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Virological evidence cannot prove transmission in HIV criminal cases

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Virological evidence cannot prove transmission in HIV criminal cases, warn experts in this week's BMJ. Viral phylogenetics provides a way of assessing the relations between viruses from different people. It allows us to estimate the probability that viruses from two particular people have a recent common origin. But there are serious limitations on what can and cannot be inferred using this technique.

The recent flurry of criminal cases brought against people in the United Kingdom accused of infecting their sexual partner(s) with HIV has resulted in several convictions, write Professor Deenan Pillay and colleagues in an editorial.

This has caused concern amongst health professionals and community groups about the detrimental effect such cases may have on disclosure of HIV infection and uptake of voluntary HIV testing.

In some cases, attempts have been made to present evidence on HIV viral sequence data in a similar way to DNA fingerprinting.

In our view, this analogy is seriously misleading, say the authors. When attempting to establish that transmission occurred between specific people, virological evidence should be used with caution and only in conjunction with the clinical and epidemiological evidence.

The greatest difficulty lies with the nature of the data, they write. Identifying a link between viruses from two people on its own says

nothing about who infected whom. Other difficulties include the unlikelihood that all sexual contacts of all HIV infected people will be available for viral testing, co-infection with genetically diverse strains, and similarities in two virus genomes as a result of convergent or parallel evolution.

They advise caution when interpreting such data because the strength of any apparent linkage between viruses will never approach the degree of certainty generally expected of DNA data in a criminal court.

Phylogenetic evidence – together with clinical and epidemiological evidence regarding likely duration of infection, sexual history, and other relevant factors – can provide support for linkage between cases but cannot prove transmission, they say.

Despite the difficulty in determining linkage between specific individuals, phylogenetics can provide important new insights in investigations, they say. A recent example is a study of the timing of HIV-1 infections among Libyan children in hospital, which showed that most infections occurred before the arrival of the accused medical workers in the country.

It will be important that sufficient checks and balances are in place to allow full use of HIV surveillance data for public health benefit, without concern that the underlying purpose for identifying possible viral genetic linkage between people will be to support criminal proceedings, they conclude.

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