



## HIV & criminal law

# Claims that phylogenetic analysis can prove direction of transmission are unfounded, say experts

Edwin J. Bernard | 24 November 2010 | Estimated reading time 7 minutes

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A report from the United States published last week in the *Proceedings of the National Academy of Sciences* claims to show for the first time that direction of HIV transmission from one individual to another for use as evidence in criminal trials can reliably be established by phylogenetic analysis. However, international experts in phylogenetics who have acted as forensic advisors in criminal courts tell **aidsmap.com** that the report "draws unwarranted conclusions".

The report, co-authored by Michael Metzker, associate professor at the Baylor College of Medicine Human Genome Sequencing Center, and David Hillis, a professor of evolutionary biology at the University of Texas, details the phylogenetic analysis methodology used in two criminal HIV transmission cases in the United States, in Washington State in 2004 and Texas in 2009, respectively.

These cases were only the second and third times that phylogenetic analysis was used as evidence in a criminal prosecution in the United States, despite at least 350 convictions under HIV-specific and/or general criminal laws for HIV non-disclosure, alleged exposure and/or transmission since prosecutions began in the mid-1980s (CHLP, 2010). Of note, both of these cases involved allegations of multiple heterosexual transmissions from a single source. Such allegations are extremely rare in criminal cases.

## Glossary

[phylogenetic analysis](#)

Phylogenetic analysis requires the use of complex computational tools to create a hypothetical diagram (known as a phylogenetic tree) that estimates how closely

hypothesis

sample

blinding

disclosure

related the samples of HIV taken from the complainant(s) and defendant are likely to be *in comparison to other samples*.

The report refers to several recent studies (including a 2008 study from Keele and colleagues) which suggest to the authors that a "significant genetic bottleneck" may occur during HIV transmission, and that at least three-quarters of infections may result from a single virus. It also notes that since HIV evolves rapidly following initial infection, this results in "increased diversity of HIV sequences within a newly infected individual".

However, the report argues that if blood samples are taken from the accused and complainant(s) "shortly after a transmission event", the population of viral sequences in one individual would be expected to be more closely related to the population in the other(s) than other populations of viral sequences used for comparison. This is known as a "paraphyletic relationship". The paper then suggests that "paraphyly provides support for the direction of transmission and, in a criminal case, could be used to identify the index case (i.e., source)".

In both cases, the investigators were blinded as to the identity of the accused and the complainants, which was only revealed in court once they had provided their report to the prosecution. Again, in both cases, the sample they identified as being the source of infection was that of the accused. It is unknown how much weight the judge and jury gave to the phylogenetic reports, but it is known that the prosecution provided a great deal of supporting evidence – including, in the Texas case, contact tracing and HIV testing of most of the complainants' prior sexual partners – and that it was the totality of such evidence that led to guilty verdicts and lengthy prison sentences in both cases.

The paper and its assertions have been widely disseminated via a press release and several articles primarily aimed at the scientific community. Such articles include quotes from the investigators that suggest their methods are unquestionably sound and it was this evidence alone that led to the guilty verdicts. "This is the first case study to establish the direction of transmission," Professor Metzker was quoted, in an AFP story with the headline ' Lab detectives use science to nab HIV criminals'.

He asserted to the *American Statesman* that "[our analysis] provided sound scientific evidence of the direction of transmission, and from that we could identify the source." The article also quotes the main prosecutor in the Texas case, who characterises phylogenetic analysis as "good evidence". Of note, the defence attorney in the case is quoted as saying they were unable to find an expert to testify in court against the reliability of Hillis and

Metzker's findings.

"It made a lot of difference in trying the case because we couldn't find an expert for our side," he said.

However, Professor Metzker's claims and the paper's assertion that he and his colleagues have established that their methodology is both a new and reliable method of proving the direction of transmission has been questioned by several international experts contacted by **aidsmap.com**. All of the experts have served as witnesses in criminal trials outside of the United States.

These experts all agree that phylogenetic analysis remains an informed but sometimes imperfect estimate of the relationship between viruses. Although there are a variety of methods by which it is possible to increase the confidence that the samples are very closely related *in comparison to other samples*, there could never be complete confidence that the defendant infected the complainant(s) based on phylogenetic analysis alone.

Anne-Mieke Vandamme, a professor at Leuven Catholic University and Rega Institute in Belgium, has serious reservations regarding the paper's assertions. "This paper draws unwarranted conclusions," she tells **aidsmap.com**. "There is still the possibility that there is a missing link, a consecutive transmission with an intermediate missing link. I would only use such paraphyletic clustering to exclude a direction of transmission. The elimination of all other possible contacts is something to be done outside the phylogenetic analysis."

Jan Albert, a professor at the Karolinska Institute and Karolinska University Hospital in Sweden, tells **aidsmap.com** that "the study suggests, but does not prove, transmission between the examined persons. The main reason for the caveat is that the analyses do not exclude the existence of unsampled persons belonging to the same clusters. The paraphyly does not exclude this possibility. In light of this it is surprising that only 20 local controls were investigated in the Washington case and none in the Texas case."

Thomas Leitner, staff scientist at Los Alamos National Laboratory in the United States, tells **aidsmap.com** that the methodology described in the paper to test the hypothesis of direction of transmission is not, in fact, new, and that along with co-author Walter Fitch he published a paper outlining a similar methodology eleven years ago. He adds that his research suggests that even when all persons involved in an alleged transmission chain are sampled, it may still be the case that the two closest samples in a phylogenetic tree are two individuals who may not have ever met.

Professor Vandamme is also lead author of a paper currently in press with *The Lancet*

*Infectious Diseases*, along with several authors including Professor Albert and Dr Anna Maria Geretti, of University College London Medical School, Royal Free Hospital, in London, which highlights the substantial risk of miscarriages of justice based on a flawed view of the science behind phylogenetic analysis. It concludes, in concurrence with a [briefing paper co-authored by Professor Vandamme and Dr Geretti and published by NAM and NAT in 2007](#), that the only 'safe' use of phylogenetic analysis in criminal HIV transmission cases is to exonerate the accused.

A fuller discussion of how phylogenetic analysis and other evidence can – and cannot – be used to establish the fact of transmission from the accused to complainant(s) in a criminal case can be found in the ['Proof' chapter](#) of NAM's new international resource, [HIV and the criminal law](#).

## References

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