypical and drug resistant strain monitoring by the Michigan Department of Health and Human Services (MDHHS) was funded by the Centers for Disease Control and Prevention (CDC) in Michigan starting in 2005. MDHHS collected remnant serum from HIV diagnostic testing across the state and genotyping was performed by the CDC. Over time, this was augmented by the collection of electronic sequence data from private and commercial laboratories nationwide that were genotyping specimens from Michigan residents. In 2010 funding from CDC ceased for genotyping remnant specimens but MDHHS partnered with the University of Michigan to continue this practice until 2012. MDHHS also was able to secure funding to genotype remnant diagnostic specimens in storage at health department labs allowing Michigan HIV genotyping to go back as far as the late 1980s. Since 2012, variant, atypical and resistant HIV genotype surveillance in Michigan has been conducted using electronically reported sequence data exclusively. However, since 2006, genotypes have been included in the list of HIV labs required by law to be reported by all laboratories. Michigan is fortunate to have the highest percentage of genotypes collected on persons living with HIV in the nation. Approximately 80% of all diagnosed and reported Michigan HIV cases have an HIV genotype sequence stored by MDHHS.

The CDC has developed four overarching goals that are made possible by the timely and accurate reporting of HIV genotypes. The four goals are as follows; asses the prevalence of drug resistant strains of HIV, describe HIV transmission patterns, identify clusters and potential outbreaks, and monitor the genetic diversity (variant and atypical strains) of HIV. The focus of this guidance is the 3rd goal, identifying clusters and potential outbreaks.

Cluster information

Each month MDHHS analyzes the complete HIV genetic sequence database to identify HIV cases that may form clusters by comparing each genetic sequences to every other genetic sequence; this allows us to determine which cases are genetically similar. MDHHS can control the degree of genetic relatedness used to establish clusters. MDHHS can also decide what additional HIV surveillance data, when used together with genetic distance, may help establish clusters; this may include data such as information generated by partner service investigations or STD data.

Responding to Clusters

There are a few crucial things to be aware of when considering genetic clusters. First, clusters identified by genotype sequence data most likely represent only a part of a larger transmission cluster. Transmission clusters can include people that have HIV but are undiagnosed, people who are not in HIV care, and individuals who are in care but have not yet had an HIV genotype. There is also an even larger risk network of people that are currently negative but are at risk of acquiring HIV. Second, directionality...
of infection cannot be determined by position in the cluster. Further, the relationship between two HIV genotype sequences may stem from direct transmission or there may be unidentified individuals between the two sequences of the cluster in the transmission network. Third, the temporal relationship of people in clusters may not be fully understood. Clusters can include members diagnosed and HIV genotyped over a wide span of time. Finally, clusters must be considered in the context of other surveillance information such as demographic, risk, and geographic information.

Clusters and HIV Care and Prevention at Local Health Departments

As HIV genetic clusters are identified by MDHHS, the question arises as to what information can be learned about the HIV epidemic locally from cluster data and how HIV genotype sequence data can be used to better allocate prevention resources. Clusters of HIV sequences indicate areas of heightened transmission patterns in our positive communities and point to possible intervention points. What possible interventions are appropriate? Should individuals whose HIV genotype was identified in a genetic cluster be included in special prevention initiatives such as heightened partner solicitation including referral to pre-exposure prophylaxis, additional post-test counseling, or supportive linkage to care services?

Clusters and Providers

Inevitably, genetic clusters will include individuals who are newly diagnosed and not in care for their HIV infection, those who may have fallen out of care and/or those who are in care but are not virally suppressed. As MDHHS, in partnership with local health departments, investigates these clusters we need to consider the role HIV care providers could play in initiating contact with these individuals and providing important care services. Clusters that contain individuals who are not in HIV care and virally suppressed may be at an increased likelihood to transmit HIV to others and should be prioritized by care resources.

Molecular clusters and Community Based Organizations (CBO)

CBOs may prove to be valuable tools to partner with MDHHS and the local health departments in reaching out to those populations that could be affected by a growing transmission cluster. CBO’s connections to at-risk communities could help in informing clients that test positive of potential future communication from MDHHS or local health representative regarding cluster connections, initiating intervention strategies, and garnering community support.