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Large Phylogenetically Linked HIV Cluster in King County, Washington, 2008 to 2014

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BACKGROUND

- To reduce ongoing transmission of HIV, King County has prioritized viral suppression as an endpoint for all people living with HIV/AIDS (PLWHA)
- 'Partner services' activities initiate at the time of HIV diagnosis and can be re-invoked when individuals display "endangering behaviors", particularly non-disclosure or inaccurate disclosure of HIV status and being named by multiple partners
- One individual (index case) in King County was named by 13 individuals newly diagnosed with HIV, many reporting the index case had misreported being HIV uninfected
- Between 2009 and 2014, the index case had 22 non-HIV sexually transmitted infection (STI) diagnoses and was named as a contact by four people with non-HIV STI diagnoses (in addition to the 13 people with HIV diagnoses; 9 of whom had concurrent non-HIV STI)
- This situation initiated multiple actions by the health department to impel the index case to receive counseling and treatment for HIV

OBJECTIVES

- Public Health—Seattle & King County (PHSKC) conducted an investigation to estimate cluster size and relatedness of the HIV strains of the index case and partners
- Current viral status of related cases are being followed to determine if additional PH work needs to be initiated to interrupt further transmission

METHODS

Characteristics of related and newly diagnosed HIV cases were examined in King County, Washington State (the metropolitan area including Seattle) 01/2008 - 12/2014

Data sources included:

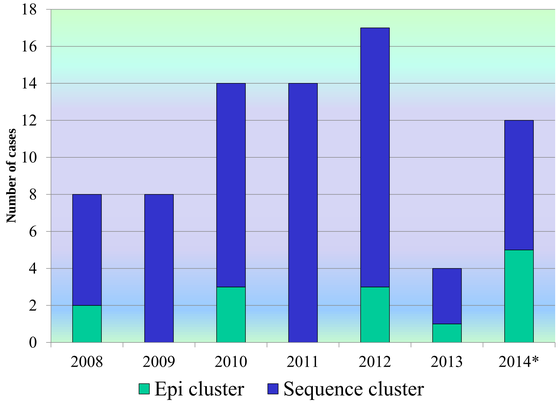
- Core HIV surveillance data (date of HIV diagnosis, transmission risk factors, viral load data)
- Partner services interview data
- Sexually Transmitted Disease infection reporting data
- Molecular HIV Surveillance (HIV-1 *pol* nucleotide sequences, ranging from 518 to 1039 bp in length)

Maximum likelihood phylogeny was reconstructed using FastTree, within Geneious v. 8.0.5

RESULTS

- *Pol* sequence s were available for 12 of 14 individuals (index case plus 13 contacts) identified through partner services investigations (Epidemiologically-linked, or "Epi" cluster, Figures1 and 3)
- Nine of the 12 Epi cluster cases with sequence data were phylogenetically linked in a cluster of 72 cases (Sequence cluster); details of this Sequence cluster include:
  - All are subtype B with transmitted
  - All but one had high-level non-nucleoside reverse transcriptase (NNRTI) resistance with Y181C
  - Largest HIV cluster identified in King County to date
  - Cluster has high local node support (FastTree SH-like local support = 1.0)
  - Mean pairwise distance for all sequences in this cluster was 1.32% (95% CI = 1.29-1.35) relative to 13.17% in other sequences (a distance of <1.50% is commonly used to define a cluster)
  - These 72 cases comprise 5% of all sequences received during the observation period (Total N== 1,546)
  - All but 1 case was male and 94% reported sex with men
  - The 72 cluster cases were 36% of all primary NNRTI resistant cases reported in the time period (Figure 2)
- Sequences from the 72 cluster cases were collected 0 to 485 days from HIV diagnosis (median 16 days); none had achieved viral suppression prior to specimen collection.
  - A most recent viral load was suppressed (< 200 copies per ml) for 63 individuals (88%)
  - Of the remaining 9: 2 were missing viral load data, 2 had > 1 log reduction in viral load, 2 relocated, and 3 remain under investigation
- The index case had a sustained period of time out of medical care; public health efforts have resulted in re-linkage to care with a most recent viral load being undetectable

Figure 1: Number of individuals in an Epidemiologically linked (Epi) cluster and an overlapping phylogenetically linked (Sequence) cluster; King County, Washington State 2008-2014



2014 data are incomplete, especially for genotypic sequence reporting

Figure 2: Molecular HIV Surveillance; King County, Washington State, 2008 - 2013

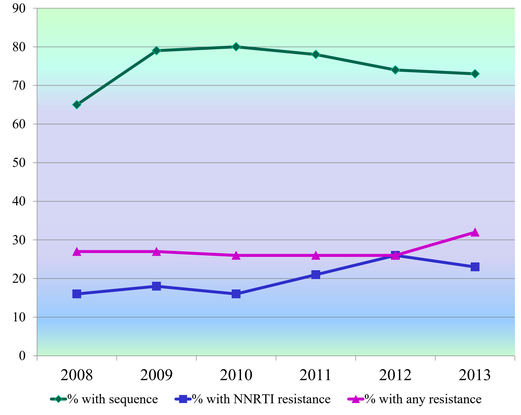
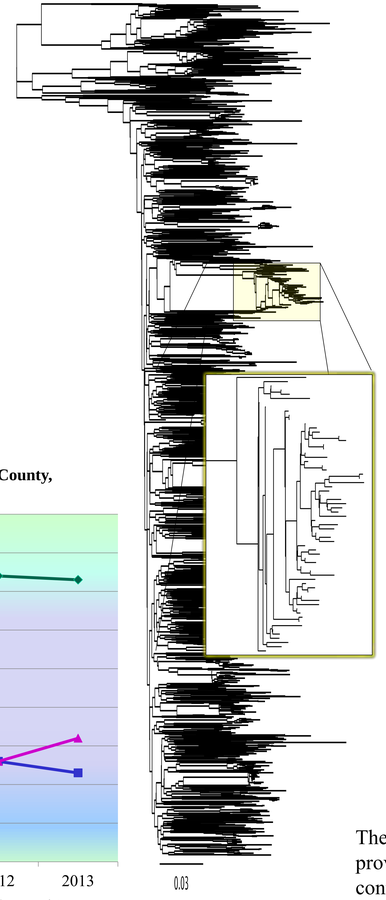


Figure 3: Phylogenetic tree showing the 66 individual cluster (in box blowout) of NNRTI resistant HIV, King County, Washington State, 2008 - 2014



KEY LIMITATIONS

- Roughly one quarter of newly diagnosed cases have no genotypic test reported to public health
- Additional people for whom we have no genotypic data could be linked to the cluster
- We cannot say how many people in the cluster might have been directly linked to the index case

SUMMARY

- Genotypic sequence data combined with partner services interview data allowed investigation of a large cluster of public health significance with NNRTI resistance
- Most cluster members have successfully linked to care and become virally suppressed
- Field staff, together with legal action, have potentially been integral in reducing further spread

IMPLICATIONS

- This large cluster of epidemiologically and molecularly-related cases supports the role of core transmission in HIV infection.
- The ability of field services staff to identify an untreated person who we believe played a central role in this transmission network demonstrates the utility of routine partner services investigations.
- Public health and clinical intervention has successfully linked the index case present to care and he is now virally suppressed.

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