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Using longitudinally sampled viral nucleotide sequences to characterize the drivers of HIV-1 transmission

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OBJECTIVES
Understanding the drivers of HIV-1 transmission is of importance for curbing the ongoing epidemic. Phylogenetic methods based on single viral sequences allow us to assess whether two individuals are part of the same viral outbreak, but cannot on their own assess who potentially transmitted the virus. We developed and assessed a molecular epidemiology method with the main aim to screen cohort studies for and to characterize individuals who are 'potential HIV-1 transmitters', in order to understand the drivers of HIV-1 transmission.

METHODS
We developed and validated a molecular epidemiology approach using longitudinally sampled viral Sanger sequences to characterize potential HIV-1 transmitters in the Swiss HIV Cohort Study.

RESULTS
Our method was able to identify 279 potential HIV-1 transmitters and allowed us to determine the main epidemiological and virological drivers of transmission. We found that the directionality of transmission was consistent with infection times for 72.9% of 85 potential HIV-1 transmissions with accurate infection date estimates. Being a potential HIV-1 transmitter was associated with risk factors including viral load [adjusted odds ratio (95% confidence interval): 1.86 (1.49-2.32)], syphilis coinfection [1.52 (1.06-2.19)], and recreational drug use [1.45 (1.06-1.98)]. By contrast for the potential HIV-1 recipients, this association was weaker or even absent [1.18 (0.82-1.72), 0.89 (0.52-1.55) and 1.53 (0.98-2.39), respectively], indicating that inferred directionality of transmission is useful at the population level.

CONCLUSIONS
Our results indicate that longitudinally sampled Sanger sequences do not provide sufficient information to identify transmitters with high certainty at the individual level, but that they allow the drivers of transmission at the population level to be characterized.

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type	journal paper/review (English)
date of publishing	25-12-2020
journal title	HIV Med
ISSN electronic	1468-1293