Introduction

- Rapid growth of an HIV transmission cluster can limit genetic diversity such that estimating the time to the most recent common ancestor from sequence data may be unreliable.
- Diagnosis dates do not account for the duration of infection, and thus a cumulative diagnosis curve may not reflect transmission dynamics.
- Serologic assays for determining recent HIV infection are used to estimate HIV incidence by differentiating recent from long-term infection. While an effective public health tool at a population level, they may also benefit outbreak investigations that are subject to common biases of respondent-driven sampling.
- Given dates of diagnosis and serologic results collected from persons who inject drugs, to determine recent HIV infection.

Methods

- Plasma samples (n=668) from recent seroconverters with known last negative/positive test dates were tested with a custom multiplex avidity assay, which measures antibody levels and avidity to three envelope (gp120, gp160, and gp41) antigens.
- A 4-parameter logistic (4PL) function was fit to a principal component logistic model’s earliest predicted dates of infection (DOI).

Results

- The earliest HIV diagnosis that was phylogenetically linked to the HIV outbreak in Scott County, Indiana occurred nearly a decade prior to 2015.
- A large dynamic range translates to higher resolution of predicted dates of seroconversion across a larger period of time.
- Our principle component logistic model's earliest predicted dates of infection correspond with the earliest HIV diagnosis.

Summary

- Serologic assays can be used to overcome sampling biases inherent to outbreak investigations and respondent-driven studies.
- The principle component 4-parameter logistic model’s earliest predicted date of seroconversion corresponds with the earliest HIV diagnosis.

References

3. Curtis, KA et al., Abstract 877, CROI 2017

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